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(54) Title: NUCLEIC ACID SEQUENCES DIFFERENTIALLY EXPRESSED IN CANCER TISSUE

(57) Abstract: This invention relates to novel nucleic acid sequences which are differentially expressed in cancer cells. The invention also relates to proteins and peptides encoded by the sequences, to diagnostic assays and therapeutic agents based on the sequences and proteins, and to probes, antisense constructs, and antibodies derived from the sequences and proteins or peptides. The subject nucleic acids have been found to be differentially expressed by tumor cells, particularly in colon cancer tissue.

INTERNATIONAL SEARCH REPORT

International application No.

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A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; A61K 38/00; C07H 21/02

US CL : 435/6; 530/300; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 530/300; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	WO 01/22920 A2 (HUMAN GENOME SCIENCES, INC.) 05 April 2001 (05.04.2002), pages 1-10, 1868-1871, 1891-2157, especially 1931-1933, 1950-1959.	14, 15, and 17-19



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:		*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A	document defining the general state of the art which is not considered to be of particular relevance	*X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B	earlier application or patent published on or after the international filing date	*Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*&	document member of the same patent family
*O	document referring to an oral disclosure, use, exhibition or other means		
*P	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/30732

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 14, 15, 17-19 and SEQ ID Number 4483 and 4484
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☒

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/30732

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1, 2, 9-12, 20-28, 30-35, 37, 39, and 40, drawn to an isolated nucleic acid, gene comprising the nucleic acid, nucleic acid with degrees of homology, a host cell comprising the nucleic acid, a pharmaceutical composition comprising the nucleic acid, probes, array comprising the probes, polypeptide, antisense, primer, a kit, and method of detecting cancer by hybridization.

Group II, claim(s) 6-8, drawn to a method of identifying a modulating agent.

Group III, claim(s) 3-5, 13, 36, and 41, drawn to an antibody, pharmaceutical composition comprising the antibody, a kit comprising the antibody, and a method of detection using the antibody.

Group IV, claim(s) 14 and 15, drawn to a method of determining a phenotype via nucleic acid expression profiling.

Group V, claim(s) 16-19, drawn to a method of determining a phenotype via protein expression profiling.

Group VI, claim(s) 29, drawn to a transgenic animal.

Group VII, claim(s) 38, drawn to a method of detecting the presence or absence of a polypeptide.

In addition, each Group detailed above reads on distinct Groups drawn to multiple sequences. The sequences are distinct because they are unrelated sequences, and a further lack of unity is applied to each Group. The Applicants must further elect one nucleic acid sequence and a corresponding polypeptide sequence (as applicable) for examination in the elected Group detailed above. Payment of fees for an additional invention will entitle the Applicants to examination of one additional sequence.

Total Number of Invention was calculated by the formula below:

Each Group x number of SEQ IDs present.

Groups I-III each have 4470 SEQ ID Numbers, therefore: $3 \times 4470 = 13410$ inventions

Groups IV and V have 4482 SEQ ID Numbers, therefore: $2 \times 4482 = 8964$ inventions

Groups VI and VII have 503 SEQ ID Numbers, therefore: $2 \times 503 = 1006$ inventions

Therefore, the total number of inventions is: $13410 + 8964 + 1006 = 23380$ inventions.

The inventions listed as Groups I-VII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Groups I, III, and VI lack unity of invention with regard to each other because they are drawn to physically distinct products not sharing a common technical feature. For example, although the antibody is derived from polypeptide of I, the polypeptide itself is not present in the product, thereby failing to "share" a special technical feature.

Groups I, lacks unity of invention with regard to Groups II, IV, V, and VII because PCT Rule 13.1 and Annex B do not provide for unity of invention between two or more products or methods of use that share a special technical feature. As the methods of Groups II, IV, V, and VII are an additional method for the use of Group I, lack of unity held.

Groups II, IV, V, and VII lack unity of invention with regard to each other because the methods are different achieving different outcome. Further, PCT Rule 13.1 and Annex B do not provide for unity of invention between two or more products or methods of use that share a special technical feature.

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Groups III and VI lack unity of invention with regard to Groups II, IV, V, and VII because the methods of Groups II, IV, V, and VII do not require the products of Groups III and VI, thereby failing to share a special technical feature.

Finally, Groups I-VII are drawn to unrelated nucleic acid/amino acid sequences, rendering the groups further lacking in unity of invention with respect to each SEQ ID Numbers disclosed (See MPEP 1850, Lack of Unity of Invention).

Continuation of B. FIELDS SEARCHED Item 3:

Sequence search on Electronic Database Genbank, Patent Database

Search term: SEQ ID Number 4484 and 4484

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- (51) International Patent Classification⁷: **C12Q** (US). **LEWIS, Marcia, E.** [US/US]; 67 Wheelwright Farm, Cohasset, MA 02025 (US).
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60/237,271 2 October 2000 (02.10.2000) US
- (71) Applicant (for all designated States except US): **BAYER CORPORATION** [US/US]; 33 Coney Street, East Walpole, MA 02032 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **BURGESS, Christopher** [US/US]; 97 Canton Terrace, Westwood, MA 02090 (US). **ASTLE, John, H.** [US/US]; 42 Short Sreet, Taunton, MA 02780 (US). **CARROLL, Eddie, III** [US/US]; 1175 Washington Street, Norwood, MA 02062 (US). **CATINO, Theodore, J.** [US/US]; 18 Jo Paul Drive, Attleboro, MA 02702 (US). **DWIVEDI, Poornima** [US/US]; 10 Haven Road, Medfield, MA 02052 (US). **MOLINO, Gary, A.** [US/US]; 3 Essex Street, Norfolk, MA 02056 (US). **THIAGLINGAM, Arunthathi** [US/US]; 26 Winchestrer Drive, Lexington, MA 02420
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- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/29086 A2

(54) Title: NUCLEIC ACID SEQUENCES DIFFERENTIALLY EXPRESSED IN CANCER TISSUE

(57) Abstract: This invention relates to novel nucleic acid sequences which are differentially expressed in cancer cells. The invention also relates to proteins and peptides encoded by the sequences, to diagnostic assays and therapeutic agents based on the sequences and proteins, and to probes, antisense constructs, and antibodies derived from the sequences and proteins or peptides. The subject nucleic acids have been found to be differentially expressed by tumor cells, particularly in colon cancer tissue.

NUCLEIC ACID SEQUENCES DIFFERENTIALLY EXPRESSED IN CANCER TISSUEField of the Invention

The present invention provides nucleic acid sequences and proteins encoded thereby
5 which are differentially expressed in cancer tissues, as well as probes derived from the nucleic
acid sequences, antibodies directed to the encoded proteins, and diagnostic methods for
determining the presence and state of cancerous cells, especially colon cancer cells.

Background of the Invention

Colorectal carcinoma is a malignant neoplastic disease. There is a high incidence of
10 colorectal carcinoma in the Western world, particularly in the United States. Tumors of this type
often metastasize through lymphatic and vascular channels. Many patients with colorectal
carcinoma eventually die from this disease. In fact, it is estimated that 62,000 persons in the
United States alone die of colorectal carcinoma annually.

However, if diagnosed early, colon cancer may be treated effectively by surgical removal
15 of the cancerous tissue. Colorectal cancers originate in the colorectal epithelium and typically
are not extensively vascularized (and therefore not invasive) during the early stages of
development. Colorectal cancer is thought to result from the clonal expansion of a single mutant
cell in the epithelial lining of the colon or rectum. The transition to a highly vascularized,
invasive and ultimately metastatic cancer which spreads throughout the body commonly takes
20 ten years or longer. If the cancer is detected prior to invasion, surgical removal of the cancerous
tissue is an effective cure. However, colorectal cancer is often detected only upon manifestation
of clinical symptoms, such as pain and black tarry stool. Generally, such symptoms are present
only when the disease is well established, often after metastasis has occurred, and the prognosis
for the patient is poor, even after surgical resection of the cancerous tissue. Early detection of
25 colorectal cancer therefore is important in that detection may significantly reduce its morbidity.

Invasive diagnostic methods such as endoscopic examination allow for direct visual
identification, removal, and biopsy of potentially cancerous growths such as polyps. Endoscopy
is expensive, uncomfortable, inherently risky, and therefore not a practical tool for screening
populations to identify those with colorectal cancer. Non-invasive analysis of stool samples for
30 characteristics indicative of the presence of colorectal cancer or precancer is a preferred

alternative for early diagnosis, but no known diagnostic method is available which reliably achieves this goal.

Summary of the Invention

5 The present invention provides nucleic acid sequences and proteins encoded thereby, as well as probes derived from the nucleic acid sequences, antibodies directed to the encoded proteins, and diagnostic methods for detecting cancerous cells, especially colon cancer cells. The sequences disclosed herein have been found to be differentially expressed in colon cancer cell lines and/or colon cancer tissue.

10 In one aspect, the invention provides an isolated nucleic acid sequence comprising SEQ ID Nos 1-503, or a sequence complementary thereto.

In another aspect, the invention provides an isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

15 In another embodiment, the nucleic acid is at least about 80% to about 100% identical to a sequence corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

20 In another aspect, the invention provides an isolated nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto. In a related embodiment, the nucleic acid is at least about 80% or about 100% identical to a sequence corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up
25 to the full length of one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503 or a sequence complementary thereto.

In one embodiment, the invention provides a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, and a transcriptional
30 regulatory sequence operably linked to the nucleotide sequence to render the nucleotide sequence suitable for use as an expression vector. In another embodiment, the nucleic acid may be

included in an expression vector capable of replicating in a prokaryotic or eukaryotic cell. In a related embodiment, the invention provides a host cell transfected with the expression vector.

5 In another embodiment, the invention provides a transgenic animal having a transgene of a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103, preferably SEQ ID Nos 1-503, or a sequence complementary thereto incorporated in cells thereof. The transgene modifies the level of expression of the nucleic acid, the stability of a mRNA transcript of the nucleic acid, or the activity of the encoded product of the nucleic acid.

10 In yet another embodiment, the invention provides a substantially pure nucleic acid comprising the nucleotide sequence of SEQ ID Nos 1-1103, or a sequence complementary thereto.

In yet another embodiment, the invention provides a substantially pure nucleic acid which hybridizes under stringent conditions to a nucleic acid probe corresponding to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides up to the full length of one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos 1-503, or a sequence complementary thereto.

The invention also provides an antisense oligonucleotide analog which hybridizes under stringent conditions to at least 12, at least 25, or at least 50 consecutive nucleotides of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 up to the full length of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, and which is resistant to cleavage by a nuclease, preferably an endogenous endonuclease or exonuclease.

25 In another embodiment, the invention provides a probe/primer comprising a substantially purified oligonucleotide comprising at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides of SEQ ID Nos 1-1103, or a sequence complementary thereto.

30 In another embodiment, the invention provides a probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least about 12, at least about 15, at least about 25, or at least about 40 consecutive nucleotides of sense or antisense sequence selected from SEQ ID Nos. 1-1103 up to the full length of one of SEQ ID Nos. 1-1103 or a sequence complementary thereto. In preferred embodiments, the probe selectively hybridizes with a target nucleic acid. In

another embodiment, the probe may include a label group attached thereto and able to be detected. The label group may be selected from radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors. The invention further provides arrays of at least about 10, at least about 25, at least about 50, or at least about 100 different probes as described above attached to a solid support.

In yet another embodiment, the invention pertains to a method of determining the phenotype of a cell comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the nucleic acid is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty.

In a still further embodiment, the invention pertains to a method of determining the phenotype of cell, comprising detecting the differential expression, relative to a normal cell, of at least one protein encoded by a nucleic acid which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the protein is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, an up to at least a factor of 50.

The invention further provides a method of determining the phenotype of cell, comprising detecting the differential expression, relative to a normal cell, of at least one polypeptide selected from the group of polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, wherein the polypeptide is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, an up to at least a factor of 50.

In yet another embodiment, the invention pertains to a method of determining the phenotype of a cell comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the nucleic acid is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty.

In another aspect, the invention provides polypeptides encoded by the subject nucleic acids. In one embodiment, the invention pertains to a polypeptide including an amino acid sequence encoded by a nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103 or a sequence complementary thereto,

or a fragment comprising at least about 25, or at least about 40 amino acids thereof. Further provided are antibodies immunoreactive with these polypeptides.

In a further aspect the invention pertains to a polypeptide encoded by one or more of the sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492,
5 and 4494.

In a still further aspect the invention pertains to a polypeptide having the sequence of one or SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 44857, 4489, 4491, and 4493.

In still another aspect, the invention provides diagnostic methods. In one embodiment, the invention pertains to a method for determining the phenotype of cells from a patient by
10 providing a nucleic acid probe comprising a nucleotide sequence having at least 10, at least about 15, at least about 25, or at least about 40 consecutive nucleotides represented in a sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 up to the full length of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, obtaining a
15 sample of cells from a patient, optionally providing a second sample of cells substantially all of which are non-cancerous, contacting the nucleic acid probe under stringent conditions with mRNA of each of said first and second cell samples, and comparing (a) the amount of hybridization of the probe with mRNA of the first cell sample, with (b) the amount of hybridization of the probe with mRNA of the second cell sample, wherein a difference of at least
20 a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty in the amount of hybridization with the mRNA of the first cell sample as compared to the amount of hybridization with the mRNA of the second cell sample is indicative of the phenotype of cells in the first cell sample. Determining the phenotype includes determining the genotype, as the term is used herein.

25 In another embodiment, the invention provides a test kit for identifying the presence of cancerous cells or tissues, comprising a probe/primer as described above, for measuring a level of a nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 in a sample of cells isolated from a patient. In certain embodiments, the kit may further include instructions
30 for using the kit, solutions for suspending or fixing the cells, detectable tags or labels, solutions for rendering a nucleic acid susceptible to hybridization, solutions for lysing cells, or solutions for the purification of nucleic acids.

In another embodiment, the invention provides a method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal or control cell, of at least one protein encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, wherein the protein is differentially expressed by at least a factor of two, at least a factor of five, at least a factor of twenty, or at least a factor of fifty. In one embodiment, the level of the protein is detected in an immunoassay. The invention also pertains to a method for determining the presence or absence of a nucleic acid, such as mRNA, which hybridizes under stringent conditions to one of SEQ ID Nos. 1-1103 in a cell, comprising contacting the cell with a probe as described above. The invention further provides a method for determining the presence or absence of a subject polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-1103 in a cell, comprising contacting the cell with an antibody as described above.

In yet another embodiment, the invention provides a method for determining the presence of an aberrant mutation (e.g., deletion, insertion, or substitution of nucleic acids) or aberrant methylation in a sequence which hybridizes under stringent conditions to a sequence of SEQ ID Nos. 1-1103 or a sequence complementary thereto, comprising collecting a sample of cells from a patient, isolating nucleic acid from the cells of the sample, contacting the nucleic acid sample with one or more probe/primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, under conditions such that hybridization and/or amplification of the nucleic acid occurs, and comparing the presence, absence, or size of an amplification product to the amplification product of a normal cell.

In one embodiment, the invention provides a test kit for identifying the presence of cancer cells, comprising an antibody specific for a protein encoded by a nucleic acid which hybridizes under stringent conditions to any one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto. In certain embodiments, the kit further includes instructions for using the kit. In certain embodiments, the kit may further include solutions for suspending or fixing the cells, detectable tags or labels, solutions for rendering a polypeptide susceptible to the binding of an antibody, solutions for lysing cells, or solutions for the purification of polypeptides.

In yet another aspect, the invention provides pharmaceutical compositions including the subject nucleic acids. In one embodiment, an agent which alters the level of expression in a cell

of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto is identified by providing a cell, treating the cell with a test agent, determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, and comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell. The invention further provides a pharmaceutical composition comprising an agent identified by this method. In another embodiment, the invention provides a pharmaceutical composition which includes a polypeptide encoded by a nucleic acid having a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto. In one embodiment, the invention pertains to a pharmaceutical composition comprising a nucleic acid including a sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

In yet another aspect, the invention provides pharmaceutical compositions including the subject nucleic acids. In one embodiment, an agent which alters the level of expression in a cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto is identified by providing a cell, treating the cell with a test agent, determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto, and comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

The invention further provides a method for identifying an agent which alters the level of expression in a cell of a polypeptide having a sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 comprising providing a cell; treating the

cell with the test agent; determining the level of expression of one or more polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 in the cell by reacting the cell with an antibody specific for one or more of the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493; and

- 5 comparing the level of expression of the polypeptide in the treated cell with the level of expression of the same polypeptide in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the polypeptide in a cell.

- 10 The invention further provides a pharmaceutical composition comprising an agent identified by the above methods. In another embodiment, the invention provides a pharmaceutical composition which includes a polypeptide encoded by a nucleic acid having a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence
- 15 complementary thereto. In a further embodiment the invention provides a pharmaceutical composition comprising one or more antibodies which bind to a polypeptide encoded by one or more of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. In a still further embodiment, the invention provides a pharmaceutical composition comprising one or more antibodies which binds to a polypeptide of one or more of SEQ ID Nos.
- 20 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. In one embodiment, the invention pertains to a pharmaceutical composition comprising a nucleic acid including a sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or a sequence complementary thereto.

- 25 In one embodiment the invention relates to a method for detecting cancer in a patient sample in which an antibody to a protein encoded by SEQ ID Nos 1-4470 is used to react with proteins in the patient sample. In a further embodiment, the invention relates to a method for detecting cancer in a patient sample in which an antibody to a protein encoded by one or more of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 is
- 30 used to react with proteins in the patient sample. In a still further embodiment, the invention provides a method for detecting cancer in a patient sample in which an antibody to a protein having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 is used to react with protein in the patient sample.

Brief Description of the Figure

Figure 1 depicts the nucleic acid sequence of SEQ ID Nos: 1-4470.

Figure 2 depicts the nucleic acid sequence of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494.

5 Figure 3 depicts the amino acid sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

Detailed Description of the Invention

The invention relates to nucleic acids having the disclosed nucleotide sequences (SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494), as
10 well as full length cDNA, mRNA, and genes corresponding to these sequences, and to polypeptides and proteins encoded by these nucleic acids and genes, and portions thereof. In particular the invention relates to the full length cDNA sequence of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 and the polypeptide sequence encoded thereby and shown in SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485,
15 4487, 4489, 4491, and 4493, respectively. The 4494 sequences disclosed herein were analyzed by comparing the sequences to those disclosed in publicly available databases. Based upon the search results, it was found that SEQ ID Nos: 1-503 contained novel sequences, SEQ ID Nos: 504-1103 contained known EST sequences, and SEQ ID Nos: 1104-4494 contained known sequences.

20 Also included in the present invention are polypeptides and proteins encoded by the nucleic acids of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, and in particular the polypeptide sequences of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. The various nucleic acids that can encode these polypeptides and proteins differ because of the degeneracy of the genetic code,
25 in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well known in this art, and this information can be used for the construction of the nucleic acids within the scope of the invention. In one embodiment, the polypeptide sequences of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 are encoded by the full length cDNA sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480,
30 4482, 4484, 4486, 4488, 4490, 4492, and 4494, respectively.

Nucleic acids encoding polypeptides and proteins that are variants of the polypeptides and proteins encoded by the present nucleic acids and related cDNA and genes are also within the scope of the invention. The variants differ from wild-type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild-type protein. Once the amino acid change is selected, a nucleic acid encoding that variant is constructed according to the invention.

The following detailed description discloses how to obtain or make full-length cDNA and human genes corresponding to the nucleic acids, how to express these nucleic acids and genes, how to identify structural motifs of the genes, how to identify the function of a protein encoded by a gene corresponding to an nucleic acid, how to use nucleic acids as probes in mapping and in tissue profiling, how to use the corresponding polypeptides and proteins to raise antibodies, and how to use the nucleic acids, polypeptides, and proteins for diagnostic purposes.

The sequences disclosed herein have been found to be differentially expressed in colon cancer cell lines and/or colon cancer tissue, and thus are useful for determining the presence of colon cancer in a cell or tissue sample. The present sequences also have utility for determining the presence or state of other types of cancer.

Accordingly, a preferred aspect of the present invention relates to nucleic acids differentially expressed in tumor cells or tissue, especially colon cancer tissue or cells, polypeptides encoded by such nucleic acids, and antibodies immunoreactive with these polypeptides, and preparations of such compositions. Moreover, the present invention provides diagnostic and therapeutic assays and reagents for detecting and treating disorders involving, for example, expression of the subject nucleic acids.

I. General

This invention relates to compositions and methods for identifying and/or classifying cancerous cells present in a human tumors, particularly in solid tumors, e.g., carcinomas and sarcomas, such as, for example, breast or colon cancers. In its broadest aspect, the method uses nucleic acids that are differentially expressed in cancer cell lines and/or cancer tissue, compared with related normal cells or tissue, and using them to identify or classify tumor cells by the upregulation and/or downregulation of expression of particular genes, an event which is implicated in tumorigenesis.

Upregulation or increased expression of certain genes such as oncogenes, act to promote malignant growth. Downregulation or decreased expression of genes, such as tumor suppressor

genes, also promotes malignant growth. Thus, alteration in the expression of either type of gene is a potential diagnostic indicator for determining whether a subject is at risk of developing or has cancer, e.g., colon cancer.

Accordingly, in one aspect, the invention also provides biomarkers, such as nucleic acid markers, for human tumor cells and tissue, particularly for colon cancer cells and tissue. The invention also provides proteins encoded by these nucleic acid markers. The invention also features methods for identifying drugs useful for treatment of such cancer cells, and for treatment of a cancerous condition, such as colon cancer. Unlike prior methods, the invention provides a means for identifying cancer cells at an early stage of development, so that premalignant cells can be identified prior to their spreading throughout the human body. This allows early detection of potentially cancerous conditions, and treatment of those cancerous conditions prior to spread of the cancerous cells throughout the body, or prior to development of an irreversible cancerous condition.

II. Definitions

For convenience, the meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below.

The term “an aberrant expression”, as applied to a nucleic acid of the present invention, refers to level of expression of that nucleic acid which differs from the level of expression of that nucleic acid in healthy tissue, or which differs from the activity of the polypeptide present in a healthy subject. An activity of a polypeptide can be aberrant because it is stronger than the activity of its native counterpart. Alternatively, an activity can be aberrant because it is weaker or absent relative to the activity of its native counterpart. An aberrant activity can also be a change in the activity; for example, an aberrant polypeptide can interact with a different target peptide. A cell can have an aberrant expression level of a gene due to overexpression or underexpression of that gene.

The term “agonist”, as used herein, is meant to refer to an agent that mimics or upregulates (e.g., potentiates or supplements) the bioactivity of a protein. An agonist can be a wild-type protein or derivative thereof having at least one bioactivity of the wild-type protein. An agonist can also be a compound that upregulates expression of a gene or which increases at least one bioactivity of a protein. An agonist can also be a compound which increases the interaction of a polypeptide with another molecule, e.g., a target peptide or nucleic acid.

The term "allele", which is used interchangeably herein with "allelic variant", refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for that gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and/or insertions of nucleotides. An allele of a gene can also be a form of a gene containing mutations.

The term "allelic variant of a polymorphic region of a gene" refers to a region of a gene having one of several nucleotide sequences found in that region of the gene in other individuals.

The term "antagonist" as used herein is meant to refer to an agent that downregulates (e.g., suppresses or inhibits) at least one bioactivity of a protein. An antagonist can be a compound which inhibits or decreases the interaction between a protein and another molecule, e.g., a target peptide or enzyme substrate. An antagonist can also be a compound that downregulates expression of a gene or which reduces the amount of expressed protein present.

The term "antibody" as used herein is intended to include whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with a vertebrate, e.g., mammalian, protein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a certain protein. Nonlimiting examples of such proteolytic and/or recombinant fragments include Fab, F(ab')₂, Fab', Fv, and single chain antibodies (scFv) containing a V[L] and/or V[H] domain joined by a peptide linker. The scFv's may be covalently or non-covalently linked to form antibodies having two or more binding sites. The subject invention includes polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies.

The phenomenon of "apoptosis" is well known, and can be described as a programmed death of cells. As is known, apoptosis is contrasted with "necrosis", a phenomenon when cells die as a result of being killed by a toxic material, or other external effect. Apoptosis involves chromatic condensation, membrane blebbing, and fragmentation of DNA, all of which are generally visible upon microscopic examination.

A disease, disorder, or condition “associated with” or “characterized by” an aberrant expression of a nucleic acid refers to a disease, disorder, or condition in a subject which can be statistically correlated with the expression of a nucleic acid.

As used herein the term “bioactive fragment of a polypeptide” refers to a fragment of a full-length polypeptide, wherein the fragment specifically agonizes (mimics) or antagonizes (inhibits) the activity of a wild-type polypeptide. The bioactive fragment preferably is a fragment capable of interacting with at least one other molecule, e.g., protein, small molecule, or DNA, which a full length protein can bind.

“Biological activity” or “bioactivity” or “activity” or “biological function”, which are used interchangeably, herein mean an effector or antigenic function that is directly or indirectly performed by a polypeptide (whether in its native or denatured conformation), or by any subsequence thereof. Biological activities include binding to polypeptides, binding to other proteins or molecules, activity as a DNA binding protein, as a transcription regulator, ability to bind damaged DNA, etc. A bioactivity can be modulated by directly affecting the subject polypeptide. Alternatively, a bioactivity can be altered by modulating the level of the polypeptide, such as by modulating expression of the corresponding gene.

The term “biomarker” refers a biological molecule, e.g., a nucleic acid, including DNA, cDNA, RNA, mRNA, tRNA, or rRNA, peptide, polypeptide, protein, hormone, etc., whose presence or concentration can be detected and correlated with a known condition, such as a disease state.

“Cells,” “host cells”, or “recombinant host cells” are terms used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A “chimeric polypeptide” or “fusion polypeptide” is a fusion of a first amino acid sequence encoding one of the subject polypeptides with a second amino acid sequence defining a domain (e.g., polypeptide portion) foreign to and not substantially homologous with any domain of the subject polypeptide. A chimeric polypeptide may present a foreign domain which is found (albeit in a different polypeptide) in an organism which also expresses the first polypeptide, or it may be an “interspecies,” “intergenic,” etc., fusion of polypeptide structures expressed by different kinds of organisms. In general, a fusion polypeptide can be represented by the general

formula $(X)_n-(Y)_m-(Z)_n$, wherein Y represents a portion of the subject polypeptide, and X and Z are each independently absent or represent amino acid sequences which are not related to the native sequence found in an organism, or which are not found as a polypeptide chain contiguous with the subject sequence, where m is an integer greater than or equal to one, and each
5 occurrence of n is, independently, 0 or an integer greater than or equal to 1 (n and m are preferably no greater than 5 or 10).

A "delivery complex" shall mean a targeting means (e.g., a molecule that results in higher affinity binding of a nucleic acid, protein, polypeptide or peptide to a target cell surface and/or increased cellular or nuclear uptake by a target cell). Examples of targeting means
10 include: sterols (e.g., cholesterol), lipids (e.g., a cationic lipid, virosome or liposome), viruses (e.g., adenovirus, adeno-associated virus, and retrovirus), or target cell-specific binding agents (e.g., ligands recognized by target cell specific receptors). Preferred complexes are sufficiently stable *in vivo* to prevent significant uncoupling prior to internalization by the target cell. However, the complex is cleavable under appropriate conditions within the cell so that the
15 nucleic acid, protein, polypeptide or peptide is released in a functional form.

As is well known, genes or a particular polypeptide may exist in single or multiple copies within the genome of an individual. Such duplicate genes may be identical or may have certain modifications, including nucleotide substitutions, additions or deletions, which all still code for polypeptides having substantially the same activity. The term "DNA sequence encoding a
20 polypeptide" may thus refer to one or more genes within a particular individual. Moreover, certain differences in nucleotide sequences may exist between individual organisms, which are called alleles. Such allelic differences may or may not result in differences in amino acid sequence of the encoded polypeptide yet still encode a polypeptide with the same biological activity.

25 The term "equivalent" is understood to include nucleotide sequences encoding functionally equivalent polypeptides. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants; and will, therefore, include sequences that differ from the nucleotide sequence of the nucleic acids shown in SEQ ID NOs: 1-4494 due to the degeneracy of the genetic code.

30 As used herein, the terms "gene", "recombinant gene", and "gene construct" refer to a nucleic acid of the present invention associated with an open reading frame, including both exon and, optionally, intron sequences.

A "recombinant gene" refers to nucleic acid encoding a polypeptide and comprising exon sequences, though it may optionally include intron sequences which are derived from, for example, a related or unrelated chromosomal gene. The term "intron" refers to a DNA sequence present in a given gene which is not translated into protein and is generally found between exons.

5 The term "growth" or "growth state" of a cell refers to the proliferative state of a cell as well as to its differentiative state. Accordingly, the term refers to the phase of the cell cycle in which the cell is, e.g., G₀, G₁, G₂, or prophase, metaphase, or telophase, or anaphase, as well as to its state of differentiation, e.g., undifferentiated, partially differentiated, or fully differentiated. Without wanting to be limited, differentiation of a cell is usually accompanied by a decrease in
10 the proliferative rate of a cell.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules, with identity being a more strict comparison. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is
15 occupied by the same base or amino acid, then the molecules are identical at that position. A degree of homology or similarity or identity between nucleic acid sequences is a function of the number of identical or matching nucleotides at positions shared by the nucleic acid sequences. A degree of identity of amino acid sequences is a function of the number of identical amino acids at positions shared by the amino acid sequences. A degree of homology or similarity of amino acid
20 sequences is a function of the number of amino acids, i.e., structurally related, at positions shared by the amino acid sequences. An "unrelated" or "non-homologous" sequence shares less than 40% identity, though preferably less than 25% identity, with one of the sequences of the present invention.

The term "percent identical" refers to sequence identity between two amino acid
25 sequences or between two nucleotide sequences. Identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules
30 can be referred to as homologous (similar) at that position. Expression as a percentage of homology, similarity, or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including FASTA, BLAST, or ENTREZ. FASTA and BLAST are

available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with, e.g., default settings. ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Md. In one embodiment, the percent identity of two sequences can be
5 determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences.

Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Preferably, an
10 alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Meth. Mol. 70-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to
15 score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases.

Databases with individual sequences are described in Methods in Enzymology, ed.
20 Doolittle, *supra*. Databases include, for example, Genbank, EMBL, and DNA Database of Japan (DDBJ).

Preferred nucleic acids have a sequence at least 70%, and more preferably 80% identical and more preferably 90% and even more preferably at least 95% identical to a nucleic acid sequence of a sequence shown in one of SEQ ID NOS: 1-4494. Nucleic acids at least 90%, more
25 preferably 95%, and most preferably at least about 98-99% identical with a nucleic sequence represented in one of SEQ ID NOS: 1-4494 are of course also within the scope of the invention. In preferred embodiments, the nucleic acid is mammalian.

The term "interact" as used herein is meant to include detectable interactions (e.g., biochemical interactions) between molecules, such as interaction between protein-protein,
30 protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule in nature. Examples of interactions between protein-protein, protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule can include binding, modifying, cleaving, processing, or catalyzing.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The terms "modulated" and "differentially regulated" as used herein refer to both upregulation (i.e., activation or stimulation e.g., by agonizing or potentiating) and downregulation (i.e., inhibition or suppression e.g., by antagonizing, decreasing or inhibiting).

The term "mutated gene" refers to an allelic form of a gene, which is capable of altering the phenotype of a subject having the mutated gene relative to a subject which does not have the mutated gene. If a subject must be homozygous for this mutation to have an altered phenotype, the mutation is said to be recessive. If one copy of the mutated gene is sufficient to alter the genotype of the subject, the mutation is said to be dominant. If a subject has one copy of the mutated gene and has a phenotype that is intermediate between that of a homozygous and that of a heterozygous subject (for that gene), the mutation is said to be co-dominant.

The designation "N", where it appears in the accompanying Sequence Listing, indicates that the identity of the corresponding nucleotide is unknown. "N" should therefore not necessarily be interpreted as permitting substitution with any nucleotide, e.g., A, T, C, or G, but rather as holding the place of a nucleotide whose identity has not been conclusively determined.

The "non-human animals" of the invention include mammals such as rodents, non-human primates, sheep, dog, cow, pigs, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying agents which can affect, for example, embryogenesis and tissue formation. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant gene is expressed in some but not all cells of the animal. The term "tissue-specific chimeric

animal” indicates that one of the recombinant genes is present and/or expressed or disrupted in some tissues but not others.

As used herein, the term “nucleic acid” refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

The term “nucleotide sequence complementary to the nucleotide sequence of SEQ ID NO. x” refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having SEQ ID NO. x. The term “complementary strand” is used herein interchangeably with the term “complement”. The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand. As used herein, a “complementary strand” to SEQ ID NO. x is a nucleic acid sequence which hybridizes under stringent conditions to SEQ ID NO. x.

The term “polymorphism” refers to the coexistence of more than one form of a gene or portion (e.g., allelic variant) thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a “polymorphic region of a gene”. A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A “polymorphic gene” refers to a gene having at least one polymorphic region.

As used herein, the term “promoter” means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in cells. The term encompasses “tissue specific” promoters, i.e., promoters which effect expression of the selected DNA sequence only in specific cells (e.g., cells of a specific tissue). The term also covers so-called “leaky” promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively expressed or that are inducible (i.e., expression levels can be controlled).

The terms “protein”, “polypeptide”, and “peptide” are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant gene, is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native polypeptide, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the polypeptide.

"Small molecule" as used herein, is meant to refer to a composition, which has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon-containing) or inorganic molecules. Many pharmaceutical companies have extensive libraries of chemical and/or biological mixtures, often fungal, bacterial, or algal extracts, which can be screened with any of the assays of the invention to identify compounds that modulate a bioactivity.

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least a portion of, for example approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400, 500, 750, or 1000 contiguous nucleotides of a nucleic acid designated in any one of SEQ ID Nos: 1-4494, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a different protein. In preferred embodiments, the oligonucleotide probe detects only a specific nucleic acid, e.g., it does not substantially hybridize to similar or related nucleic acids, or complements thereof.

"Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of one of the genes is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally occurring forms of the polypeptide.

As used herein, the term “transfection” means the introduction of a nucleic acid, e.g., via an expression vector, into a recipient cell by nucleic acid-mediated gene transfer.

“Transformation”, as used herein, refers to a process in which a cell’s genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of the target gene is disrupted.

The term “treating” as used herein is intended to encompass curing as well as ameliorating at least one symptom of the condition or disease.

The term “vector” refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as “expression vectors”. In general, expression vectors of utility in recombinant DNA techniques are often in the form of “plasmids” which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, “plasmid” and “vector” are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

The term “wild-type allele” refers to an allele of a gene which, when present in two copies in a subject results in a wild-type phenotype. There can be several different wild-type alleles of a specific gene, since certain nucleotide changes in a gene may not affect the phenotype of a subject having two copies of the gene with the nucleotide changes.

III. Nucleic Acids of the Present Invention

As described below, one aspect of the invention pertains to isolated nucleic acids, variants, and/or equivalents of such nucleic acids.

Nucleic acids of the present invention have been identified as differentially expressed in tumor cells, e.g., colon cancer-derived cell lines and colon cancer tissue (relative to the expression levels in normal cells or tissue, e.g., normal colon tissue and/or normal non-colon tissue). The present differentially expressed sequences comprise SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos.

1-1103, even more preferably SEQ ID Nos. 1-503, or sequence complementary thereto. In another embodiment, the invention comprises sequences which hybridize under stringent conditions with any of the sequences of SEQ ID Nos 1-4494. In a preferred aspect, sequences of the invention hybridize to SEQ ID Nos 1-4494 with about 50% identity, preferably about 70%
5 identity, more preferably about 90% identity, and still more preferably about 100% identity. In preferred embodiments, the subject nucleic acids are differentially expressed by at least a factor of two, preferably at least a factor of five, even more preferably at least a factor of twenty, still more preferably at least a factor of fifty. Preferred nucleic acids are those sequences identified as differentially expressed both in colon cancer tissue and colon cancer cell lines. In preferred
10 embodiments, nucleic acids of the present invention are upregulated in tumor cells, especially colon cancer tissue and/or colon cancer-derived cell lines. In another embodiment, nucleic acids of the present invention are downregulated in tumor cells, especially colon cancer tissue and/or colon cancer-derived cell lines.

Genes which are upregulated, such as oncogenes, or downregulated, such as tumor
15 suppressors, in aberrantly proliferating cells can be used as targets for diagnostic or therapeutic applications. For example, upregulation of the *cdc2* gene induces mitosis. Overexpression of the *myt1* gene, a mitotic deactivator, negatively regulates the activity of *cdc2*. Aberrant proliferation may thus be induced either by upregulating *cdc2* or by downregulating *myt1*. Similarly, downregulation of tumor suppressors such as p53 and Rb have been implicated in
20 tumorigenesis.

Particularly preferred polypeptides are those that are encoded by nucleic acid sequences at least about 70%, 75%, 80%, 90%, 95%, 97%, or 98% similar to a nucleic acid sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. Preferably, the nucleic acid includes all or a portion (e.g., at least about 10, at least about
25 15, at least about 25, or at least about 40 nucleotides) of the nucleotide sequence corresponding to the nucleic acid of SEQ ID Nos. 1-1103, most preferably SEQ ID Nos. 1-503, or a sequence complementary thereto.

Still other preferred nucleic acids of the present invention encode a polypeptide comprising at least a portion of a polypeptide encoded by one of SEQ ID Nos. 1-4470, 4472,
30 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. For example, preferred nucleic acid molecules for use as probes/primers or antisense molecules (i.e., noncoding nucleic acid molecules) can comprise at least about 10, 20, 30, 50, 60, 70, 80, 90, or 100 base pairs in length up to the length of the complete sequence of any of SEQ ID Nos 1-4494. Coding nucleic

acid molecules can comprise, for example, from about 50, 60,70,80,90, or 100 base pairs up to the full length of the entire sequence of any of SEQ ID Nos 1-4494.

Another aspect of the invention provides a nucleic acid which hybridizes under low, medium, or high stringency conditions to a nucleic acid sequence represented by one of SEQ ID
5 Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto. Appropriate stringency conditions which promote DNA hybridization, for example, about 6.0 x sodium chloride/sodium citrate (SSC) at about 45 °C, followed by a wash of about 2.0 x SSC at about 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-12.3.6. For example, the salt concentration in
10 the wash step can be selected from a low stringency of about 2.0 x SSC at about 50°C to a high stringency of about 0.2 x SSC at about 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22 °C, to high stringency conditions at about 65 °C. Both temperature and salt may be varied, or temperature or salt concentration may be held constant while the other variable is changed. In a preferred
15 embodiment, a nucleic acid of the present invention will bind to one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, under moderately stringent conditions, for example at about 2.0 x SSC and about 40°C. In a particularly preferred embodiment, a nucleic acid of the present invention will bind to one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, under high stringency
20 conditions.

In one embodiment, the invention provides nucleic acids which hybridize under low stringency conditions of about 6 x SSC at about room temperature followed by a wash at about 2 x SSC at about room temperature.

In another embodiment, the invention provides nucleic acids which hybridize under high
25 , stringency conditions of about 2 x SSC at about 65 °C followed by a wash at about 0.2 x SSC at about 65 °C.

Nucleic acids having a sequence that differs from the nucleotide sequences shown in one of SEQ ID Nos. 1-1103, preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, due to degeneracy in the genetic code, are also within the scope of the invention. Such nucleic
30 acids encode functionally equivalent peptides (i.e., a peptide having equivalent or similar biological activity) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and

CAC each encode histidine) may result in "silent" mutations which do not affect the amino acid sequence of a polypeptide. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the subject polypeptides will exist among mammals. One skilled in the art will appreciate that these variations in one or more nucleotides (e.g., up to about 3-5% of the nucleotides) of the nucleic acids encoding polypeptides having an activity of a polypeptide may exist among individuals of a given species due to natural allelic variation.

Also within the scope of the invention are nucleic acids encoding splicing variants of proteins encoded by a nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, or natural homologs of such proteins. Such homologs can be cloned by hybridization or PCR, as further described herein.

The polynucleotide sequence may also encode for a leader sequence, e.g., the natural leader sequence or a heterologous leader sequence, for a subject polypeptide. For example, the desired DNA sequence may be fused in the same reading frame to a DNA sequence which aids in expression and secretion of the polypeptide from the host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of the polypeptide from the cell. The protein having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the protein.

The polynucleotide of the present invention may also be fused in frame to a marker sequence, also referred to herein as "Tag sequence" encoding a "Tag peptide", which allows for marking and/or purification of the present invention. In a preferred embodiment, the marker sequence is a hexahistidine tag, e.g., supplied by a PQE-9 vector. Numerous other Tag peptides are available commercially. Other frequently used Tags include myc-epitopes (e.g., see Ellison et al. (1991) J Biol Chem 266:21150-21157) which includes a 10-residue sequence from c-myc, the pFLAG system (International Biotechnologies, Inc.), the pEZZ-protein A system (Pharmacia, NJ), and a 16 amino acid portion of the Haemophilus influenza hemagglutinin protein. Furthermore, any polypeptide can be used as a Tag so long as a reagent, e.g., an antibody interacting specifically with the Tag polypeptide is available or can be prepared or identified.

As indicated by the examples set out below, nucleic acids can be obtained from mRNA present in any of a number of eukaryotic cells or tissue, e.g., and are preferably obtained from metazoan cells or tissue, more preferably from vertebrate cells or tissue, and even more preferably from mammalian cells and tissue, and most preferably from human cells or tissue. It

also is possible to obtain nucleic acids of the present invention from genomic DNA from both adults and embryos. For example, a gene can be cloned from either a cDNA or a genomic library in accordance with protocols generally known to persons skilled in the art. cDNA can be obtained by isolating total mRNA from a cell, e.g., a vertebrate cell, a mammalian cell, or a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention.

The invention includes within its scope a polynucleotide having the nucleotide sequence of nucleic acid obtained from this biological material, wherein the nucleic acid hybridizes under stringent conditions (at least about 4 x SSC at 65 °C, or at least about 4 x SSC at 42 °C; see, for example, U.S. Patent No. 5,707,829, incorporated herein by reference) with at least 15 contiguous nucleotides of at least one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. By this is intended that when at least 15 contiguous nucleotides of one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 will hybridize with the same gene or mRNA if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

Because the present nucleic acids are cDNAs which represent partial mRNA transcripts, two or more nucleic acids of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene. Nucleic acid-related polynucleotides can also be isolated from cDNA libraries. These libraries are preferably prepared from mRNA of human colon cells, more preferably, human colon cancer specific tissue, designated as the 100-101, and 103-112 clones in Table 1. In another embodiment the nucleic acids are isolated from libraries prepared from normal colon specific tissue, designated herein as the 102 clones in Table 1. Alignment of SEQ ID Nos. 1-4470, 4472,

4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, as described above, indicated that a cell line or tissue source of a related protein or polynucleotide can also be used as a source of the nucleic acid-related cDNA.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). The cDNA can be prepared by using primers based on a sequence from SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. In one embodiment, the cDNA library can be made from only polyadenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA. Alignment of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 can result in identification of a related polypeptide or polynucleotide. Some of the polynucleotides disclosed herein contains repetitive regions that were subject to masking during the search procedures. The information about the repetitive regions is discussed below.

Constructs of polynucleotides having sequences of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by Stemmer et al, Gene (Amsterdam) (1995) 164(i):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, Nature (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process. For example, a 1.1-kb fragment containing the TEM-1 beta-lactamase-encoding gene (bla) can be assembled in a single reaction from a total of 56 oligos, each 40 nucleotides (nt) in length. The synthetic gene can be PCR amplified and cloned in a vector containing the tetracycline-resistance gene (Tc-R) as the sole selectable marker. Without relying on ampicillin (Ap) selection, 76% of the Tc-R colonies were Ap-R, making this approach a general method for the rapid and cost-effective synthesis of any gene.

IV. Identification of Functional and Structural Motifs of Novel Genes Using Art-Recognized Methods

Translations of the nucleotide sequence of the nucleic acids, cDNAs, or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For

example, sequences that show similarity with a chemokine sequence may exhibit chemokine activities. Also, sequences exhibiting similarity with more than one individual sequence may exhibit activities that are characteristic of either or both individual sequences.

5 The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the nucleic acid. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the nucleic acid.

Typically, the nucleic acids are translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence
10 Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences.

Nucleic acid sequences can be compared with known genes by any of the methods disclosed above. Results of individual and query sequence alignments can be divided into three
15 categories: high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure.

Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value.

20 The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment. This number is divided by the total residue length of the query sequence to find a percentage.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number
25 of residues of the individual sequence found in the region of strongest alignment. For the example above, the percent identity would be 10 matches divided by 11 amino acids, or approximately 90.9%.

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin et al., Proc. Natl. Acad. Sci. 87:
30 2264 (1990) and Karlin et al., Proc. Natl. Acad. Sci. 90: (1993). The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach

described in Altschul et al., Genet. 6:119(1994). Alignment programs such as BLAST program can calculate the p value.

The boundaries of the region where the sequences align can be determined according to Doolittle, Methods in Enzymology, *supra*; BLAST or FASTA programs; or by determining the
5 area where the sequence identity is highest.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences.

10 High Similarity

For the alignment results to be considered high similarity, the percent of the alignment region length, typically, is at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more
15 usually, as much as about 64%; even more usually, as much as about 66%.

Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

20 The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} more typically; no more than or equal to about 10^{-10} ; even more typically; no more than or equal to
25 about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity

For the alignment results to be considered weak there is no minimum percent length of the alignment region no minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in
30 length; more typically, at least about 20; even more typically; at least about 25 amino acid

residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues.

Further, for weak similarity, the region of alignment, typically, exhibits at least about
5 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2} ; more usually; less
10 than or equal to about 10^{-3} even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} more usually; no more than or equal to about 10^{-10} ; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity

15 Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about
20 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

25 Determining Activity from Alignments with Profile and Multiple Aligned Sequences

Translations of the nucleic acids can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the nucleic acids can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to
30 determine the activity of the polypeptides encoded by nucleic acids or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating a MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney et al., Nucl. Acid Res. 25(14): 2730-2739 (1996).

5 MSAs of some protein families and motifs are publicly available. For example, these include MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer et al., Proteins 28: 405-420 (1997). Other sources are also available in the world wide web. A brief description of these MSAs is reported in Pascarella et al., Prot. Eng. 9(3): 249-251 (1996).

10 Techniques for building profiles from MSAs are described in Sonnhammer et al., *supra*; Birney et al., *supra*; and Methods in Enzymology, vol. 266: "Computer Methods for Macromolecular Sequence Analysis," 1996, ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by
15 (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif.

Typically, a program such as Searchwise can be used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney et al., *supra*. Other techniques to compare the sequence and profile are
20 described in Sonnhammer et al., *supra* and Doolittle, *supra*.

Next, methods described by Feng et al., J. Mol. Evol. 25:351-360 (1987) and Higgins et al., CABIOS 5:151-153 (1989) can be used to align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng et al., *infra*.

25 The following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number
30 of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between

the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts.

Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids that are found at a particular position in all or some of the family or motif members. For example, most known chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position may contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member, more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA more typically, at least about 50%; even more typically; at least about 55%.

V. Probes and Primers

The nucleotide sequences determined from the cloning of genes from tumor cells, especially colon cancer cell lines and tissues will further allow for the generation of probes and primers designed for identifying and/or cloning homologs in other cell types, e.g., from other tissues, as well as homologs from other mammalian organisms. Nucleotide sequences useful as probes/primers may include all or a portion of the sequences listed in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or sequences complementary thereto or sequences which hybridize under stringent conditions to all or a portion of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. For instance, the present invention also provides a probe/primer comprising a substantially purified oligonucleotide, which oligonucleotide comprising a nucleotide sequence that hybridizes under stringent conditions to at least approximately 12, preferably 25, more preferably 40, 50, or 75 consecutive nucleotides up to the full length of the sense or anti-sense sequence selected from the group consisting of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, or naturally occurring mutants thereof. For instance, primers based on a nucleic acid represented in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and even still more preferred SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, can be used in PCR reactions to clone homologs of that sequence.

In yet another embodiment, the invention provides probes/primers comprising a nucleotide sequence that hybridizes under moderately stringent conditions to at least approximately 12, 16, 25, 40, 50 or 75 consecutive nucleotides up to the full length of the sense or antisense sequence selected from the group consisting of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or naturally occurring mutants thereof.

In particular, these probes are useful because they provide a method for detecting mutations in wild-type genes of the present invention. Nucleic acid probes which are complementary to a wild-type gene of the present invention and can form mismatches with mutant genes are provided, allowing for detection by enzymatic or chemical cleavage or by shifts in electrophoretic mobility. Likewise, probes based on the subject sequences can be used to

detect transcripts or genomic sequences encoding the same or homologous proteins, for use, for example, in prognostic or diagnostic assays. In preferred embodiments, the probe further comprises a label group attached thereto and able to be detected, e.g., the label group is selected from radioisotopes, fluorescent compounds, chemiluminescent compounds, enzymes, and
5 enzyme co-factors.

Full-length cDNA molecules comprising the disclosed nucleic acids are obtained as follows. In a preferred embodiment, the invention provides the full length cDNA sequence of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. A subject nucleic acid or a portion thereof comprising at least about 12, 15, 18, or 20 nucleotides
10 up to the full length of a sequence represented in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, may be used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques as described in U.S. Patent No.
15 5,654,173, "Secreted Proteins and Polynucleotides Encoding Them," incorporated herein by reference. Libraries of cDNA may be made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as that used to generate the nucleic acids, as both the nucleic acid and the cDNA represent expressed genes. Most preferably, the cDNA library is made from
20 the biological material described herein in the Examples. Alternatively, many cDNA libraries are available commercially. (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. (Cold Spring Harbor Press, Cold Spring Harbor, NY 1989). The choice of cell type for library construction may be made after the identity of the protein encoded by the nucleic acid-related gene is known. This will indicate which tissue and cell types are likely to express the
25 related gene, thereby containing the mRNA for generating the cDNA.

Members of the library that are larger than the nucleic acid, and preferably that contain the whole sequence of the native message, may be obtained. To confirm that the entire cDNA has been obtained, RNA protection experiments may be performed as follows. Hybridization of a full-length cDNA to an mRNA may protect the RNA from RNase degradation. If the cDNA is
30 not full length, then the portions of the mRNA that are not hybridized may be subject to RNase degradation. This may be assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. (Cold Spring Harbor Press, Cold Spring Harbor, NY 1989). In order to obtain additional sequences 5' to the end of a partial cDNA, 5'

RACE (PCR Protocols: A Guide to Methods and Applications (Academic Press, Inc. 1990)) may be performed.

Genomic DNA may be isolated using nucleic acids in a manner similar to the isolation of full-length cDNAs. Briefly, the nucleic acids, or portions thereof, may be used as probes to
5 libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the nucleic acids. Most preferably, the genomic DNA is obtained from the biological material described herein in the Example. Such libraries may be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook et al., 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are
10 commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking may be performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are isolated. These may be mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

15 Using the nucleic acids of the invention, corresponding full length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, may be performed on a number of cell types to determine which cell lines express the gene of interest at the highest rate.

Classical methods of constructing cDNA libraries in Sambrook et al., supra. With these
20 methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods may be used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert may contain sequence from the full length cDNA
25 that corresponds to the instant nucleic acids. Such PCR methods include gene trapping and RACE methods.

Gene trapping may entail inserting a member of a cDNA library into a vector. The vector then may be denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, may be used to trap cDNA inserts of interest. Biotinylated probes can
30 be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence may be based on the nucleic acids of the invention, e.g., SEQ ID Nos. 1-1103, preferably SEQ

ID Nos. 1-503, or a sequence complementary thereto. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber et al., PCT WO 95/04745 and Gruber et al., U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life
5 Technologies, Gaithersburg, Maryland, USA.

“Rapid amplification of cDNA ends,” or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs may be ligated to an oligonucleotide linker and amplified by PCR using two primers. One primer may be based on sequence from the instant nucleic acids, for which full length sequence is desired, and a second primer may comprise a
10 sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this method is reported, for example, in PCT Pub. No. WO 97/19110.

In preferred embodiments of RACE, a common primer may be designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques*, 15:890-893, 1993; Edwards et al., *Nuc. Acids Res.*, 19:5227-5232, 1991). When a single gene-specific
15 RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without specific knowledge of the cDNA sequence. The method uses lock-docking primers (1-
20 VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT). This method is described, for example, in PCT Pub. No. WO 96/40998.

The promoter region of a gene generally is located 5' to the initiation site for RNA
25 polymerase II. Hundreds of promoter regions contain the “TATA” box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by “walking up.”

30 If the gene is highly expressed or differentially expressed, the promoter from the gene may be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on the disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

5 As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more nucleic acids of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 12 nucleotides (corresponding to at least 12 contiguous nucleotides which hybridize under stringent conditions to or are at least 80% identical to a nucleic acid represented by one of SEQ
10 ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at
15 least one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral
20 particle comprising (a) or (b). Construction of (c) can be accomplished as described below in part VI.

The sequence of a nucleic acid of the present invention is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired
25 function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired.

VI. Vectors Carrying Nucleic Acids of the Present Invention

The invention further provides plasmids and vectors, which can be used to express a gene in a host cell. The host cell may be any prokaryotic or eukaryotic cell. Thus, a nucleotide
30 sequence derived from any one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, encoding all or a

selected portion of a protein, can be used to produce a recombinant form of an polypeptide via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard
5 procedures well known in the art.

Vectors that allow expression of a nucleic acid in a cell are referred to as expression vectors. Typically, expression vectors contain a nucleic acid operably linked to at least one transcriptional regulatory sequence. Regulatory sequences are art-recognized and are selected to direct expression of the subject nucleic acids. Transcriptional regulatory sequences are described
10 in Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). In one embodiment, the expression vector includes a recombinant gene encoding a peptide having an agonistic activity of a subject polypeptide, or alternatively, encoding a peptide which is an antagonistic form of a subject polypeptide.

The choice of plasmid will depend on the type of cell in which propagation is desired and
15 the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The nucleic acid or full-length gene is inserted into a vector typically by means
20 of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence may be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion
25 of the desired nucleotide sequence.

Nucleic acids or full-length genes are linked to regulatory sequences as appropriate to obtain the desired expression properties. These may include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters may be regulated or constitutive. In some situations it
30 may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art may be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to the nucleic acid is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670, "Protein Production and Protein Delivery."

A number of vectors exist for the expression of recombinant proteins in yeast (see, for example, Broach *et al* (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye, Academic Press, p. 83, incorporated by reference herein). In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, a polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning one of the nucleic acids represented in one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The various methods employed in the preparation of plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning: A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

When it is desirable to express only a portion of a gene, e.g., a truncation mutant, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat *et al.*, (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller *et al.* (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing polypeptides in a host which produces

MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller *et al.*, *supra*).

Moreover, the nucleic acid constructs of the present invention can also be used as part of a gene therapy protocol to deliver nucleic acids such as antisense nucleic acids. Thus, another
5 aspect of the invention features expression vectors for *in vivo* or *in vitro* transfection with an antisense oligonucleotide.

In addition to viral transfer methods, non-viral methods can also be employed to introduce a subject nucleic acid, e.g., a sequence represented by one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ
10 ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, into the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral targeting means of the present invention rely on endocytic pathways for the uptake of the subject nucleic acid by the targeted cell.
15 Exemplary targeting means of this type include liposomal derived systems, polylysine conjugates, and artificial viral envelopes.

A nucleic acid of any of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, the corresponding cDNA, or the full-
20 length gene may be used to express the partial or complete gene product. Appropriate nucleic acid constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Press, Cold Spring Harbor, New York), and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant
25 DNA research. The polypeptides encoded by the nucleic acid may be expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described, for example, in U.S. Patent No. 5,654,173.

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature*
30 (1978) 275:615, Goeddel *et al.*, *Nature* (1979) 281 :544, Goeddel *et al.*, *Nucleic Acids Rec.* (1980) 8:4057; EP 0 036,776, U.S. Patent No. 4,551,433, DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:2125, and Siebenlist *et al.*, *Cell* (1980) 20:269.

- Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) 75:1929; Ito *et al.*, *J. Bacteriol.* (1983) 153:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 6:142; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132:3459, Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202:302) Das *et al.*, *J. Bacteriol.* (1984) 158:1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) 154:737, Van den Berg *et al.*, *Bio/Technology* (1990) 8:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5:3376, U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) 300:706; Davidow *et al.*, *Curr. Genet.* (1985) 10:380, Gaillardin *et al.*, *Curr. Genet.* (1985) 10:49, Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) 112:284289;
- 5 *Tilburn et al.*, *Gene* (1983) 26:205221, Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) 81:14701474, Kelly and Hynes, *EMBO J.* (1985) 4:475479; EP 0 244,234, and WO 91/00357.

- Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051, Friesen *et al.*, (1986) "The Regulation of Baculovirus Gene Expression" in: *The Molecular Biology Of Baculoviruses* (W. Doerfler, ed.), EP 0 127,839, EP 0 155,476, and Vlak *et al.*, *J. Gen. Virol.* (1988) 69:765776, Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42:177, Carbonell *et al.*, *Gene* (1988) 73:409, Maeda *et al.*, *Nature* (1985) 315:592594, Lebacqz Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985) 82:8404, Miyajima *et al.*, *Gene* (1987) 58:273; and Martinet *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells
- 15 from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6:4755, Miller *et al.*, *Generic Engineering* (Setlow, J.K. *et al.* eds.), Vol. 8 (Plenum Publishing, 1986), pp. 277279, and Maeda *et al.*, *Nature*, (1985) 315:592-594.

- Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) 4:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1982) 79:6777, Boshart *et al.*, *Cell* (1985) 41:52 1 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58:44, Barnes and Sato, *Anal. Biochem.* (1980) 102:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.
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VII. Therapeutic Nucleic Acid Constructs

- 30 One aspect of the invention relates to the use of the isolated nucleic acid, e.g., SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, in antisense therapy. As used herein, antisense therapy refers to

administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g., bind) under cellular conditions with the cellular mRNA and/or genomic DNA, thereby inhibiting transcription and/or translation of that gene. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA
5 duplexes, through specific interactions in the major groove of the double helix. In general, antisense therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary
10 to at least a unique portion of the cellular mRNA. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell, causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a subject nucleic acid. Such oligonucleotide probes are preferably modified oligonucleotides which are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, and are
15 therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphorothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol *et al.* (1988) *BioTechniques* 6:958-976; and Stein *et al.* (1988) *Cancer Res* 48:2659-2668. With
20 respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the nucleotide sequence of interest, are preferred.

Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to mRNA. The antisense oligonucleotides will bind to the mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. In the
25 case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable
30 degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most

efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. Nature 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a gene could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are typically less efficient inhibitors of translation but could also be used in accordance with the invention. Whether designed to hybridize to the 5', 3', or coding region of subject mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably less than about 100 and more preferably less than about 50, 25, 17 or 10 nucleotides in length.

Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, e.g., Letsinger *et al.*, 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre *et al.*, 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO 88/098 10, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10 134, published April 25, 1988), hybridization-triggered cleavage agents (See, e.g., Krol *et al.*, 1988, BioTechniques 6:958-976), or intercalating agents (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to

another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxytriethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)_w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

The antisense oligonucleotide can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, e.g., in Peny-O'Keefe *et al.* (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom *et al.* (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methyphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet a further embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier *et al.*, 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, Nucl. Acids Res. 15:6131-12148), or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, FEBS Lett. 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein *et al.* (1988, Nucl. Acids Res. 16:3209), methylphosphonate
5 oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin *et al.*, 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to a coding region sequence can be used, those complementary to the transcribed untranslated region and to the region comprising the initiating methionine are most preferred.

10 The antisense molecules can be delivered to cells which express the target nucleic acid *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be
15 administered systemically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation on endogenous mRNAs. Therefore, a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pot II promoter. The use of such a construct to transfect target cells
20 in the patient will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the target mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the
25 desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not
30 limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-3 10), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster

et al., 1982, Nature 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced directly into the tissue site; e.g., the choroid plexus or hypothalamus. Alternatively, viral vectors can be used which selectively infect the desired tissue (e.g., for brain, herpesvirus vectors may be used), in which
5 case administration may be accomplished by another route (e.g., systemically).

In another aspect of the invention, ribozyme molecules designed to catalytically cleave target mRNA transcripts can be used to prevent translation of target mRNA and expression of a target protein (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225 and U.S. Patent No. 5,093,246). While ribozymes
10 that cleave mRNA at site specific recognition sequences can be used to destroy target mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art
15 and is described more fully in Haseloff and Gerlach, 1988, Nature, 334:585-591. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter
20 "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224:574-578; Zaug and Cech, 1986, Science, 231:470-475; Zaug, et al., 1986, Nature, 324:429-433; published International patent application No. W088/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47:207-216). The
25 Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in a target gene.

As in the antisense approach, the ribozymes can be composed of modified
30 oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells which express the target gene *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy

endogenous messages and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antisense RNA, DNA, and ribozyme molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include
 5 techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the
 10 T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications
 15 include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

VIII. Full-length cDNA Sequences of the Present Invention

20 The present invention also relates to full length cDNA sequences corresponding to one or more of the partial sequences of SEQ ID Nos. 1-4470. In particular the invention provides the full length cDNA sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. The full length sequences may be obtained as described above. These sequences are shown in Figure 2, and summarized below in Table 2. Also shown in Table
 25 2 are the SEQ ID Nos and GenBank accession numbers for the polypeptides which are encoded by the full length cDNA sequences and which correspond to SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

cDNA SEQ ID NO.	Gene Name	GenBank Accession No.	Protein SEQ ID NO.	GenBank Accession No.
4472	Reg IV	NM 032044	4471	NP 114433
4474	XAG-2	NM 006408	4473	NP 006399

4476	SPARC/Osteonectin	NM 003118	4475	NP 003109
4478	GW112 protein	NM 006418	4477	NP 006409
4480	HSBP1	NM 001540	4479	NP 001531
4482	SKD1 Homolog	NP 004869	4481	NP 004860
4484	9-27	NM 003641	4483	NP 003632
4486	Defensin 5	NM 021010	4485	NP 066290
4488	p0071	NM 003628	4487	NP 003619
4490	UBE2I	NM 003345	4489	NP 003336
4492	Cytoplasmic dynein light chain	NM 003746	4491	NP 003737
4494	10Ckshs1	NM 001798	4493	NP 001789

IX. Polypeptides of the Present Invention

The present invention makes available isolated polypeptides which are isolated from, or otherwise substantially free of other cellular proteins, especially other signal transduction factors and/or transcription factors which may normally be associated with the polypeptide. Subject

5 polypeptides of the present invention include polypeptides encoded by the nucleic acids of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and

10 4494, or a sequence complementary thereto, or polypeptides encoded by genes of which a sequence in SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, or a sequence complementary thereto, is a fragment. In a preferred embodiment, polypeptides, useful in the present invention have the amino acid sequence of one or more of SEQ ID Nos. 4471,

15 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. Polypeptides of the present invention include those proteins which are differentially regulated in tumor cells, especially colon cancer-derived cell lines (relative to normal cells, e.g., normal colon tissue and

non-colon tissue). In a preferred embodiment the differentially regulated polypeptides are one or more of the polypeptides having the sequence set forth in SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. In preferred embodiments, the polypeptides are upregulated in tumor cells, especially colon cancer cancer-derived cell lines. In other embodiments, the polypeptides are downregulated in tumor cells, especially colon cancer-derived cell lines. Proteins which are upregulated, such as oncogenes, or downregulated, such as tumor suppressors, in aberrantly proliferating cells may be targets for diagnostic or therapeutic techniques. For example, upregulation of the *cdc2* gene induces mitosis. Overexpression of the *myt1* gene, a mitotic deactivator, negatively regulates the activity of *cdc2*. Aberrant proliferation may thus be induced either by upregulating *cdc2* or by downregulating *myt1*.

The term "substantially free of other cellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of polypeptides having less than about 20% (by dry weight) contaminating protein, and preferably having less than about 5% contaminating protein. Functional forms of the subject polypeptides can be prepared, for the first time, as purified preparations by using a cloned nucleic acid as described herein. Full length proteins or fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least about 5, 10, 25, 50, 75, or 100 amino acids in length are within the scope of the present invention.

For example, isolated polypeptides can be encoded by all or a portion of a nucleic acid sequence shown in any of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503 and most preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto. Isolated peptidyl portions of proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as either agonists or antagonists of a wild-type (e.g., "authentic") protein.

Another aspect of the present invention concerns recombinant forms of the subject proteins. Recombinant polypeptides preferred by the present invention, in addition to native proteins, as described above are encoded by a nucleic acid, which is at least 60%, more preferably at least 80%, and more preferably 85%, and more preferably 90%, and more preferably 95% identical to an amino acid sequence encoded by SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. Polypeptides which are encoded by a nucleic acid that is at least about 98-99% identical with the sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 are also within the scope of the invention. Also included in the present invention are peptide fragments comprising at least a portion of such a protein.

In a preferred embodiment, a polypeptide of the present invention is a mammalian polypeptide and even more preferably a human polypeptide. In particularly preferred embodiment, the polypeptide retains wild-type bioactivity. It will be understood that certain post-translational modifications, e.g., phosphorylation and the like, can increase the apparent molecular weight of the polypeptide relative to the unmodified polypeptide chain.

The present invention further pertains to recombinant forms of one of the subject polypeptides. Such recombinant polypeptides preferably are capable of functioning in one of either role of agonist or antagonist of at least one biological activity of a wild-type ("authentic") polypeptide of the appended sequence listing. The term "evolutionarily related to", with respect to amino acid sequences of proteins, refers to both polypeptides having amino acid sequences which have arisen naturally, and also to mutational variants of human polypeptides which are derived, for example, by combinatorial mutagenesis.

In general, polypeptides referred to herein as having an activity (e.g., are "bioactive") of a protein are defined as polypeptides which include an amino acid sequence encoded by all or a portion of the nucleic acid sequences shown in one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and most preferably SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, or a sequence complementary thereto, and which mimic or antagonize all or a portion of the biological/biochemical activities of a naturally occurring protein. According to the present invention, a polypeptide has biological activity if it is a specific agonist or antagonist of a naturally occurring form of a protein.

Assays for determining whether a compound, e.g, a protein or variant thereof, has one or more of the above biological activities are well known in the art. In certain embodiments, the polypeptides of the present invention have activities such as those outlined above.

In another embodiment, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a polypeptide (see, for example, EP Publication No: 0259149; and Evans *et al.* (1989) *Nature* 339:3 85; Huang *et al.* (1988) *J. Virol.* 62:3 855; and Schlienger *et al.*, (1992) *J. Virol.* 66:2). In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, and, accordingly, can be used in the expression of the polypeptides of the present invention (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* (N.Y. John Wiley & Sons, 1991)). In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the recombinant protein, can allow purification of the expressed fusion protein by affinity chromatography using a Ni²⁺ metal resin. The purification leader sequence can then be subsequently removed by treatment with enterokinase to provide the purified protein (e.g., see Hochuli *et al.* (1987) *J. Chromatography* 411:177; and Janknecht *et al.* *PNAS* 88:8972).

Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed to generate a chimeric nucleic acid sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992).

The present invention further pertains to methods of producing the subject polypeptides. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. Suitable media for cell culture are well

known in the art. The recombinant polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred
5 embodiment, the recombinant polypeptide is a fusion protein containing a domain which facilitates its purification, such as GST fusion protein.

Moreover, it will be generally appreciated that, under certain circumstances, it may be advantageous to provide homologs of one of the subject polypeptides which function in a limited capacity as one of either an agonist (mimetic) or an antagonist, in order to promote or inhibit
10 only a subset of the biological activities of the naturally occurring form of the protein. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of naturally occurring forms of subject proteins.

Homologs of each of the subject polypeptide can be generated by mutagenesis, such as
15 by discrete point mutation(s), or by truncation. For instance, mutation can give rise to homologs which retain substantially the same, or merely a subset, of the biological activity of the polypeptide from which it was derived. Alternatively, antagonistic forms of the polypeptide can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to a receptor.

20 The recombinant polypeptides of the present invention also include homologs of the wild-type proteins, such as versions of those proteins which are resistant to proteolytic cleavage, for example, due to mutations which alter ubiquitination or other enzymatic targeting associated with the protein.

Polypeptides may also be chemically modified to create derivatives by forming covalent
25 or aggregate conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of proteins can be prepared by linking the chemical moieties to functional groups on amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

Modification of the structure of the subject polypeptides can be for such purposes as
30 enhancing therapeutic or prophylactic efficacy, stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation), or post-translational modifications (e.g., to alter phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the

naturally occurring form of the protein, or to produce specific antagonists thereof, are considered functional equivalents of the polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. The substitutional variant may be a substituted conserved amino acid or a substituted non-conserved amino acid.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e., isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tiyptophan; (5) amide = asparagine, glutamine; and (6) sulfur -containing = cysteine and methionine. (see, for example, *Biochemistry*, 2 ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional homolog (e.g., functional in the sense that the resulting polypeptide mimics or antagonizes the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response.

Polypeptides in which more than one replacement has taken place can readily be tested in the same manner. The variant may be designed so as to retain biological activity of a particular region of the protein. In a non-limiting example, Osawa et al., 1994, *Biochemistry and Molecular International* 34:1003-1009, discusses the actin binding region of a protein from several different species. The actin binding regions of the these species are considered homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, an S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

Additional guidance on amino acid substitution is available from studies of protein evolution. Go et al., 1980, *Int. J. Peptide Protein Res.* 15: 211-224, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group. Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp, and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Intergroup replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Querol et al., 1996, *Prot. Eng.* 9:265-271, provides general rules for amino acid substitutions to enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, 1991, *J. Gen. Microbiol.* 137 :579-585. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, 1984, *Science* 226:555-557; Pantoliano et al., 1987, *Biochemistry* 26:2077-2082; Matsumura et al., 1989, *Nature* 342:291-293; Nishikawa et al., 1990, *Protein Eng.* 3:443-448; Takagi et al., 1990, *J. Biol. Chem.* 265:6874-6878; Clarke et al., 1993, *Biochemistry* 32:4322-4329; and Wakarchuk et al., 1994, *Protein Eng.* 7:1379-1386.

An additional metal binding site can be introduced, according to Toma et al., 1991, *Biochemistry* 30:97-106, and Haezebrouck et al., 1993, *Protein Eng.* 6:643-649. Substitutions with prolines in loops can be made according to Masul et al., 1994, *Appl Env. Microbiol.* 60:3579-3584; and Hardy et al., *FEBS Lett.* 317:89-92.

Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses how to substitute other amino acids for cysteines, and how to determine biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine residues suitable for such substitutions, for example to eliminate disulfide bond formation.

To learn the identity and function of the gene that correlates with an nucleic acid, the nucleic acids or corresponding amino acid sequences can be screened against profiles of protein families. Such profiles focus on common structural motifs among proteins of each family. Publicly available profiles are described above.

5 In comparing a new nucleic acid with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) 25:35 1-360. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) 48:443-453. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize
10 the number of matches using the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* (1981) 2:482-489.

X. Diagnostic & Prognostic Assays and Drug Screening Methods

 The present invention provides method for determining whether a subject is at risk for developing a disease or condition characterized by unwanted cell proliferation by detecting the
15 disclosed biomarkers, i.e., the present nucleic acids (SEQ ID Nos: 1-4494) and/or polypeptide markers (preferably SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493) for colon cancer encoded thereby.

 In clinical applications, human tissue samples can be screened for the presence and/or absence of the biomarkers identified herein. Such samples could consist of needle biopsy cores,
20 surgical resection samples, lymph node tissue, or serum. For example, these methods include obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumor cells to about 80% of the total cell population. In certain embodiments, nucleic acids extracted from these samples may be amplified using techniques well known in the art. The levels of selected markers detected would be compared with statistically valid groups of metastatic, non-metastatic
25 malignant, benign, or normal colon tissue samples.

 In one embodiment, the diagnostic method comprises determining whether a subject has an abnormal mRNA and/or protein level of the disclosed markers, such as by Northern blot analysis, reverse transcription-polymerase chain reaction (RT-PCR), in situ hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the
30 method, cells are obtained from a subject and the levels of the disclosed biomarkers, protein or mRNA level, is determined and compared to the level of these markers in a healthy subject. An

abnormal level of the biomarker polypeptide or mRNA levels is likely to be indicative of cancer such as colon cancer.

Accordingly, in one aspect, the invention provides probes and primers that are specific to the unique nucleic acid markers disclosed herein. Accordingly, the nucleic acid probes comprise
5 a nucleotide sequence at least 10 nucleotides in length, preferably at least 15 nucleotides, more preferably, 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto.

- 10 In one embodiment, the method comprises using a nucleic acid probe to determine the presence of cancerous cells in a tissue from a patient. Specifically, the method comprises:
1. providing a nucleic acid probe comprising a nucleotide sequence at least 10 nucleotides in length, preferably at least 15 nucleotides, more preferably, 25
15 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto and is differentially expressed in tumors cells, such as colon cancer cells;
 2. obtaining a tissue sample from a patient potentially comprising cancerous cells;
 - 20 3. providing a second tissue sample containing cells substantially all of which are non-cancerous;
 4. contacting the nucleic acid probe under stringent conditions with RNA of each of said first and second tissue samples (e.g., in a Northern blot or in situ hybridization assay); and
 - 25 5. comparing (a) the amount of hybridization of the probe with RNA of the first tissue sample, with (b) the amount of hybridization of the probe with RNA of the second tissue sample; wherein a statistically significant difference in the amount of hybridization with the RNA of the first tissue sample as compared to the amount of hybridization with the RNA of the second tissue sample is indicative of
30 the presence of cancerous cells in the first tissue sample.

In one aspect, the method comprises *in situ* hybridization with a probe derived from a given marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto. The method comprises contacting the labeled hybridization probe with a sample of a given type of tissue potentially containing cancerous or pre-cancerous cells as well as normal cells, and determining whether the probe labels some cells of the given tissue type to a degree significantly different (e.g., by at least a factor of two, or at least a factor of five, or at least a factor of twenty, or at least a factor of fifty) than the degree to which it labels other cells of the same tissue type.

Also within the invention is a method of determining the phenotype of a test cell from a given human tissue, e.g., whether the cell is (a) normal, or (b) cancerous or precancerous, by contacting the mRNA of a test cell with a nucleic acid probe at least 12 nucleotides in length, preferably at least 15 nucleotides, more preferably at least 25 nucleotides, and most preferably at least 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto, and which is differentially expressed in tumor cells as compared to normal cells of the given tissue type; and determining the approximate amount of hybridization of the probe to the mRNA, an amount of hybridization either more or less than that seen with the mRNA of a normal cell of that tissue type being indicative that the test cell is cancerous or pre-cancerous.

Alternatively, the above diagnostic assays may be carried out using antibodies to detect the protein product encoded by the marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID Nos: 1-4494 or a sequence complementary thereto. Accordingly, in one embodiment, the assay would include contacting the proteins of the test cell with an antibody specific for the gene product of a nucleic acid represented by SEQ ID Nos: 1-4494, preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, the marker nucleic acid being one which is expressed at a given control level in normal cells of the same tissue type as the test cell, and determining the approximate amount of immunocomplex formation by the antibody and the proteins of the test cell, wherein a statistically significant difference in the amount of the immunocomplex formed with the proteins of a test cell as compared to a normal cell of the same tissue type is an indication that the test cell is cancerous or pre-cancerous. Preferably, the antibody is specific for one of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

The method for producing polyclonal and/or monoclonal antibodies which specifically bind to polypeptides useful in the present invention is known to those of skill in the art and can be found in, for example Dymecki et al., 1992, J. Biol. Chem., 267:4815; Boersma & Van Leeuwen, 1994, J. Neurosci. Methods, 51:317; Green et al., 1982, Cell, 28:477; and Arnheiter et al., 1981, Nature, 294:278.

Another such method includes the steps of: providing an antibody specific for the gene product of a marker nucleic acid sequence represented by SEQ ID Nos 1-4494, the gene product being present in cancerous tissue of a given tissue type (e.g., colon tissue) at a level more or less than the level of the gene product in non-cancerous tissue of the same tissue type; obtaining from a patient a first sample of tissue of the given tissue type, which sample potentially includes cancerous cells; providing a second sample of tissue of the same tissue type (which may be from the same patient or from a normal control, e.g. another individual or cultured cells), this second sample containing normal cells and essentially no cancerous cells; contacting the antibody with protein (which may be partially purified, in lysed but unfractionated cells, or in situ) of the first and second samples under conditions permitting immunocomplex formation between the antibody and the marker nucleic acid sequence product present in the samples; and comparing (a) the amount of immunocomplex formation in the first sample, with (b) the amount of immunocomplex formation in the second sample, wherein a statistically significant difference in the amount of immunocomplex formation in the first sample less as compared to the amount of immunocomplex formation in the second sample is indicative of the presence of cancerous cells in the first sample of tissue.

The subject invention further provides a method of determining whether a cell sample obtained from a subject possesses an abnormal amount of marker polypeptide which comprises (a) obtaining a cell sample from the subject, (b) quantitatively determining the amount of the marker polypeptide in the sample so obtained, and (c) comparing the amount of the marker polypeptide so determined with a known standard, so as to thereby determine whether the cell sample obtained from the subject possesses an abnormal amount of the marker polypeptide. Such marker polypeptides may be detected by immunohistochemical assays, dot-blot assays, ELISA and the like.

Immunoassays are commonly used to quantitate the levels of proteins in cell samples, and many other immunoassay techniques are known in the art. The invention is not limited to a particular assay procedure, and therefore is intended to include both homogeneous and heterogeneous procedures. Exemplary immunoassays which can be conducted according to the

invention include fluorescence polarization immunoassay (FPIA), fluorescence immunoassay (FIA), enzyme immunoassay (EIA), nephelometric inhibition immunoassay (NIA), enzyme linked immunosorbent assay (ELISA), and radioimmunoassay (RIA). An indicator moiety, or label group, can be attached to the subject antibodies and is selected so as to meet the needs of various uses of the method which are often dictated by the availability of assay equipment and compatible immunoassay procedures. General techniques to be used in performing the various immunoassays noted above are known to those of ordinary skill in the art.

In another embodiment, the level of the encoded product, i.e., the product encoded by SEQ ID Nos 1-4494 or a sequence complementary thereto, or alternatively the level of the polypeptide of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, in a biological fluid (e.g., blood or urine) of a patient may be determined as a way of monitoring the level of expression of the marker nucleic acid sequence in cells of that patient. Such a method would include the steps of obtaining a sample of a biological fluid from the patient, contacting the sample (or proteins from the sample) with an antibody specific for a encoded marker polypeptide, and determining the amount of immune complex formation by the antibody, with the amount of immune complex formation being indicative of the level of the marker encoded product in the sample. This determination is particularly instructive when compared to the amount of immune complex formation by the same antibody in a control sample taken from a normal individual or in one or more samples previously or subsequently obtained from the same person.

In another embodiment, the method can be used to determine the amount of marker polypeptide present in a cell, which in turn can be correlated with progression of a hyperproliferative disorder, e.g., colon cancer. The level of the marker polypeptide can be used predictively to evaluate whether a sample of cells contains cells which are, or are predisposed towards becoming, transformed cells. Moreover, the subject method can be used to assess the phenotype of cells which are known to be transformed, the phenotyping results being useful in planning a particular therapeutic regimen. For instance, very high levels of the marker polypeptide in sample cells is a powerful diagnostic and prognostic marker for a cancer, such as colon cancer. The observation of marker polypeptide level can be utilized in decisions regarding, e.g., the use of more aggressive therapies.

As set out above, one aspect of the present invention relates to diagnostic assays for determining, in the context of cells isolated from a patient, if the level of a marker polypeptide is significantly reduced in the sample cells. The term "significantly reduced" refers to a cell

phenotype wherein the cell possesses a reduced cellular amount of the marker polypeptide relative to a normal cell of similar tissue origin. For example, a cell may have less than about 50%, 25%, 10%, or 5% of the marker polypeptide that a normal control cell. In particular, the assay evaluates the level of marker polypeptide in the test cells, and, preferably, compares the measured level with marker polypeptide detected in at least one control cell, e.g., a normal cell and/or a transformed cell of known phenotype.

Of particular importance to the subject invention is the ability to quantitate the level of marker polypeptide as determined by the number of cells associated with a normal or abnormal marker polypeptide level. The number of cells with a particular marker polypeptide phenotype may then be correlated with patient prognosis. In one embodiment of the invention, the marker polypeptide phenotype of the lesion is determined as a percentage of cells in a biopsy which are found to have abnormally high/low levels of the marker polypeptide. Such expression may be detected by immunohistochemical assays, dot-blot assays, ELISA and the like.

Where tissue samples are employed, immunohistochemical staining may be used to determine the number of cells having the marker polypeptide phenotype. For such staining, a multiblock of tissue is taken from the biopsy or other tissue sample and subjected to proteolytic hydrolysis, employing such agents as protease K or pepsin. In certain embodiments, it may be desirable to isolate a nuclear fraction from the sample cells and detect the level of the marker polypeptide in the nuclear fraction.

The tissue samples are fixed by treatment with a reagent such as formalin, glutaraldehyde, methanol, or the like. The samples are then incubated with an antibody, preferably a monoclonal antibody, with binding specificity for the marker polypeptides. This antibody may be conjugated to a label for subsequent detection of binding. Samples are incubated for a time sufficient for formation of the immunocomplexes. Binding of the antibody is then detected by virtue of a label conjugated to this antibody. Where the antibody is unlabeled, a second labeled antibody may be employed, e.g., which is specific for the isotype of the anti-marker polypeptide antibody. Examples of labels which may be employed include radionuclides, fluorescers, chemilumescers, enzymes and the like.

Where enzymes are employed, the substrate for the enzyme may be added to the samples to provide a colored or fluorescent product. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art.

In one embodiment, the assay is performed as a dot blot assay. The dot blot assay finds particular application where tissue samples are employed as it allows determination of the average amount of the marker polypeptide associated with a single cell by correlating the amount of marker polypeptide in a cell-free extract produced from a predetermined number of cells.

- 5 It is well established in the cancer literature that tumor cells of the same type (e.g., breast and/or colon tumor cells) may not show uniformly increased expression of individual oncogenes or uniformly decreased expression of individual tumor suppressor genes. There may also be varying levels of expression of a given marker gene even between cells of a given type of cancer, further emphasizing the need for reliance on a battery of tests rather than a single test.
- 10 Accordingly, in one aspect, the invention provides for a battery of tests utilizing a number of probes of the invention, in order to improve the reliability and/or accuracy of the diagnostic test.

- In one embodiment, the present invention also provides a method wherein nucleic acid probes are immobilized on a DNA chip in an organized array. Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up
- 15 to 250,000 oligonucleotides (GeneChip, Affymetrix). These nucleic acid probes comprise a nucleotide sequence at least about 12 nucleotides in length, preferably at least about 15 nucleotides, more preferably at least about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence represented by SEQ ID Nos: 1-4494 and is
- 20 differentially expressed in tumor cells, such as colon cancer cells. The present invention provides significant advantages over the available tests for various cancers, such as colon cancer, because it increases the reliability of the test by providing an array of nucleic acid markers on a single chip.

- The method includes obtaining a biopsy, which is optionally fractionated by cryostat
- 25 sectioning to enrich tumor cells to about 80% of the total cell population. The DNA or RNA is then extracted, amplified, and analyzed with a DNA chip to determine the presence of absence of the marker nucleic acid sequences.

- In one embodiment, the nucleic acid probes are spotted onto a substrate in a two-dimensional matrix or array. Samples of nucleic acids can be labeled and then hybridized to the
- 30 probes. Double-stranded nucleic acids, comprising the labeled sample nucleic acids bound to probe nucleic acids, can be detected once the unbound portion of the sample is washed away.

The probe nucleic acids can be spotted on substrates including glass, nitrocellulose, etc. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. The sample nucleic acids can be labeled using radioactive labels, fluorophores, chromophores, etc.

5 Techniques for constructing arrays and methods of using these arrays are described, for example, in EP No. 0 799 897; PCT No. WO 97/292 12; PCT No. WO 97/127317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.

10 Further, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant nucleic acid sequences can be used to determine if any of the nucleic acid sequences are differentially expressed between normal cells and cancer cells, for example. High expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein.

15 In one embodiment nucleic acid molecules useful in the present invention, such as those of SEQ ID Nos 1-4494, preferably those of SEQ ID Nos 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, may be used to generate macroarrays on a solid surface such as a membrane such that the arrayed nucleic acid molecules can be used to determine if any of the nucleic acids are differentially expressed between normal cells or tissue and cancerous
20 cells or tissue. In one embodiment, the nucleic acid molecules of the invention are either cDNA or may be used to generate cDNA molecules to be subsequently amplified by PCR and spotted on nylon membranes. The membranes are then reacted with radiolabeled target nucleic acid molecules obtained from equivalent samples of cancerous and normal tissue or cells. Methods of cDNA generation and macroarray preparation are known to those of skill in the art and may be
25 found, for example in Bertucci et al., 1999 *Hum. Mol. Genet.* 8:2129; Nguyen et al., 1995, *Genomics*, 29: 207; Zhao et al., *Gene*, 156:207; Gress et al., 1992, *Mammalian Genome*, 3:609; Zhumabayeva et al., 2001, *Biotechniques*, 30:158; and Lennon et al., 1991, *Trends Genet.* 7:314.

In yet another embodiment, the invention contemplates using a panel of antibodies which are generated against the marker polypeptides of this invention, which polypeptides are encoded
30 by one or more of SEQ ID Nos: 1-4494, preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494. Preferably, the antibodies are generated against one or more polypeptides having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. Such a panel of antibodies may be used as a

reliable diagnostic probe for colon cancer. The assay of the present invention comprises contacting a biopsy sample containing cells, e.g., colon cells, with a panel of antibodies to one or more of the encoded products to determine the presence or absence of the marker polypeptides.

5 The diagnostic methods of the subject invention may also be employed as follow-up to treatment, e.g., quantitation of the level of marker polypeptides may be indicative of the effectiveness of current or previously employed cancer therapies as well as the effect of these therapies upon patient prognosis.

Accordingly, the present invention makes available diagnostic assays and reagents for detecting gain and/or loss of marker polypeptides from a cell in order to aid in the diagnosis and
10 phenotyping of proliferative disorders arising from, for example, tumorigenic transformation of cells.

The diagnostic assays described above can be adapted to be used as prognostic assays, as well. Such an application takes advantage of the sensitivity of the assays of the invention to events which take place at characteristic stages in the progression of a tumor. For example, a
15 given marker gene may be up- or downregulated at a very early stage, perhaps before the cell is irreversibly committed to developing into a malignancy, while another marker gene may be characteristically up or down regulated only at a much later stage. Such a method could involve the steps of contacting the mRNA of a test cell with a nucleic acid probe derived from a given marker nucleic acid which is expressed at different characteristic levels in cancerous or
20 precancerous cells at different stages of tumor progression, and determining the approximate amount of hybridization of the probe to the mRNA of the cell, such amount being an indication of the level of expression of the gene in the cell, and thus an indication of the stage of tumor progression of the cell; alternatively, the assay can be carried out with an antibody specific for the gene product of the given marker nucleic acid, contacted with the proteins of the test cell. A
25 battery of such tests will disclose not only the existence and location of a tumor, but also will allow the clinician to select the mode of treatment most appropriate for the tumor, and to predict the likelihood of success of that treatment.

The methods of the invention can also be used to follow the clinical course of a tumor. For example, the assay of the invention can be applied to a tissue sample from a patient;
30 following treatment of the patient for the cancer, another tissue sample is taken and the test repeated. Successful treatment will result in either removal of all cells which demonstrate differential expression characteristic of the cancerous or precancerous cells, or a substantial

increase in expression of the gene in those cells, perhaps approaching or even surpassing normal levels.

In yet another embodiment, the invention provides methods for determining whether a subject is at risk for developing a disease, such as a predisposition to develop cancer, for example colon cancer, associated with an aberrant activity of any one of the polypeptides encoded by nucleic acids of SEQ ID Nos: 1-4494, preferably, any one of the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, wherein the aberrant activity of the polypeptide is characterized by detecting the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a marker polypeptides, or (ii) the mis-expression of the encoding nucleic acid. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the nucleic acid sequence, (ii) an addition of one or more nucleotides to the nucleic acid sequence, (iii) a substitution of one or more nucleotides of the nucleic acid sequence, (iv) a gross chromosomal rearrangement of the nucleic acid sequence, (v) a gross alteration in the level of a messenger RNA transcript of the nucleic acid sequence, (vi) aberrant modification of the nucleic acid sequence, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, (viii) a non-wild type level of the marker polypeptide, (ix) allelic loss of the gene, and/or (x) inappropriate post-translational modification of the marker polypeptide.

The present invention provides assay techniques for detecting lesions in the encoding nucleic acid sequence. These methods include, but are not limited to, methods involving sequence analysis, Southern blot hybridization, restriction enzyme site mapping, and methods involving detection of absence of nucleotide pairing between the nucleic acid to be analyzed and a probe.

Specific diseases or disorders, e.g., genetic diseases or disorders, are associated with specific allelic variants of polymorphic regions of certain genes, which do not necessarily encode a mutated protein. Thus, the presence of a specific allelic variant of a polymorphic region of a gene in a subject can render the subject susceptible to developing a specific disease or disorder. Polymorphic regions in genes, can be identified, by determining the nucleotide sequence of genes in populations of individuals. If a polymorphic region is identified, then the link with a specific disease can be determined by studying specific populations of individuals, e.g, individuals which developed a specific disease, such as colon cancer. A polymorphic region can

be located in any region of a gene, e.g., exons, in coding or non coding regions of exons, introns, and promoter region.

In an exemplary embodiment, there is provided a nucleic acid composition comprising a nucleic acid probe including a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of a gene or naturally occurring mutants thereof, or 5' or 3' flanking sequences or intronic sequences naturally associated with the subject genes or naturally occurring mutants thereof. The nucleic acid of a cell is rendered accessible for hybridization, the probe is contacted with the nucleic acid of the sample, and the hybridization of the probe to the sample nucleic acid is detected. Such techniques can be used to detect lesions or allelic variants at either the genomic or mRNA level, including deletions, substitutions, etc., as well as to determine mRNA transcript levels.

A preferred detection method is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip". Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) *Human Mutation* 7:244. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment.

In certain embodiments, detection of the lesion comprises utilizing the probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligase chain reaction (LCR) (see, e.g., Landegran et al. (1988) *Science* 241:1077-1080; and Nakazawa et al. (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the gene (see Abravaya et al. (1995) *Nuc Acid Res* 23:675-682). In a merely illustrative embodiment, the method includes the steps of (i) collecting a sample of cells from a patient, (ii) isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, (iii) contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence under conditions such that hybridization and amplification of the nucleic acid (if present) occurs, and (iv) detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR

and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. *et al.*, 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. *et al.*, 1989, Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. *et al.*, 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

10 In a preferred embodiment of the subject assay, mutations in, or allelic variants, of a gene from a sample cell are identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

Another aspect of the invention is directed to the identification of agents capable of modulating the differentiation and proliferation of cells characterized by aberrant proliferation. In this regard, the invention provides assays for determining compounds that modulate the expression of the marker nucleic acids (SEQ ID Nos: 1-4494, preferably SEQ ID Nos 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494) and/or alter for example, inhibit the bioactivity of the encoded polypeptide such as those of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493.

Several *in vivo* methods can be used to identify compounds that modulate expression of the marker nucleic acids (SEQ ID Nos: 1-4494) and/or alter for example, inhibit the bioactivity of the encoded polypeptide.

Drug screening is performed by adding a test compound to a sample of cells, and monitoring the effect. A parallel sample which does not receive the test compound is also monitored as a control. The treated and untreated cells are then compared by any suitable phenotypic criteria, including but not limited to microscopic analysis, viability testing, ability to replicate, histological examination, the level of a particular RNA or polypeptide associated with the cells, the level of enzymatic activity expressed by the cells or cell lysates, and the ability of

the cells to interact with other cells or compounds. Differences between treated and untreated cells indicates effects attributable to the test compound.

Desirable effects of a test compound include an effect on any phenotype that was conferred by the cancer-associated marker nucleic acid sequence. Examples include a test
5 compound that limits the overabundance of mRNA, limits production of the encoded protein, or limits the functional effect of the protein. The effect of the test compound would be apparent when comparing results between treated and untreated cells.

The invention thus also encompasses methods of screening for agents which inhibit expression of the nucleic acid markers (SEQ ID Nos: 1-4494, preferably SEQ ID Nos. 4472,
10 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494) *in vitro*, comprising exposing a cell or tissue in which the marker nucleic acid mRNA is detectable in cultured cells to an agent in order to determine whether the agent is capable of inhibiting production of the mRNA; and determining the level of mRNA in the exposed cells or tissue, wherein a decrease in the level of the mRNA after exposure of the cell line to the agent is indicative of inhibition of the
15 marker nucleic acid mRNA production.

Alternatively, the screening method may include *in vitro* screening of a cell or tissue in which marker protein is detectable in cultured cells to an agent suspected of inhibiting production of the marker protein; and determining the level of the marker protein in the cells or tissue, wherein a decrease in the level of marker protein after exposure of the cells or tissue to
20 the agent is indicative of inhibition of marker protein production.

The invention also encompasses *in vivo* methods of screening for agents which inhibit expression of the marker nucleic acids, comprising exposing a mammal having tumor cells in which marker mRNA or protein is detectable to an agent suspected of inhibiting production of marker mRNA or protein; and determining the level of marker mRNA or protein in tumor cells
25 of the exposed mammal. A decrease in the level of marker mRNA or protein after exposure of the mammal to the agent is indicative of inhibition of marker nucleic acid expression.

Accordingly, the invention provides a method comprising incubating a cell expressing the marker nucleic acids (SEQ ID Nos: 1-4494) with a test compound and measuring the mRNA or protein level. The invention further provides a method for quantitatively determining the level of
30 expression of the marker nucleic acids in a cell population, and a method for determining whether an agent is capable of increasing or decreasing the level of expression of the marker nucleic acids in a cell population. The method for determining whether an agent is capable of

increasing or decreasing the level of expression of the marker nucleic acids in a cell population comprises the steps of (a) preparing cell extracts from control and agent-treated cell populations, (b) isolating the marker polypeptides from the cell extracts, (c) quantifying (e.g., in parallel) the amount of an immunocomplex formed between the marker polypeptide and an antibody specific to said polypeptide. The marker polypeptides of this invention may also be quantified by
5 assaying for its bioactivity. Agents that induce increased the marker nucleic acid expression may be identified by their ability to increase the amount of immunocomplex formed in the treated cell as compared with the amount of the immunocomplex formed in the control cell. In a similar manner, agents that decrease expression of the marker nucleic acid may be identified by their
10 ability to decrease the amount of the immunocomplex formed in the treated cell extract as compared to the control cell.

mRNA levels can be determined by Northern blot hybridization. mRNA levels can also be determined by methods involving PCR. Other sensitive methods for measuring mRNA, which can be used in high throughput assays, e.g., a method using a DELFIA endpoint detection and
15 quantification method, are described, e.g., in Webb and Hurskainen (1996) *Journal of Biomolecular Screening* 1:119. Marker protein levels can be determined by immunoprecipitations or immunohistochemistry using an antibody that specifically recognizes the protein product encoded by SEQ ID Nos: 1- 4494, and preferably one or more of the proteins having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487,
20 4489, 4491, and 4493.

Agents that are identified as active in the drug screening assay are candidates to be tested for their capacity to block cell proliferation activity. These agents would be useful for treating a disorder involving aberrant growth of cells, especially colon cells.

A variety of assay formats will suffice and, in light of the present disclosure, those not
25 expressly described herein will nevertheless be comprehended by one of ordinary skill in the art. For instance, the assay can be generated in many different formats, and include assays based on cell-free systems, e.g., purified proteins or cell lysates, as well as cell-based assays which utilize intact cells.

In many drug screening programs which test libraries of compounds and natural extracts,
30 high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays of the present invention which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins or with lysates, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively

easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with
5 other proteins or changes in enzymatic properties of the molecular target.

A. Use of Nucleic Acids as Probes in Mapping and in Tissue Profiling Probes

Polynucleotide probes as described above, e g , comprising at least 12 contiguous nucleotides selected from the nucleotide SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more
10 preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, are used for a variety of purposes, including identification of human chromosomes and determining transcription levels. Additional disclosure about preferred regions of the nucleic acid sequences is found in the accompanying tables.

15 The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label, and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations which are complementary
20 to the nucleotide sequence of the probe. A probe that hybridizes specifically to a nucleic acid should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

In a non-limiting example, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Nucleic acids of the invention
25 can be used to probe these regions. For example, if, through profile searching, a nucleic acid is identified as corresponding to a gene encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the nucleic acid constitutes a new material for isolating a specific protein that has potential for
30 developing a cancer diagnostic or therapeutic.

Nucleotide probes are used to detect expression of a gene corresponding to the nucleic acid. For example, in Northern blots, mRNA is separated electrophoretically and contacted with

- a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are also used to detect products of amplification by polymerase chain reaction. The products of the reaction are hybridized to the probe and hybrids are detected.
- 5 Probes are used for *in situ* hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels may be used such as chromophores, fluorophores, and enzymes.

- Expression of specific mRNA can vary in different cell types and can be tissue specific.
- 10 This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to nucleic acids of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more
- 15 preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, can determine the presence or absence of target cDNA or mRNA.

- Examples of a nucleotide hybridization assay are described in Urdea *et al.*, PCT W092/02526 and Urdea *et al.*, U.S. Patent No. 5,124,246, both incorporated herein by reference.
- 20 The references describe an example of a sandwich nucleotide hybridization assay.

- Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids, as described in Mullis *et al.*, *Met/i. Enzymol.* (1987) 155:335-350; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202, all incorporated herein by reference. Two primer polynucleotides nucleotides hybridize with the target nucleic acids and
- 25 are used to prime the reaction. The primers may be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the
- 30 polymerase, it is detected by methods such as Southern blots. When using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are
5 then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

Mapping

Nucleic acids of the present invention are used to identify a chromosome on which the
10 corresponding gene resides. Using fluorescence *in situ* hybridization (FISH) on normal metaphase spreads, comparative genomic hybridization allows total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Current Opinions in Biotechnology* (1994) 8:70-74; Kallioniemi *et al.*, *Seminars in Cancer Biology* (1993) 4:41-46; Valdes and Tagle, *Methods in Molecular Biology* (1997) 68:1, Boultonwood, ed., Human Press,
15 Totowa, NJ.

Preparations of human metaphase chromosomes are prepared using standard cytogenetic techniques from human primary tissues or cell lines. Nucleotide probes comprising at least 12 contiguous nucleotides selected from the nucleotide sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos.
20 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, are used to identify the corresponding chromosome. The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label, and detected by well known methods appropriate for the particular label
25 selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations that are complementary to the nucleotide sequence of the probe. A probe that hybridizes specifically to a target gene provides a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with unrelated coding
30 sequences.

Nucleic acids are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) 33:63-99; Walter *et al.*, *Nature Genetics* (1994) 7:22-28; Walter and Goodfellow, *Trends in*

Genetics (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at <http://F/shgc-www.stanford.edu>, and other locations. The statistical program RHMAP can be used to construct a map based on the data from radiation
5 hybridization with a measure of the relative likelihood of one order versus another, RHMAP is available via the world wide web at <http://www.sph.umich.edu/group/statgen/software>.

Such mapping can be useful in identifying the function of the target gene by its proximity to other genes with known function. Function can also be assigned to the target gene when particular syndromes or diseases map to the same chromosome.

10 Tissue Profiling

The nucleic acids of the present invention can be used to determine the tissue type from which a given sample is derived. For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a nucleic acid is expressed only in a specific tissue type, and a metastatic
15 lesion is found to express that nucleic acid, then the developmental source of the lesion has been identified. Expression of a particular nucleic acid is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods may be used to detect particular mRNA species, including but not limited to *in situ* hybridization and Northern
20 blotting.

Use of Polymorphisms

A nucleic acid will be useful in forensics, genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. A particular polymorphic form of the nucleic acid may be used to either identify a sample as
25 deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to an allele-specific probe.

B. Use of Nucleic Acids and Encoded Polypeptides to Raise Antibodies

30 Expression products of a nucleic acid, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies for experimental,

diagnostic, and therapeutic purposes. For nucleic acids to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The nucleic acid or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the encoded polypeptide, and can precipitate or
5 bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an *in vitro* expression system.

Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the nucleic acids of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins. Polypeptides are also covalently linked to other
10 larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly. Immunogens are administered to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art. According to another method
15 known in the art, the nucleic acid is administered directly, such as by intramuscular injection, and expressed *in vivo*. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for nucleic acid-encoded proteins and polypeptides are made using standard methods known in the art. The antibodies
20 specifically bind to epitopes present in the polypeptides encoded by a nucleic acid of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-1103, even more preferably SEQ ID Nos. 1-503, and still more preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto. In a preferred embodiment the antibodies bind to
25 epitopes on the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493. Typically, at least about 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve noncontiguous amino acids may require more, for example, at least about 15, 25, or 50 amino acids. A short sequence of a nucleic acid may then be unsuitable for use as an epitope to raise antibodies for identifying the
30 corresponding novel protein, because of the potential for cross-reactivity with a known protein. However, the antibodies may be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a nucleic acid of the invention.

Antibodies that specifically bind to human nucleic acid-encoded polypeptides should provide a detection signal at least about 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically bind nucleic acid T-encoded polypeptides do not detect
5 other proteins in immunochemical assays and can immunoprecipitate nucleic acid-encoded proteins from solution.

To test for the presence of serum antibodies to the nucleic acid-encoded polypeptide in a human population, human antibodies are purified by methods well known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which a nucleic acid-
10 encoded protein, polypeptide, or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, genetically engineered antibody derivatives are made, such as single chain antibodies.

Antibodies may be made by using standard protocols known in the art (See, for example,
15 Antibodies: A Laboratory Manual ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, hamster, or rabbit can be immunized with an immunogenic form of the peptide (e.g., a mammalian polypeptide or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described above).

In one aspect, this invention includes monoclonal antibodies that show a subject
20 polypeptide is highly expressed in colorectal tissue or tumor tissue, especially colon cancer tissue or colon cancer-derived cell lines. Therefore, in one embodiment, this invention provides a diagnostic tool for the analysis of expression of a subject polypeptide in general, and in particular, as a diagnostic for colon cancer.

Techniques for conferring immunogenicity on a protein or peptide include conjugation to
25 carriers or other techniques well known in the art. An immunogenic portion of a protein can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of a protein
30 of a mammal, e.g., antigenic determinants of a protein encoded by one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 or closely related homologs (e.g., at least 90% identical, and more preferably at least 95% identical).

Following immunization of an animal with an antigenic preparation of a polypeptide, antisera can be obtained and, if desired, polyclonal antibodies isolated from the serum. To produce monoclonal antibodies, antibody-producing cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) *Nature*, 256: 495-497), the human B cell hybridoma technique (Kozbar *et al.*, (1983) *Immunology Today*, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, (1985) *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with a polypeptide of the present invention and monoclonal antibodies isolated from a culture comprising such hybridoma cells.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with one of the subject polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab)₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab)₂ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific, single-chain, and chimeric and humanized molecules having affinity for a polypeptide conferred by at least one CDR region of the antibody. In preferred embodiments, the antibodies, the antibody further comprises a label attached thereto and able to be detected, (e.g., the label can be a radioisotope, fluorescent compound, chemiluminescent compound, enzyme, or enzyme co-factor).

Antibodies can be used, e.g., to monitor protein levels in an individual for determining, e.g., whether a subject has a disease or condition, such as colon cancer, associated with an aberrant protein level, or allowing determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of polypeptides may be measured from cells in bodily fluid, such as in blood samples.

Another application of antibodies of the present invention is in the immunological screening of cDNA libraries constructed in expression vectors such as gt11, gt18-23, ZAP, and ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose

carboxyl termini consist of a foreign polypeptide. Antigenic epitopes of a protein, e.g., other orthologs of a particular protein or other paralogs from the same species, can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with antibodies. Positive phage detected by this assay can then be isolated from the infected plate.

- 5 Thus, the presence of homologs can be detected and cloned from other animals, as can alternate isoforms (including splicing variants) from humans.

In another embodiment, a panel of monoclonal antibodies may be used, wherein each of the epitope's involved functions are represented by a monoclonal antibody. Loss or perturbation of binding of a monoclonal antibody in the panel would be indicative of a mutational alteration of the protein and thus of the corresponding gene.

10

C. Differential Expression

The present invention also provides a method to identify abnormal or diseased tissue in a human. For nucleic acids corresponding to profiles of protein families as described above, the choice of tissue may be dictated by the putative biological function. The expression of a gene corresponding to a specific nucleic acid is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The normal tissue is any tissue of the human, especially those that express the target gene including, but not limited to, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon.

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20 The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. A difference between the target gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased.

25

The target genes in the two tissues are compared by any means known in the art. For example, the two genes are sequenced, and the sequence of the gene in the tissue suspected of being diseased is compared with the gene sequence in the normal tissue. The target genes, or portions thereof, in the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to nucleotide probes selected from a

30

corresponding nucleotide sequence shown SEQ ID No. 1-4494. A difference in the nucleotide sequence of the target gene in the tissue suspected of being diseased compared with the normal nucleotide sequence suggests a role of the nucleic acid-encoded proteins in the disease, and provides a lead for preparing a therapeutic agent. The nucleotide probes are labeled by a variety of methods, such as radiolabeling, biotinylation, or labeling with fluorescent or chemiluminescent tags, and detected by standard methods known in the art.

Alternatively, target mRNA in the two tissues is compared. PolyA⁺RNA is isolated from the two tissues as is known in the art. For example, one of skill in the art can readily determine differences in the size or amount of target mRNA transcripts between the two tissues using Northern blots and nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing. Increased or decreased expression of a target mRNA in a tissue sample suspected of being diseased, compared with the expression of the same target mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a therapeutic agent.

Any method for analyzing proteins is used to compare two nucleic acid-encoded proteins from matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect nucleic acid-encoded proteins in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of nucleic acid-encoded protein expression in a tissue suspected of being diseased, compared with the same nucleic acid-encoded protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides another lead for preparing a therapeutic agent.

Similarly, comparison of gene sequences or of gene expression products, e.g., mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons of genes, mRNA, or protein are made as described above.

For example, increased or decreased expression of the target gene in the tissue suspected of being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of the target gene in the neoplastic tissue relative to expression of the gene in normal tissue, or differences in the amount of increased expression of the target gene in the neoplastic tissue over time, is used to assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is detected by comparing an target gene, mRNA, or protein in a fetal tissue with a normal target gene, mRNA, or protein.

5 Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an *in vitro*-fertilized embryo. The comparable normal target gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the target gene is expressed. Differences such as alterations in the nucleotide sequence or size of the fetal target gene or mRNA, or alterations in the molecular
10 weight, amino acid sequence, or relative abundance of fetal target protein, can indicate a germline mutation in the target gene of the fetus, which indicates a genetic predisposition to disease.

In a preferred embodiment nucleic acid macroarrays comprising the one or more of the sequences of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488,
15 4490, 4492, and 4494 may be used to evaluate differential expression of nucleic acid sequences in cancerous cells or tissue relative to the expression of the same sequences in normal cells or tissue as described above. Preferably, such sequences are differentially expressed by at least 3 fold in cancerous cells or tissue relative to normal cells or tissue. More specifically, the present invention provides the full length sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480,
20 4482, 4484, 4486, 4488, 4490, 4492, and 4494 which are differentially expressed in cancerous colonic cells/tissue by at least 3 fold relative to normal patient samples. Thus, the sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, as well as the encoded polypeptides (SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, respectively) serve as valuable diagnostic markers for
25 identifying and screening for colon cancer in a patient.

D. Use of Nucleic Acids, and Encoded Polypeptides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant nucleic acids, e.g., SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, preferably SEQ ID Nos. 1-
30 1103, even more preferably SEQ ID Nos. 1-503, and most preferably SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, or a sequence complementary thereto, and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Preferably, the

polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493 may be used screen for binding partners.

A library of peptides may be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175, and in PCT WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (e.g., a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (e.g., hexamers) is formed. Note that one need not include all amino acids in each step: one may include only one or two amino acids in some steps (e.g., where it is known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin. The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction may be easily driven to completion. Additionally, one may maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step. This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, e.g., 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, e.g., 20-100 candidates, and reassayed. Positive sub-subpools may be resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO

91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis may be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide may require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide may be added in concentrations on the order of the native concentration.

The end results of such screening and experimentation will be at least one novel polypeptide binding partner, such as a receptor, encoded by a nucleic acid of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding may help in developing improved agonists/antagonists of the known receptor.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989); *DNA Cloning*, Volumes I and II (D.N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis *et al.* U.S. Patent No. 4,683,195; *Nucleic Acid Hybridization* (B.D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods in Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M.P. Calos

- eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C.C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

As mentioned above, the sequences described herein are believed to have particular utility in regards to colon cancer. However, they may also be useful with other types of cancers and other disease states.

- The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

XI. Examples

A. Identification of differentially expressed sequences.

Description of the Libraries

- SEQ ID Nos: 1-4470 were derived from libraries designated as 101, 102, 103, 104, 109, 110, 111, and 112 as described below briefly and in the accompanying table (Table 1). For example, the 101 library is a normalized, colon cancer specific, subtracted cDNA library. It is specific for sequences expressed in colon cancer [proximal and distal Dukes' B, microsatellite instability negative (MSI-)] but not expressed in normal tissues, including normal colon tissue.
- The 102 library is a normalized, colon specific, subtracted cDNA library. It is specific for sequences expressed in normal colon tissue but not expressed in other normal tissues.
- Characteristics of the remaining libraries are described in Table 1.

Table 1 Library designation and description

Library Designation	Description
101	Specific for sequences expressed in colon cancer (proximal and distal Dukes' B, MSI-) but not expressed in normal tissues ⁴ , including colon ²
102	Specific for sequences expressed in normal colon (normal tissue from proximal and distal Dukes' B, MSI-matrix patients) ³ , but not expressed in

	other normal tissues ⁴
103	Specific for sequences expressed in proximal Dukes' B, MSI- colon cancer, but not expressed in normal colon tissue ³
104	Specific for sequences expressed in distal Dukes' B, MSI- colon cancer, but not expressed in normal colon tissue ³
109	Specific for sequences expressed in proximal Dukes' B, MSI+ colon cancer, but not expressed in normal colon tissue ³
110	Specific for sequences expressed in proximal Dukes' B, MSI+ colon cancer, but not expressed in other normal tissues ⁴ , including colon ²
111	Specific for sequences expressed in distal, Dukes' D, MSI- colon cancer, but not expressed in normal colon tissue ³
112	Specific for sequences expressed in distal, Dukes' D, MSI- colon cancer, but not expressed in normal tissues ⁴ , including colon ²

¹ cDNA synthesized from SW480 poly A+ RNA obtained from Clontech, Palo Alto, CA

² cDNA synthesized from normal colon tissue total RNA obtained from OriGene Technologies, Inc.; Rockville, MD

³ Corresponding normal colon epithelium from colon cancer patients.

- 5 ⁴ A pool of cDNAs synthesized from the following normal tissue RNAs (poly A+ or total) obtained from OriGene Technologies, Inc.: heart, kidney, spleen, liver, peripheral blood lymphocytes, small intestine, skeletal muscle, lung and prostate.

Construction of the normalized and subtracted cDNA libraries

10 The normalized and subtracted cDNA libraries were constructed according to published procedures (Daitchenko et al., 1996 PNAS 93:6025-6030, Gurskaya et al., 1996 Analytical Biochemistry 240:90-97). Commercially available kits from Clontech Laboratories, Inc., Palo Alto, California were utilized (Clontech SMART cDNA synthesis kit, catalog number K1052-1, and Clontech PCR-Select cDNA Subtraction kit, catalog number K1804-1). For each subtracted library, the specific or "tester" cDNA was comprised of amplified cDNA from four similar
15 sample types that were pooled together. Likewise, the reference or "driver" cDNA was comprised of a pool of sample types as illustrated in Table 1. During the subtraction process, the genes or transcripts unique to the tester are retained, and the genes or transcripts common to both the tester and driver are removed. Thus, in principle, the clones present in the subtracted libraries indicate those genes or transcripts that are expressed (or overexpressed) in the tester, but

not expressed (or underexpressed) in the driver. Reverse-subtracted libraries were also constructed in which the tester and driver materials were reversed. These libraries were only utilized to prepare labeled targets (see below).

To construct the libraries, one microgram of total RNA from each sample was
5 representatively amplified using the Clontech SMART cDNA synthesis kit. The amplified cDNA was purified and pooled to create the individual tester and driver samples that were used for the subsequent library construction. To construct the normalized and subtracted libraries, the Clontech PCR-Select cDNA Subtraction kit was utilized. A forty-five fold mass excess of driver cDNA (450 nanograms) was used for each subtraction experiment. Subtractive hybridization of
10 tester with driver cDNAs was performed twice, each time for about 8-12 hours. Subtracted cancer specific cDNA was ligated into the pCR2.1-TOPO plasmid vector (Invitrogen Corporation, Carlsbad CA) and chemically transformed into ultracompetent Epicurian E. coli XL10-Gold cells (Stratagene, La Jolla, CA). The transformed cells were plated onto LB-ampicillin plates containing IPTG and X-gal. Individual white colonies, representing those with
15 cloned inserts, were picked and grown overnight in LB-ampicillin broth. Plasmid DNA was purified using QIAprep 96 Turbo kits from Qiagen (Valencia, CA).

Sequencing of the clones

The nucleotide sequence of the inserts from clones was determined by single-pass sequencing from either the T7 or M13 promoter sites using fluorescently labeled
20 dideoxynucleotides via the Sanger sequencing method. The nucleotide sequences of the individual clones were compared to those in public databases (GenBank, dbEST, Geneseq) via Blast 2 homology searches according to methods described in the text.

The sequences derived from individual clones from the libraries described above represents a sequence from a partial mRNA transcript, since the cDNA used for making the
25 subtracted library was restricted with *RsaI*, a four base cutter restriction endonuclease that generates fragments with an average size of about 600 base pairs.

The nucleic acids of the invention were assigned a sequence identification number (see Figure 1). The nucleic acid sequences are provided in the attached Sequence Listing.

Validation of differential expression in colon cancer

30 To validate that the differentially expressed sequences found in this library were specific to colon cancer, the inserts from the plasmid DNA were amplified by PCR using vector-specific

primers. The amplification products were arrayed onto nylon membranes and hybridized with ³³P-labeled cDNAs prepared from both the subtracted library cDNA as well as the corresponding reverse-subtracted cDNA library. Each membrane array comprises approximately 3,456 clones. Four such membranes were generated comprising the clone libraries shown in Table 1 as indicated below in Table 3.

Membrane ID Number	Library Clones
101-1	Clones from subtracted library 101
101-2	Clones from subtracted library 101 and 102
103104109	Clones from subtracted libraries 103, 104, and 109
110111112	Clones from subtracted libraries 110, 111, and 112

The set of four membranes is hybridized, using techniques known to those of skill in the art and further described above, with ³²P-labeled target nucleic acid molecules obtained from human colon cancer tissue. A second, identical set of membranes is hybridized with ³²P-labeled target nucleic acid molecules obtained from normal human colon tissue. The signals of the hybridization products on the cancer membrane are subsequently compared to those on the normal membrane. A difference in hybridization, indicative of a difference in expression of the sequence in colon cancer vs. normal, of at least 3 fold is considered to be indicative of differential expression.

Using this validation technique, the full length cDNA sequences of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 have been identified as significantly differentially expressed in colon cancer relative to normal colon tissue.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All patents, published patent applications, and publications cited herein are incorporated by reference as if set forth fully herein.

What is claimed is:

CLAIMS

1. A method for detecting cancer in which one or more of SEQ ID Nos. 1-4470,
4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 are used as probes,
5 said method comprising:
 - (a) collecting a sample of cells from a patient,
 - (b) isolating nucleic acid from the cells of the sample,
 - (c) contacting the nucleic acid sample with one or more primers which
specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-4470, 4472, 4474, 4476,
10 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494 under conditions such that
hybridization and amplification of the nucleic acid occurs, and
 - (d) comparing the presence, absence, or size of an amplification product to the
amplification product of a normal cell.
2. A method of claim 1 in which said cancer is colon cancer.
- 15 3. A method for detecting cancer in a patient sample in which an antibody to a
protein encoded by SEQ ID Nos. 1-4470 is used to react with proteins in said sample.
4. A method for detecting cancer in a patient sample in which an antibody to a
protein encoded by one or more of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484,
4486, 4488, 4490, 4492, or 4494 is used to react with proteins in said sample.
- 20 5. A method for detecting cancer in a patient sample in which an antibody to a
protein having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485,
4487, 4489, 4491, or 4493 is used to react with proteins in said sample.
6. A method for identifying an agent which alters the level of expression in a cell of
a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a
25 sequence complementary thereto, comprising
 - (a) providing a cell;
 - (b) treating the cell with a test agent;

(c) determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a sequence complementary thereto; and

(d) comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

7. A method for identifying an agent which alters the level of expression in a cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, or 4494 or a sequence complementary thereto, comprising

(a) providing a cell;

(b) treating the cell with a test agent;

(c) determining the level of expression in the cell of a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, or 4494 or a sequence complementary thereto; and

(d) comparing the level of expression of the nucleic acid in the treated cell with the level of expression of the nucleic acid in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the nucleic acid in a cell.

8. A method for identifying an agent which alters the level of expression in a cell of a polypeptide of one or more of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493 comprising

(a) providing a cell;

(b) treating the cell with a test agent;

(c) determining the level of expression of one or more polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493 in said cell

by reacting said cell with an antibody specific for one or more of the polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493; and

- (d) comparing the level of expression of said one or more polypeptides in the treated cell with the level of expression of said one or more polypeptides in an untreated cell, wherein a change in the level of expression of the nucleic acid in the treated cell relative to the level of expression of the nucleic acid in the untreated cell is indicative of an agent which alters the level of expression of the polypeptide in a cell.

9. A pharmaceutical composition comprising an agent identified by the method of claim 29, 30, or 31.

10. A pharmaceutical composition comprising a nucleic acid which includes a nucleotide sequence which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a sequence complementary thereto.

11. A pharmaceutical composition comprising a polypeptide encoded by a nucleic acid which includes a nucleotide sequence that hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470 or a sequence complementary thereto.

12. A pharmaceutical composition comprising a polypeptide having the sequence of one of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493.

13. A pharmaceutical composition comprising an antibody which binds to one or more polypeptides having the sequence of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, or 4493.

14. A method of determining the phenotype of a cell, comprising detecting the differential expression, relative to a normal cell, of at least one nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the nucleic acid is differentially expressed by at least a factor of two.

15. A method for determining the phenotype of cells in a sample of cells from a patient, comprising:

(a) providing a nucleic acid probe comprising a nucleotide sequence having at least 12 consecutive nucleotides of any of SEQ ID Nos. 1-4470, 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494;

(b) obtaining a sample of cells from a patient;

5 (c) providing a second sample of cells substantially all of which are non-cancerous;

(d) contacting the nucleic acid probe under stringent conditions with mRNA of each of said first and second cell samples; and comparing (a) the amount of hybridization of the probe with mRNA of the first cell sample, with (b) the amount of hybridization of the probe
10 with mRNA of the second cell sample, wherein a difference of at least a factor of two in the amount of hybridization with the mRNA of the first cell sample as compared to the amount of hybridization with the mRNA of the second cell sample is indicative of the phenotype of cells in the first cell sample.

16. A method of determining the phenotype of cell, comprising detecting the
15 differential expression, relative to a normal cell, of at least one polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-4470, wherein the polypeptide is differentially expressed by at least a factor of two.

17. A method of determining the phenotype of cell, comprising detecting the
differential expression, relative to a normal cell, of at least one polypeptide encoded by a nucleic
20 acid which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID Nos. 4472, 4474, 4476, 4478, 4480, 4482, 4484, 4486, 4488, 4490, 4492, and 4494, wherein the polypeptide is differentially expressed by at least a factor of two.

18. A method of determining the phenotype of cell, comprising detecting the
differential expression, relative to a normal cell, of at least one polypeptide selected from the
25 group of polypeptides of SEQ ID Nos. 4471, 4473, 4475, 4477, 4479, 4481, 4483, 4485, 4487, 4489, 4491, and 4493, wherein the polypeptide is differentially expressed by at least a factor of two.

19. The method of claim 16, 17, or 18, wherein the level of said polypeptide is detected in an immunoassay.

20. A method for detecting a mutation in a test nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-4470 or a sequence complementary thereto, comprising

- (a) collecting a sample of cells from a patient,
- 5 (b) isolating nucleic acid from the cells of the sample,
- (c) contacting the nucleic acid sample with one or more primers which specifically hybridize to a nucleic acid sequence of SEQ ID Nos. 1-4470 under conditions such that hybridization and amplification of the nucleic acid occurs, and
- (d) comparing the presence, absence, or size of an amplification product to the
10 amplification product of a normal cell.

21. An isolated nucleic acid comprising a portion of a nucleotide sequence of SEQ ID Nos. 504-1103 or a sequence complementary thereto.

22. A gene which hybridizes to one of SEQ ID Nos. 1-503.

23. An isolated nucleic acid comprising a nucleotide sequence which hybridizes
15 under stringent conditions to a sequence of SEQ ID Nos. 1-503 or a sequence complementary thereto.

24. An isolated nucleic acid comprising a nucleotide sequence at least 80% identical to a sequence corresponding to at least about 15 consecutive nucleotides of one of SEQ ID Nos. 1-503 or a sequence complementary thereto.

20 25. An isolated nucleic acid comprising a nucleotide sequence of SEQ ID Nos. 1-503 or a sequence complementary thereto.

26. A nucleic acid according to claim 25, further comprising a transcriptional regulatory sequence operably linked to said nucleotide sequence so as to render said nucleotide sequence suitable for use as an expression vector.

25 27. An expression vector, capable of replicating in at least one of a prokaryotic cell and eukaryotic cell, comprising the nucleic acid of claim 26.

28. A host cell transfected with the expression vector of claim 27.

29. A transgenic animal having a transgene of the nucleic acid of claim 25 incorporated in cells thereof, which transgene modifies the level of expression of the nucleic acid, the stability of an mRNA transcript of the nucleic acid, or the activity of the encoded product of the nucleic acid.,
- 5 30. A substantially pure nucleic acid which hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1-1103 or a sequence complementary thereto.
31. A polypeptide including an amino acid sequence encoded by a nucleic acid of claim 25 or a fragment comprising at least 25 amino acids thereof.
- 10 32. A probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 12 consecutive nucleotides of sense or antisense sequence selected from SEQ ID Nos. 1-1103.
- 15 33. An array including at least 10 different probes of claim 32 attached to a solid support.
34. The probe/primer of claim 32, further comprising a label group attached thereto and able to be detected.
35. The probe/primer of claim 34, wherein said label group being selected from radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors.
- 20 36. An antibody immunoreactive with a polypeptide of claim 31.
37. A method for determining the presence or absence of a nucleic acid which hybridizes under stringent conditions to one of SEQ ED Nos. 1-1103 in a cell, comprising contacting the cell with a probe of claim 32.
- 25 38. A method for determining the presence of absence of a polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to one of SEQ ID Nos. 1-503 in a cell, comprising contacting the cell with an antibody of claim 36.
39. An antisense oligonucleotide analog which hybridizes under stringent conditions to at least 12 consecutive nucleotides of one of SEQ ID Nos. 1-503 or a sequence complementary thereto, and which ~ resistant to cleavage by a nuclease.

40. A test kit for determining the phenotype of transformed cells, comprising the probe/primer of claim 34, for measuring a level of a nucleic acid which hybridizes under stringent conditions to a nucleic acid of SEQ ID Nos. 1-4470 in a sample of cells isolated from a patient.
- 5 41. A test kit for determining the phenotype of transformed cells, comprising an antibody specific for a protein encoded by a nucleic acid which hybridizes under stringent conditions to any one of SEQ Nos. 1-4470.

Figure 1

SEQ ID NO: 1 GGTACATTGAATTACAAAAGGATCCAAGAATATTGAAATAGTTACCAAAAAA
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SEQ ID NO: 32 ACGCGGGACTCAAAGAGACTAACAGTATTGTAAATTCTAAGCTCTGTAAAGA
AATTCCAAGTTAGTTTAACTACAGAGCTACAAAAATGTCACAGAAAAATTGTTCTAGTGGCAATAT
TAAAGAAATAAAAAATTATTAGGCCAGGCACGGTGGCTCACACCTGTAATCCTTGCCTTTGGGAG
GCTGAGGTGGCGGATCACCTGTGGTCAGGAGTTCAAACCCAGTCTCTACTAAAAATACAAAAATT
ANCCAGGTGTGGTGGCCATGCCTGTAATCCAGTACTTTGAGGGGCTGAAGTATGGANAATCNNTT
TGAACCCANGANGTGGAGGCTNGNANTAAGCCCCAAAAATGNGGCCNNTGTATT

SEQ ID NO: 33 AATTGNGCCCTCTAGATGCCANGCTCGAGNCGGGGCGAATTCGAGCTCGGTA
CCCGGGGATCCTCTANAGTCNACCTGCAGGCATGCAAGCTNACNTNTTCNATTGAGAAGCCCCAA
CAGCNTTGNNGNCATCATNGACCTGGCTNCCTCCTGCACTGAAAAA

SEQ ID NO: 34 ACGCGGGGCGNGTGCTGTTGGGAGTTGCTTGGAGGTNGGCGGCGCGNGGGCTN
AANGCTAGCAAAACCGAGCGATCATGTNGCACAACAAATTTACTATTCCGACAAATACAACCTACN
AGGAGTTTGNGTATCNACATGTNATGCTGCCNAGGACATATCCA

SEQ ID NO: 35 ACAGCACTCCATTACACAGAGTAACCCCACTCTTGATTAATCTGTTCTAAAG
TGCCAGTATTATTACACTTTTTTTTTTTTTTANCCAAAAAGTCTGGCCAGTTGTGGCATCAGGTGAA
GATTGTCACTCCANCTCTATTATCATTNACATTNANCAAGGGAATTCNATAATNCAGNTCTATG
TCCCTGGTCCCNAGAAGGTTTACNTNGNCATTGGCANCNCTAAANTGGNGAACTTNTTCCNGNTCTN
GGANCNTGAAAGNGGAGNCNAGGTANTGGCTGTTCAAAGG

SEQ ID NO: 36 ACCATTNTATTTAGTGTGTAGGAAATGTTGGGTACTTCTTAAAAACGAAAC
CAAAGAAATCAAAAAGTCCCAAAGAAAGAGGAGAGTGACATTGCCTAGGGCATGGGCCAGAGTT
TGGGCGATCCTTCAATNGGAGGAANANGCGCTCANTTAANTAGCTCACACTGTANATNTGGANAC
ACCATATGGANATACGGAGTTAAGNTNGGTGGATACTAGGAATTAANTTCTCCCCCTAANGC
TAAATNTTTCAGNCTTGANAGATNANTNGTAGTTCTAGAAAAANANATAAAGTTTACTGNAGAA
NGTGGGAGGGAAGGACGGCNTGGC

SEQ ID NO: 37 ACTTTTTTTTTTTTTTTTTTTTTTTTNGANACANAGTCTTGCTCAGTTGCT
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AAACTCCNNGGCTCAAGTAATCCTTCTCCTTGGCTTCCCTAAATGGTTGGATTACAGGTGGGAGT
CACTCTGCCTGCCCTGNCAAGTCTTTNCCATNAAAACTTTTATGTTTTTTTTTAAAT

SEQ ID NO: 38 TGAGAGGAAGTTCCATCGCCTAGGTTCTGGGAGAAGCAATACGTCACAATCC
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TTGTAAGTTGATGAGCCCTGAGATATGTACAATGTCCCCCGAACAGATTCAAGGCAGGAGAT
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AAAGAGCAACACCAACTTGGTATTGAGGCCAACCATATGCCACAATCCACTCTGGGAGCAGTTGT
CAGGCAGGAGAAAAGAGTCACAACACCTGGGTTATGGCCCAATACATATGTTACAATCTTGCCCA
TGGGCAAAAGCCAGGTTGAGACAGGAGAATCACATTNAA

SEQ ID NO: 39 ACTTCAGCCTGGTGACAGAGGGAGAGTCCATCTCAAAAAAGAAAAA
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ATCATGAACCTAGTTTTTCCACACTGGCCAGCCCATCTTTGGCTTTTCTCTCACGCTTTCAACTAA
TGTAACAATTAGTCTGGCTATGGTCTAGTTAAGGAAGTAATTTGAACACGAATCCTCCAAAGTG

GCTACATTTGTTCTTTCTACTGTCACATATAAGAGTGATGAAGTGCATTGATTTTAAAAAGCTGGTG
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AAATTATCAGTAGATATTTATAAGTGAGGNATCTTATATTGGTTACTTA

SEQ ID NO: 40 ACGCGGGCAACTACGCTAAAGAATTTTGAGAACACCAGTGTGTCTACATTCA
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ATCCCTACCAAAGTTCATCTTATGCCTCTTCAAATCTACATAGCTTATGTCTCCAACCTTATGTTCTC
CCATTCAACTAATTAATAATAAGCATTTTGTTCCTTTAGCTAATTTAAGTTTTCAAATAA
GGCCACAACAACAGGTCTCTGACAATCTCCAAATATCCTTGGGTTTATCACATCATCTATATTTTC
CAACAGGGACTTGGGCTCTACCAAGTATTCAGTATAAATCTTTGTAAAGTAAACATGGCCGGGT
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CNGAGTCAAGACCAGCCTGGGCAAAATGGGTGAAACCCCAT

SEQ ID NO: 41 ACTAAGGTTACAGCTGTTCTGTTGGTCTAGGCTCTGAGTAGACAGAGCCAA
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AGTTGTAGCTGCTCAGCTGCAGAATGGTGTGCTGCCATTAGTAGGTGGTGTAGTGGCAGTGAA
GCCTAGGGTATGGGAAGATACAGTGGCTATAGACCCCAAATGAGAAGGCACCCTAGCAGTGGCT
TCAGTCTCAAGATGCCATTACACAGCAGCAGCTTGGATAATAGGGCAGGAGGAGACACAATGTGG
GCTCCTTGTGGAGTAACATAGTCATGTGAACCTCCAGGCAACCCCTCAGGCTGGGCTTAAGGACC
TGTGAGGACTACAGTGATCTCCATGAGCCAAAGATGTGGGTGTCCACATTTTAATTTTGATTGTC
TGAAAGGCCTTCCTGCATACCTTTCTNTTGAAGGAGAGTCCGCTTGGCTCTTGACCTNATNCC
ACTAGGANAGACNAGATGGTNAAGCAAAATGTTTCATTCCCTTTTTAT

SEQ ID NO: 42 GAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCGCCAGTGTGATGGATATC
TAGCATAATTTCCCCTTAGCGTGGNCNCGCCGATGTACTGAANTATACTNGTCCNATGCTACAGG
AATTCTTTGGAATTTTATTACTATGNTTNTTCTAAGAAGAGGTATGNACCAA

SEQ ID NO: 43 ACGCGGGGACTGAGAACAGGGACAGGCGACCCGACCCCGAGGCCCGGTG
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TTGAAAAGGCAAGACTCTGCCAGATCACAGCAGCATGTCAACCTCAGCCCGTCTCCTGCTACCCA
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GTTCTTGATATTGGCCCAAAAGAACATTTTATTGATGCTGAAACAACACTGTNAACAAATGAA
ACTCANGTCATTGGAATGAAGCGGTGTGGTGGTNTCTTTTTANATATTTGCATTCT

SEQ ID NO: 44 ACTGGTGTGGAGTGAAGCAGGGCCACTTCTATGGAGAGACTGCAGCCGTCTA
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TGGCTGTAAGAGGCTGAAAGTGGAGAGTGGGAAGGGAGGGGACATTTAGGTCTATATAGCCTCG
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TAACCTCGGCATTNAGACAACCTCCCACTGAATGAGTGGCTCACACCTGTATCCCATCACTTTGGGA
GGCCGANGTAGGCANATCACTTAGGCCNGGANTTCAACACATCTGNTGACATGGAGAAAAT

SEQ ID NO: 45 ACTTTTTTTTTTTTTTTTTTTTTTTTGGNTAGTTCTATGACTATGTCTAACAG
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TGTGTGTGATGAAAAAN

SEQ ID NO: 46 ACGCGGGATATGCTTGCAAATTCATTTAGTTAAATTAACACAGTCTTTAAAA
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GCCAATTCATAGTCATGATATCTTCAAATATCCTAACCTTATCANCAAAATCTTTGTTCTTCCAAA
TTTAGCTACTTATTTAAACTACATAATGTCTTTTTTTCCTTTTTCTTTGCAAGNTNACATAATGT
NTTTTTTNTCTGNGCTACNAAGATGTTTNCCTATNTATGAAAAGNNCTANATTATTGCCAGTTGC
GGGTGGNTTA

SEQ ID NO: 47 ATGNGGATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGA
TATCTGNTGGAATATCCGCCTTTTCGAGCGGNCGCCCGGGCAGGTACAAAAGGAACTTGCACATTT
CNCAAAAAGCAATTTCACTTGAACCTCTGCTTAAAAAACTGNTTCCNANCANCGTNATGAANACA
AACCANTAAATGTTAATNAAANCTACAAGATTTATGGCTCTGAGAGAAATATACTGANTGATGCA
TCNTAANTATCCACAAATACCNATTAAATGNAATGTTTAATACTATATNAT

SEQ ID NO: 48 ACAAGTAGAGAATGTCTTTACTTTTTTCCAACCACTGCCATCTCTTACTCTGAT
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SEQ ID NO: 49 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCAATATTTAAAAATATAATTG
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ANATTTTAGGGGATTTCTATGCAAAACAATCATGTTGTCTGTGAATANACATGGCTTCAATTTATTT
TCAATCTGTATGTCTTTATTTCTTTTGTCTTACTGCAANGGCTAGGACCTGTAGTGCAATTTTGAA
TATGAGNNGGGAAAGNNGGACATCCTCAGTTTGTCTTAATCTTACAAGGGGAGCATTTAGTCATTC
ACCTTTGAATATAAAGTTAGCTGCAGCTTTTTGNGGATCCCATTATGAGGTTGAGGAAATTTCTC
TCTAAATNGTAAGAGTTTGTATCATCAACAAATGTAAATTTCTATCAAAATGGTTTCTGATCTATTG
ANAGANCAAAATGCTTTTCTTCTATCTGN

SEQ ID NO: 50 ACATTTACATTCTGTAAGAGATTGAGCCTGAACTCTCTTAGTCATAAAAAACAT
CAAATGGCCACATGTCCACTACCAAGCTTCTCTATGTTAAAAAAATAATAAAAGCAGTTTAA
CCTGAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 51 ACGCGGGGTATGGGGTTTCTTTTTGAGGTGATGGAAATGTTCTGGAATTAGAT
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ATTGTATACTTTAAAAATGTTGAATTTTATGCTATGTGAATTATATCTCAACTTTTTTAAAAAGAGG
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AANACAGGTTGGCCANACCATGCANCAGTNGCCTGTCAACATNTGAGACCTTCTTCATAAAATTG
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SEQ ID NO: 52 ACGCGGACACAGGCAGTCACTAAAGGGATGGCAAAGACAGAAAGAAATCTT
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CTTATTTTAAATTTGATTGCCTTACGTCAACAGCAGTATTTGATCTATACCATGGCTGCCTAAGT
GATGTAGCGTGATTGCAGTAAATATGCCTTGATCTCACATACACTTTGTCTAGG

SEQ ID NO: 53 ACTNTGTGATCTTGCTGAAGACTACAGGCAGCCAANTGGTTCCAGATACTTC
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TNTTGATTTAAGGANAAAAATAATCANAATGAATTTNTTGCATAAACNTTAAAGTCA

SEQ ID NO: 54 ACGCGGGGAGGCTAGCCAGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTT
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TAACCCCATGTCTACAAAAAAAAAAAAAATTAGCCAGGTGTGGTGGTGGNCACTGTAAATCCNAGN
TACTGANAAAGCTGAGGCAAGAGAATTGTNTNGAACTGGGGAGGNGGCTNNACCAGGNGAGGCA
NANGTTGAA

SEQ ID NO: 55 ACCACTTTGGAATGCACTGACTCTTTAAAGCCACATAAATGTTTCAAGCCATT
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TTTTATCTTCATTCTTGGTNGGAAAAAATAAATCTATTATTGAATCTTTTACACACTNNCNTTAA
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GATNATACCAACCCCTTGGGAAGGGGGGGNGCNTTGGCCANCCNAAANCAACCNATGGGGNANG
GGCAGNCTA

- SEQ ID NO: 56 ACCAGCGGATCGCANCGTTGCCATGAAATCTGTGCATTTC AAGGCCCGTTTGGATGTGGGTAACTCAGTGGTTCTCAGGTGGGGAGGTATCATGATTACCTCCAGGGAATACTTGGCCATGTTTGGAGACCTTTTTGGTTGTACAGCTAGGGGAGGGGTGCTATTGGCATCTGGTGGGTCAAGGCTAGGGATGCCGNTGAATATTCTACANTCCACAGGACCAACCCGCCNCAAAGAAGGNTCCCANCTGATATGTNAGGCTTGCCACNGGNGGGGAAACCCCTNATTAAAGTATTA AAAATTTGAANCTACATNTNTTTANTNCCNCGGGCTTTTGTTTTA
- SEQ ID NO: 57 ACAACCACTATGGGGAATAGTTTGGAGGTTTCTCAAAAACTAAAAATAGAGCTACCATAAGATCCAGCAATCCCACTGCTGGGTATACACCCAAAAGAAAGGAAATCAGTTTATCTAAGAGATATCTGCACTCCCATGTTTATTGCCAACACTATTACAATAGCCAAGATATGGAAGCAACCTAAGTGCCATCAACACATGAACAGATAAAGGATATGTGGTATATATACGCAATGAAGTATTATCAACCATAAAAAGAATGAGATCCTGACATGAGGTCATTATGTTAAGCAAAATAAGCCAGGCAAGAAAGACAAACATCACATGCTCTCACTTATCTGTGGGAGCTAAAATTAACAATTGAAATCATGGAAATAGAGAGTAGAAGGATAGTTCTAGAGGTTAAAAGTNCCTCGGCCGACCCNTTAAGGCNATCCACNCCTGCGCCGTACTATGGTCCACTCGGACAANTGGGNATATGGATACTGTTCTCTGGGAATGTNTCCGTC
- SEQ ID NO: 58 ACGGCCAGGGCTATTNTTGAATGAGTAGGCTGATGGTTTCGATAATAACTAGTATGGGGATAAGGGGTGTAGGTGTCCTTGTGGNAAAAGTGGNCTAGGGCATTTTAAATCTTNANCGGAAAGCNTATANTCACTGNCNCCGCTCATAAGGGNTTGNCTTGGCNNGGTTTATATATAGTNGGGGGGTGCGTGTAATTNAATGA
- SEQ ID NO: 59 ACCTAGAAGAGAGGCGNTTCAAAGAAGTAGTGAAGAAGCATTCTCAGNNCA TANGCTATCCCATCNCCTTNTTNGGAGAAGGAACGAGANAAGGAAATTANNGATGATGAGGCTGAGGAANAGAAAGGTGAGAAAAATGAGGTAAATCNTTATTGATTGATGAAAAANCCAAAAATC
- SEQ ID NO: 60 CGCGGCGAGCTATCNTTTGAATANTGAGACAGAAATNAATCAATATAGAGGCTGTGCACGGTGGATCACGCCTGTAATCCAGCACTTTTGGGAGGCCANAGGCAGGTGGATCGAGACCATNCTGGCTAACATGGTNAAACCCGGTCTTTACTAAAAATACAAAATTTNCTGCNTGNGGGTACCGGNCACCNGTAT
- SEQ ID NO: 61 ACGCGGGATATCAATAATGGGTCTGATATAGACTGAGGATTTCATATTAACCTCACATGCCTCCAAAAAGGCAACCTAGAGTCATGACTAATACATGGAAATTTGGTGCCTCCACCCGAGCTGACCCCTTTGGTCTCTTAAGAAAAGAACTAGAACTTTTAAAGGTCTGAGATCAAGATCTTACTTTTTTTGTTTAGTAAGTATTTAGCAAATATTTTGAATAATTTTCCATGAGAAGCATGAACATGAGCTACATGTTTGAAGTAAAGGATGTAATTGTAGCTTCCACTTGCCTNTCAACATGGAAATGCTAGAAAGTTTACTTACAGGGTTCAAAAACATGTATACAGTCATCCCTCTGTATCTGNGAAGGATTGATTCAGGACCTTTCACGGATACCAAAATCTGNANATGCTNAAAGTCTTTGACATAAAATTTGGCATNTNTTNNCATATNNACTTATGCNNNTCTCCTATATTACNNNTANNATTTNTCTACATTACTTATTTTACC AAANNCAATGTAAATAGTTCTTTAACTGGCATTGGNTTAAGGGGAACNAC
- SEQ ID NO: 62 ACGGGGGAGACTGTGGAGCANTTATTCAAAACTCGGAGGGAGTGGCATGGGAGGATCCATATAATTTACGCTAAATTTGTCNCGTCTGTTTGTGAAATGTGAAGNGCACATTGT TTTCTGGAAGGCAAATTTCAATTTNTTATACCACCTTGCCAGAAAGATCTGTGATCCCAANGAAC TGCTGTGTTANAAACAANGACAATCAATTTTANGCAANAAATGATGGTTCCAACNAGGGAGGGAGTAACCATGGATATTGCTGAAATGCAGTTGGTGCCAGGGATTATTANGACATGATTAGTTCTGNAATCATCCCTAANGTAGCGATGAAGTCTCNCTATGTTGCCAGNCTGATCTCAAACCTCCGGCTCTAAGTGATCTCCACCTCATCACTCCCAAANGTGCTGGGAATTAAGGCCCTGANCCATTGTNGCCCAAACCTNAC
- SEQ ID NO: 63 GGGGACTGAGAACAGGGACAGGCGACCCGACCCCAAGGGCCCGGTGCTCAGGACAGAGTAAAAGGCCAAGCTATGATAGCAACTGGTGGAGTGATAACTGGCCTGGCCGCTTGAA AAGGCAAGACTCTGCCAGATCACAGCAGCATGTCAACCTCAGCCCGTCTCCTGCTACCCAAGAGAAGAAGCCCATCAGGCGCGGCCCGGGCAGATGTTGTGGTTGTCGTGGCAAAATCCGGCTTTATT CCCCATCTGGTTTTTTTTCTTATTTTAGGAGTGCTCATCTCCATTATAGGAATTGCTATGGCCGTTCCTGGATATGGCCCCAAAAAGAACATTTTATTGATGCTGAAACAACACTGTCAACAAATGAAACTCA GGTCAATTCGGAATGAANGCGGTGTGGTGGGTTGCTTCTTTGAGCACATTTGCATTCTGATAAGATGAAAATGCTTGCCCATTCACCATGGGGATTGGCATTTTTCATTTTCTGCTAATGCCATCTTCA TGAAAACCGTGACAAAGAGACCAAAATCATACCATGAGGGATATCTTTCCAGTCATTGACATTCACACGCTAAGAAATAAGGAGCAAAAGCAAATG

SEQ ID NO: 64 ACGCGGGGCGGTCGAAAAAGAGATAAAGTTGAAGGAAATAAAATTGGCAGC
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TGAACANTTCANGAACCNATGCTTGAGAAAAAGAAAAANTCTNTCGAGCAGCTTTCNGATCTANAA
GNTTCCAACGAGTNCTTATAAATAC

SEQ ID NO: 65 ACGCGGGCACCACGATGAAAGGGCACTGGCAATGGGAATGGCATCTATAGT
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SEQ ID NO: 66 GGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGANACANAGTCTCACTNTGTT
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SEQ ID NO: 67 ACTGAAGTCAAAAACAGCACATGGGCCTTGACGATCTGGGGTGACGCAAGC
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SEQ ID NO: 68 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGACGGAGTCTCACCGTGTGCCCA
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CTGGTNTTTNACTCTNGCCCTGGAANTNCCCCACCTTTGGC

SEQ ID NO: 69 ACTTAAAGTAATGGTGATCCTTATTCAGGGCTTCGCCGCCAGGATTTCTTGC
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SEQ ID NO: 70 ACCACCTTCTTAACACAAATGATTTAATTTAACCATTAAGTCAAGTCTGCAAT
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SEQ ID NO: 71 GGCATGCTCNAGCGGCCGCCANAGTGATGGATATCTGCANAATTCGCCCTTT
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SEQ ID NO: 72 ACTTTTTTTTTTTTTTTTTTTTTTGAAAANATGAGGTTTTGCCATATTGCCCAGG
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CTTNTCTTCCAAGTTTTT

SEQ ID NO: 73 ATCTTTATATTATTTNCTTAAATTGATTGGGCCCTCTAGATGCATGCTCGAGC
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TAAAGCAAGAAGTTGGAGAATATGAGATACATCTCATCTCTTTAAATACTTAAATGACTTCCCT
CCTCCGGAGTNTATCACAATTTTCGNGATNNANNTGACNGACGTANGTGAANACNCTGTTGGGA
ACTTACANACTAAACTTG

SEQ ID NO: 74 ACCAGCCCAGAGAGGCTCTCTGCTACCTGACTTTCCTACTCTATGGTAATGT
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CATGCCTAAACTCCACAGGAATGAGTTGTCTTTACTATGTGAGAAGTCAAATGTAATGTTGGCAA
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TTGCTCTATTCTGCATTAGGTACGCCAAACGCTTCTGTCAAGACTCAGTAACCTTACCATAACAT
TTTTGTCTATTCTATGGTCTATGGGCAGGAATGTCTTATAAAGCACACATTACTAAGTGCTTTATAT
ACATCACCTATTCTTAAAAAAATTCTATAAGAAGTATTATTNTCATTTAGAGATTAAAAATTGA
AGCTCCAGGCCCTTACCAATTTTCAACTAATAACTAATTAACAGGGCTGGGATTGAAATTCAGGCT
ACCTNCTTTAAATNTGGTTTTTTCATTGGTTAGG

SEQ ID NO: 75 ACTNTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGGTGTTGTTTCACTTCTTGGN
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TGTTTTCTTCGGAGTTTATACCTTTAGCTTACATTTAAGTTTTTGATGCNTTTANAGTTAATTTTAA
CACATGATANAAAGTAGGGATTCAAGTTTNTCTTTNGCAAATGAATATCCACGTTGCCAACATC
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SEQ ID NO: 76 TTTCAATTTTGTANGCATTTGGGCCCTCTAAAGCATGCTCGAGCGGCCGCCAGC
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CTNTGNTATCCTGNGGAACACACAACATTACAGTGAANCCTTCTGTGAAAGATGCCAATGGTNTA
GTATGGAAGACTGGTCCCAGAACTACCATATTTGTAAATTCCTGGAAGACCTTATTCNCAGCAA
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SEQ ID NO: 77 ACTTAAATGTAGTAGATTCTATGCCTATGCATATTTCCCAAATTTGTAAGTG
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AGAGGAGACTAAAGCACCCCTCCAGGCACAAATTAACCAAGTTCCCAAATAAACCTTTTACCAAC
TCACTATGACAAAAGCATAGATGAGAGAAATAACAGCATGCCAGGTTCAACCGAGTCCATAGGTGA
GTGTAGCTGCTCANTAAGTGTGGTTGATTAAATTAAGGGTGACTNAAATCCATGCCCAAACCTGAG
TCCTTACNAAATGCCCCATAAAATTTAAATTTAGAAGAGTTAGTAAAGACTTCTTGAATACTAA
CTGCATGGAGATACTACACAAAACAGTCATNTTAATTCCTACANCTTCANAACAAAAGAGTCC
AACTGAAAGTAAGATCCCTGTNATTATGTTGATCCTGGCT

SEQ ID NO: 78 ACCTTTTTTTTCTTATTTAAAGCACAAAGAGGCCCATAAATCTTGAGTTACTTTA
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SEQ ID NO: 79 ACTTTTTTTTTTTTTTTTTTTTTTTTNGANACATGGTCCCGTTCTGTCAACCCAGG
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SEQ ID NO: 80 ACGCGGGGATTCTGAAGCTGGCAGCATTGGGCGGAGATGTCTCGTCCGT
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CTATTCCGGTTAAATCCATTCAATCCATTCCATTCCATTCCATTCCATTCCATTCAATTACATTNC
NTTCCATTCTATTCCGAACCTCGGCGGACCAAGCTAAG

SEQ ID NO: 81 ACAGTTCCCATCACGTATGTCAGTTTTGTGTATGCAGCAGAAATGATACCTA
AATAAAAAACAAGGACACATANAACAGGAGGTGCTGACCAAAGTCTTNAACANGGAGAGGGGAG
TAAAAAGGGGAAAGGAAAGAAAAAGTAACCTATTATCAGCATCAAAGTATGTGGTACCTGC
CCGGCGGNCNTCCAAAGGGCAN

SEQ ID NO: 82 ACGCGGGGACATAAAATNTNCTTTAACGCATTTAAATAAACAGAAATCATAC
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CAAAATTTGGAAATAAATATATCTAAATAACTCATGGGCCAAAGAGGGAGCTAGTGTAAAAAC
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AAATGGAAATTGNNAACAGAAAAATAGAGAAAAATAANATGGAAATTAANGTTAGGTATTAT
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SEQ ID NO: 83 ACAAGGAAAACTACAAAATATGTATGAAAGAAATTGGAGATGACACAAACA
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CGTGGTTTGATTAAAAACAGACNCTTCCCATGGAACAGAATAGATACCCAGAAATNATCCTTT
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TAAACGGTGTAGGAAACTAGATTTCCTTATCCAGAAGAATGAAGTGAAGTCTATCTTCACTATN
TACAAAAGCCAACTCAAGATGAGATTAAANGCTTAT

SEQ ID NO: 84 ACCGCCGGGCANGTACNCGGGACCATACCATATCCACCAGAGAGTGACTCC
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SEQ ID NO: 85 ACGCGGGAAGCGTGAGCCACCGAGCCCGGCCACAATGTGTTTATATACACAA
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CACCGTAGAATCTAAAAATAGTCAAAATCATAGANAAGTANCATGGTGATTTCCTGCGTGTTA
ATTACCAATCTTCCCATATAGGTAAATCCATATGGCACAACTGCCCTTACTTGNAGAGCCACCNC
CCCTGTGNCATGAAGTGNAGGTGNTCTTCATGGTTGCTTGGCCANTCAGGGCCTGTATCTCTTC
ACACTACCTTACANTTCNCAACTGNCTTTGNTTTTNGTNGGTGTTGNGTAGTATTTATTA

AAANG

SEQ ID NO: 86 ACGCGGGGAAAAATGGGGAGCAGGAGGCTGACAATGAGGTAGACGAAGAA
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CCAANCTTGATATTCNCAGGGGANGAANANACCAAANTTTCAGGNCNTNTTTTTTAAANNCTT
GNCNNANCNCTNTGCNATTTCTNCNTTGGCNCNTNTTTTGGTTCNACTTNTCCANCTTGNNTTAT
TGTTATTTTNTTTTTT

SEQ ID NO: 87 ACTCTGTATACACACATGAGAATGACAGTGACAAAGGCAAATAATGTCTTAG
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AGGGTAAGGCAGAGTAGGTAGTTGCTCTATTATGACTTTTCTTGGTTCAGCAAAATAAAACCGC
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SEQ ID NO: 88 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTGTTTTGANACANAGTCTCA
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SEQ ID NO: 89 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTNAGAANANATGGGGTTTNTCCATGTT
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SEQ ID NO: 90 ACGCGGAAAGGGACATTTCAAAGCCTATTGATGCTTGTAGTAAAAACCTTA
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CATGCGATCTGTGAAGATACATCTTCACAGATTCATCTGTGGATTCATCTACAGAGTAAAAAGCTTT
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SEQ ID NO: 91 GAGTCTAGCTCCACACAGCAGTCGGGCCTGCCTCCTGCAAAAGAGGGGAAAG
AGAAGAANGAGAAACCCANGANCAAAACAGCCCATCATATTGCCAAANACATGGAACGCTGGGC
TAATATGTTTGAATAATCACAAAGAAAACTTTAAAAATAGNCTNTCATCTGNCAATTCCTTTGA
TGGAANAANAAAGGANAAGAATCTNTTTGNA

SEQ ID NO: 92 CGTGGCGCGGCCGAGGTACTTTGACCAAAAAATTGACCAAAAGTAAGAAAAAT
GCAAGTTCTAAAAATAGACTAAGGATGCCTTTGCAGAACACCAAAGCTTCCCAAAGGAAGTGTA
GGGAAAGTGGCCCCCTGTCTCCTGGAAGTGGNAANAAGCCCTGCTCCCTGGCCTTTGGGTTGCTT
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SEQ ID NO: 93 ACTTTTTTTTTTTTTTTTTTTTTTTCAANATGGAGTCTTGCTCTGTACCTAGG
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TCTGTATANATNAAAAAATGGAAACTGANACCCGNGTACCTTGGNCGGGACCACCC

SEQ ID NO: 94 ACTCCGAGGCTTTANATTNATTTTGGGTCTTTGGGGGGGACCTNTATCATTAC
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AATCCNATCCC

SEQ ID NO: 95 GCCGTGGCGCGGCCGAGGTACTTTTGATATTAAGGCTAATTTTTAAAAACCC
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SEQ ID NO: 96 ACTTNTTTTTTTTTTTTTTTTTTNGGACAATTGTTATTTAGTTTTATTTCTATAA
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CCATGGCTCACAAATNTCNNGCCTTTTTTCANTTTTCCAAA

SEQ ID NO: 97 ACAATCTTACTATCTTTCTTTTCAGTTTGTGCCTTTAATTTCTCTGCATACCTC
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SEQ ID NO: 98 ACTTNTTTTTTTTTTTTTTTTTTNGCGGTGCCTCTAATACTGGGTGATGCTA
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SEQ ID NO: 99 ACGTGTCTAAGTTCTAGAGCCTCCTGACGTGAGCATGGCTGAGAGTGAGGGA
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CANGGGTTTTTGAACCAAGGGAAACCTGGANACCACCTTGAAGGAAATTAAGCGGTTNATTATN
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SEQ ID NO: 100 ACTACCTGGGGGGGTTGCTTTCTGCCTTTTCTCTGTTGGTCAACATCTTCT
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ATCCNTCT

SEQ ID NO: 101 ACGAGTGGTGGAACAACAGTGCCCTGGGGAAACAGCCCATACCATCGGGCTCCT
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ATATCCTGNGAAGAAAAATAAATTNTNTTCATTCAAAAAAAAAAAAAAAAAAAAAANTCCTG
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SEQ ID NO: 102 ACACCCGCACGAGGAGCGGGGACGGCGGGCGCAGAAGTGGGCCACCATATC
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AGCAACNAGTTTGTGCCANATTTGGNAAAGNGTCACTTGTGAAANTANCTNTCCNGGANCAAGG
ANGCTTNCCTTGAAAAAATATTCATTCTTNTTGGGCTNGGNGGATGGAATGGGGATAAACAGG
GGT

SEQ ID NO: 103 TNGATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATAT
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TGGGTGGGGGTANGGGT

SEQ ID NO: 104 ACNCGGGCACTCACAGACATGACACACTCACAGACATGACACGCTCACAGAC
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GCACCGATGTCTACACAGATCAATTNACAGACACTGTGACACAAAGTTACACAGTCATGTGCAC
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SEQ ID NO: 105 ACTTTNNTTTTNTNTTTTCTTTTAAAAATTTGAACACATATTTNATAATTT
GNGATAATGGTTTTGNGGCTAACTCNAAAAANGAACGGCCCAATCTTAAAAAGTCTACNCTGA
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SEQ ID NO: 106 ACTTTCTATGANAAGCGTATGGCCACAGAANTTGCTGCTGACTCTCTGGGTGA
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NAGGTGNTCTTGCCATGGCCGAGTCTCCTGTACTGATTAAGGGNACT

SEQ ID NO: 107 ACAAACAATGNTTATTTGTTGTAAAGTGCCAGGTTTATATTTANNTAAACAT
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TAATCTN

SEQ ID NO: 108 ACGCGGGGCTCTTTTCCGGCTGGAACCATGGAGGGTGTAGAAGAGAAGAN
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SEQ ID NO: 109 GCGTTGGGCCCTCTATNGCATNAATCGAGCGGCCGCCAGTGTGATGGATATC
TGCAGAATTCGCCCTTAGCTNATCCGGCCGAGGTACAANACNCTACGGGAACAGNTTGCCTCCCT
NCCAGCCTCAACCACAATTCTTCCATGCTGGGGCTGATGTGGGCTAGTAANACTCCAGTTCTTANA
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SEQ ID NO: 110 TGGGCCCTCTANAGCATGNTCGAGCGGCCGCCAGNGTGATGGATATCTGNNN
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SEQ ID NO: 111 ACCCTCCAGAAAATTGGTGACTTINCTTTTGTGACTGACAACACTTATACTAAG
CACCAAAATCAGACAGATGGAAATGAAGATTCTTAAGAGCTTTAACTTTGGTCTGGGGTGGCCT
CTACCTTTGANNCTCCTCGGAGAAAGCTTCTTAANATTGGAGAAGGTTGGATGTCAACCAACANTA
NTTNGGCCAATTACTTGANGGACCTANTTATGTNGGANCTTTAACAANGGNCNTTNTCTTTT
TAANATNGNACAAAGGACCTTTNNCTAACCNNTNAAAATTNNGGNTANTGGGGGAT

SEQ ID NO: 112 ACITTTTGGGTTTTTTTTTTTTTTTGTATAATCTATTCATGGATCTCCACTTT
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SEQ ID NO: 113 ACTTGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAAGGACCA
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SEQ ID NO: 114 ACGCGGGCAGTCAAGCTGGTTGCTCTGAAAGTAACCCAGCTTGTTGCTCTAA
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SEQ ID NO: 115 ACTTTTTTTTTTTTTTTTTTAAAGCAACCACATTTTAATCAATAAATATGAA
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CCAATGGAAATAATGATTGGATGGGAAAAATTGGTGAGCATTAGNGAATACCTATGGTCACTTATGG
GCCCGGCTTACCTTCATTTCTTGGTCTTTTCCGGCTTACTGNCCTTGNTNTTCCAAGGCCTTGGN
GANGGGGCTTCAAAAAGCCTGGGCANTAANGGGCTGGTGGAAAAATGTGANGGGCAGGATAGGG
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CCCTN

SEQ ID NO: 116 ACTTCTTGTGTTAAGTATTCAGCCACTGTTTTAGATCTAGTTAATAGGTTCT
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CTTTTTTNGGGACCTNATTCCTTGAAGATTGGGCTTGCTATCAGGGGTTTATCCTTTTTCTCCA
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NANGTTGGG

SEQ ID NO: 117 ACTTTTTTTTTTTTTTTTTTNNTTTTTTTTTNGCATCAAAAAGCTTTATTTCCATT
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AANCCCTATTACTTTGCAAGGGGCCCTTAAAAAGTCGNTGGGCTCAAAAGGNCTTTTAATNCTCCTT
TAAANNTANGCCTTTTCGNAANAATTCNTNNGCCAANCAANGCTTNGGGCCACNCAAA

SEQ ID NO: 118 ACCACTTGAAGCCAGAATAGTTNGNTTATGTGAAACCACGGGACCNGGAAA
ATTTTCATCTTNATNGAAGATTTCGANGGTTTGGANATTTAAATTTTAAAGTNACCCANATNCCATNNA
GCTACGGTCTTTATCCNCAGAGCCGGTGGCTAAAAATAANAC

SEQ ID NO: 119 ACACTTGATTGAGATTCCACCTGGGATTCGACAAATTTTTCTTTTTTGTTTTT
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AATTCITTTGTTTCTTTTACTTCATCTTTTTTGGGCTTTTGGACTCCTTTAGTTCTTCTTTGGCTTCA
GAAATTCITTTCTTTTGTCTTAAATCAAAAACCTTTCCAAAGGAGCTTCCAGGCTGGTTTGG
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GGGCTCCAAGGCCNCGCTCTGGGCCCGGACCACNCTTAAGG

SEQ ID NO: 120 GTACCTCAAGGTTCTCAGGACCTCCTTTCCCAGATCTTAGGGTCTGCCCTG
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AGGA

SEQ ID NO: 121 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTTTTAAAC
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CCAAGCTGGANTGTANTGGAACAATCANANTTCACTGGANCATNNGCCTCCNNGGCTCAANNAN
NTTANTTGTCTAACCCCCCGAGTNGCTTGAANTANCNGGTGAACAAAAACCACANCCAAGNTTA
TTTTTTATGTTTTTGNAAAAACGGGGCTTTGCT

SEQ ID NO: 122 ACGCGGGTGCCATTCCCTCCTCTTCTGGATTTTTTCTTTGACCATATCAAGC
TGAAGAGATGAACCTGTTTTCTCAAACCTTTGCATCAAATTAAGAGTAAAAACAATAAAGTAAT
ATCAAATGAGGCAGGCCAACTAAAAACAAGAAATAGGTAGAGAATATTGACTCTCCGCCGGGCAT
GGTGGCTCATGCTGTAAATCCCAACAGTTTATAGGAGGCTGAGATGGGCAGATCACTTGAGGNCAGG
AGTTCAAGACCATGCCTGGCCAAACANTGGTTGAAACCTTGTCTCTACTAAAAAATACAAAAATT
AGCCAGGCGTGGTANTGGGCCCTGNAATCCNAGCTACTTNGGANGCTGANGCAGGA

SEQ ID NO: 123 GTACTCTNTTTATACNTAATCTGGNGGATANCTATTTAATTTATGTTATTC
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SEQ ID NO: 124 ACTTTTTTTTTTTTTTTTTTTTTTNTGGGGAAAAATCCTTTTCTTTACAACTTCCAT
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ATGTTTANNTTGGCGNAANGCTCCCNATTATTTCCATCTNAATTTGGNNCTNATTCAAAGTNCAC
NNTANTCC

SEQ ID NO: 125 ACTTTTTTTTTTTTTTTTTTTTTTGTATTNNGGCTNCCTTAAACAGTTGGACCTTC
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CATTTTTCCTTTTTTTAAAGCCTTATTTGGAATTGNNTNTTCTTNNAATTCNCTTINANCCTCNCCN
NAGGGTTNGGTACCAAAAAAT

SEQ ID NO: 126 ACCCTTGCCTTTCTCACATCATNAGATCAAGTCACTCTTGTGCATCCCTTCCT
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CTAAAAAGTANAANGACTTCAGCATATNTGANNTCAACCNAATCTGTANGTATCAGATATCTGNA
CTTA

SEQ ID NO: 127 ACAGTGTGGCTCATGCCTGTAATCCCAGCACTTCGGGAGGCTGAGGTGGGAC
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AATACAAGAATTAGCTGAGTGTGGTGGCACATGCCTGTANTAGCCACAGCTACTTGGGAGGCTAA
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CCAGCCTGNGTGACAGAGCAAGACCCTGTCTTTAATACANTNAAAAATNAAAAAANATNNTT

SEQ ID NO: 128 ACACGGCAGTCTTAGAGAAGCAAATGGCTCAGATGATGATAATTAAGAGTAG
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AATCCTCTTGCTCAGGAAGTGATACAACTTTTTTAAAAATTATACCTTGTTATTATTCTACTTCTCT
CTTCTATGACAACTCTAGTGCAATATTAGAGTTTCATTTATTCACAAATATATTTTACTGTTTTTTT
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ATTATTTTACTTTCAAATGTATANTTAATTGCTAACATGTTTTTATTTTCATATATTGNTG

SEQ ID NO: 129 ACAGTAGAAACAAGCAGAGCTACTGATACTCTCACAGCTCATTTCAGTTTGTG
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AATGCACATAATATTGATACTGCGTTGTAAACATTTAGGCCCGTAAAATTACTGAAGGACTGTAGA
ATGAAAGAGAATCNCANAATAAACTTAAGGTTANAGAACACTTAATGTTTCCTGCCTNAAAGTGNG
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TCATT

SEQ ID NO: 130 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGANANACAGGGTCTTGCCACTTTGCC
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ANANATTCTTTTTTTTTTTTTTTTTTTTTTTTNGGGAATGGAGTNTACTNNTTGGCCAGGCT
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CCCCCTTATTNTCCCAAAGTCTGGGATTACAGGCGTNAGCCACCGNCTGGCCAATATTNCCGC
NCCCTNCCGGGGCGNCGTTTAAAAGGGCAANTCCANCACTGGGNGGNCNTNTTNGTGGATN
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C

SEQ ID NO: 131 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGAATGCAACAACCTTTATTGAAAGGAAAGTG
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AAATTAATCAACCTNTGCTGATNAAGAGGGATNCNTTCATATATTTANNATNTTTAGTNTTGANT
TTTTAAATGGTNATNATT

SEQ ID NO: 132 ACCTACATCAGATCTAACCTTGATCCCAGCAATGTGGATTCCCTCTTCTACGC
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CTANGA

SEQ ID NO: 133 ACAAATGTTTTTTTATTCAAANGTNCAAAAATAAATTATCTGTAGGCATGGACA
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NNAC

SEQ ID NO: 134 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGGATTANTAAAATAAATGTAT
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SEQ ID NO: 135 ACATAGTAACTGTGGGTATTCAGGGAGATAAAAGTTTTTTGTTTGTGTTT
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SEQ ID NO: 136 ACCTTTTTTTTTTTTTTTTTTTTNGGTAAACANGGCGGGTAAAGATTGCCGA
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CATCATAAAATCGNCCCA

SEQ ID NO: 137 ACTTGACCCACAGCCGTCNGGGATGAGCCGCTTCTCAGCCACCATGTCTTCA
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TGAANACTTGTC

SEQ ID NO: 138 ACACAGCTGTCAGGGAAAGTCCTGATGGCCACAGTGAAAAANGTCATGGTTN
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SEQ ID NO: 139 ACGCGGGGGCGAAGGCGGGGTCGGCGCTGCCGGGTGAAATCGTAGGACAGT
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GCQCGGTGGCTCCAANTTTGGCGGATTGCGTGGANATTTNTGAAACTCTGGCNNAACNCAAA
ANTNTANTGAAGGNNCNTCTGAAAATC

SEQ ID NO: 140 ACTTTTTTTTTTTTTTTTTTTTTTCCGGTTTTTTTTTTTTTTTTTTTTTAAA
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AACNTGAGGGNGTTTTCTCGNGTNAATGAGGGTTTTATGTTGTAATGNGGGGGGTGAGGGACCC
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SEQ ID NO: 141 ACTTTTTTTTTTTTTTTTTTTTTTGGANAAGGAANAGGTTTTTATTCGGCCG
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CTTGGGTTT

SEQ ID NO: 142 ACTTTTTTTTTTTTTTTTTTTTTTGGCTGGATTGCCTTTATAGGANAG
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GAAAGCNGGATTTTNTCCNACTCCCNNTTANCTCNTAAGNNAGCTGGTNAANTGGGATNTTGN
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AATACTT

SEQ ID NO: 143 ACCGAGTGTGGCACCTAGGACAGCAGGCAGTAGTGACAGATAAGGTGTGACTC
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SEQ ID NO: 144 CTGAAGNAACTANCNTCAANAAGTAGCCTCTGTATGGGAATAGAGCTAAGGA
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AACACATTTGTCAACTTGACAGGGAGCTTGGGCTGCAGATTCTGCCCTTGTGAGACTCTGAGGCC
CGGCAGAAAGAGCCAGGCATGGGAGTCAGACTCATGGGAGGGTGTGGGGTAAATCCTGGCCA
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CCCTT

SEQ ID NO: 145 ACTGTTCAATAAAATTTAATTCATATAAATCAATTTTTTAAAAATTAATTATA
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SEQ ID NO: 146 ACTTTTTTTTTTTTTTTTTTTTTTTTATTGGCTTTTAAAAAACCCTTTATTTTTT
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GGA CTGAAACTG

SEQ ID NO: 147 ACTTTTTTTTTTTTTTTTTTTAATATNACAAAATNAAAACTTANACACTTTAG
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CAATGNTNTNACTAATACATTANTACTNAAAGGTGCTTAAAAAT

SEQ ID NO: 148 ACTTCCGGTGCTAAGGGNTNTCCGATTTGTAGAAGGCACAAATATTAATAGG
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CCCTTACAGGAAATAGTAAGCTTACTCGCTTGTAAAGGATTCTCTGGAGGAACTGTCAAATA
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SEQ ID NO: 149 ACGCGGGGCCATACCAGCCTAGGTGTGGAGCAAGAGGTAGGGAGGCCCTCG
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AAACANITTTAAATTANATANTTCTATTCAITGA

SEQ ID NO: 150 GTACGCNCGGACGACGAAGATGATGAANATGATGATGATGAAGATGATGAG
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SEQ ID NO: 151 ACTTTTTTTTTTNTTANTTTGTTTTTGACATANATNTANTCTNTGGTNANGGTGG
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CCATGTTNACACTGACCTAATGCAAANTATGGAACCATTTGGGCTGGTTATACATTTCTGTTTCTTA
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SEQ ID NO: 152 ACGCGGGGAGACTGAAAACTGCCTCATGCATGTGTTCTATTTATTGATATATG
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SEQ ID NO: 153 ACTTTTTTTTTTTTTTTTTTTTTTGGAGACAGNCTCACTCTATTGCTGAGGCT
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CTCAACCT

SEQ ID NO: 154 ACGCGGGGAGAAAGGAACACAGTAACTGAATTGATCCGTTTGAAGTTTAC
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ACATGCCTGGAAAAATAAATTTGTCTATTNGGTGAAAGATACTTANAANAATTTNTTGCCTTTNN
TANANTCATTTNTATNAANAGANATNTTNAATATTNGTATATNTT

SEQ ID NO: 155 ACTTATGTCCATTTTCAGTTTCCCCACCTATAAACAAGAGCCAATTTCTCTTATT
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SEQ ID NO: 156 ACCACTGNATTGATTAGNGGTGTATNTAAACANGGCTCCCTTCATTGCATCTG
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ACTACCCAGTTTGNNGTTCCTTGGGANAATGTAAGTGNACAGTTACCTTTCAATTAAGACA
CTTACCCCAAAANAAAAAATTAAAAANAANTNCCGTCCNCTTTTGTGT

SEQ ID NO: 157 ACCTGGAGGCTCAACGGTTTAAGCTTCACCACAAAAGCNAAATGGGCACACC
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TNCNTAT

SEQ ID NO: 158 ACTGTAAAAGTTCTGACACAAGACAGTGGCAGTGGTTACTTTTCATCGACTTT
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SEQ ID NO: 159 ACAACTATGATACATAAAATTAATAACAAAAAAGGAGGGGGCAGGC
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TTAANGNTTNTATNATTAATATC

SEQ ID NO: 160 ACCCCCTCTCCACGTAGCCACGGCTCCCTACTATCAACATCCTGCACTA
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SEQ ID NO: 161 ACGCGGGAGTGAAGAAAAAGAAATTCTGATACGGGACAAAAATGCTCTTCA
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SEQ ID NO: 162 ACAAATTTTGGGATTAAGCTGCTCCCAAGACAGTCTTCATCACCTTTGTGAAC
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ATAAATGTAT

SEQ ID NO: 163 ACATATTGGCATTTCATCCTCAAAGGAATCATCAAAAGAAAATTCAGTGAGT
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TCCCTTGACTCTGATAGTAAACCTGCCCTCTCANCAATTGACGCCTGGGTATTTTATGGATATTTA
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GCA

SEQ ID NO: 164 ACATATTGGCATTTCATCCTCAAAGGAATCATCAAAAGAAAATTCAGTGAGT
AATCTTTTACCATGACTGTTGAAGTGAAGGGTCCCTATGAATACCTNACACTTGAAGACTATCCC
TTGATGATTTTTTNTATGGNGATGNGNATTGNATATGTCCNGNTAGGNNTNAAANCGTTNGTTNG

[illegible]

TTTTTTACTTTAACCATCCTGATAGGCGTGTGCTGGTATCTCACTGTGTTTTTTAAGTTTGCATTTTC
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AATGTCTGCCGCGTACCTGCCN

SEQ ID NO: 171 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGGAAGTCCTATTTATCATTTTAAAG
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SEQ ID NO: 172 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGTTTGATTCTCTTCATTCTC
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CACCCGCGT

SEQ ID NO: 173 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTAGAGACAATGTTTCACTATGT
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SEQ ID NO: 174 ACCCGGGGGCANNCCNNGTGGTCCCATAGCACAAAGCTGTGAGGGGATTCACTT
GTGTGCGNAACTCCTCGGAACCNCTGGTGTCCCTAAACATNTTCTGGGAACAGCCNTNCTAAGA
CCCTGATGACTANNGAGCTANCTAAGATCAGCTGANTTA

SEQ ID NO: 175 ACTTTTTTTTTTTTTTTTTTTTTTTTTNNTGAGTGAGGCAGGAGTCCAANGAGGNTAT
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ATGGNTATCANTCGAATTGAGGTTA

SEQ ID NO: 176 ACTGGGATTACAGGCATGAGCCACTGCGCCTGGCCCANAAATCTCTTTGAA
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GAACANAATAA

SEQ ID NO: 177 TATACCACTCACTATGGGCGAATTCGAGCTCGTACCGGGGATCCTCTAAGTC
ACCTGCAGCATGCAAGCTTGAGTATTCTATATGTACCTAAATNCNCCGNGAAGAAGGCNGTTTT
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NGCCTGCGGCNGAAGCCGTATACANGNTCACTCAAAANGCG

SEQ ID NO: 178 ACTTTNG
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TAANCCTGTAAATTTAAGGGGAGTTGGGGTGGGGCGTAANAGCAAANGGACAGCCGGANAAN
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NTNAA

SEQ ID NO: 179 ACAGGCTTGAACAGAAATTGGAGAATGCCTTGAAGACAATAGAAAGTGCC
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TTTCCANANAAACCTTGGGCCTCCANAAAGGGCACATTNNACCTTGGGTTCAAAACTTTTTTTTC
CCTTTNTTTGGGCCAAGGCCCTTTAACCCNGCCCN

SEQ ID NO: 180 CCCCCCGGGGCACCTGGAGCAGAGGGGTAATGACCACTGGAAACACTTGCG
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CACCGAGAGAGAACTGGTCCGCTTACCTCAAGGAAGCCATCAGACTAACAGCCGATCTCTCTGG
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AATGATT

SEQ ID NO: 181 ACTNTTTTTTTTTTTTTTTTTTTTTTCTAAAAACCACTTCTGAATTTGTGTAT
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TGANATCTTTCTAACTTTTTCATGTGGCCATTAGTGCTATAAACTTCCCTCCTAAAACTGTGTGG
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ATGGCATTTAAGTAAATTCACAATGTTGNGCAACCATCACCATTATATATTTCCANACTTTTACA
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SEQ ID NO: 182 ACGCGGGGAGAAATTAGGGGCTGCAGCGGCGCTGGCTTTAGGTGAACGACGT
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CCAACCTGTTAGAAAAGACAGGAGGAGTGATTTCCATATGAAAAGCTGTGCCAGGGACAGAAGTT
CCATGGCATAAGATTGGGTTTGTGAGCNAATTTGGGAAGAGTCTTACCTGTTTCTCACCTTAAA
AATCAACATANNCGTAAAAATCATCTNATATGGATCCCTCAAAATTCGCCCAACCTG

SEQ ID NO: 183 ACGCGGGTGGCCAACATGGTGAAACCTGTCTCTACTAAAAATACAAAAACT
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AGAGCAAGATTCCACCTCAAAAAACAAAAACAAAAACCAACCCAAAAATAAAAATAAGTAA
ATAAATAAATAAAGGTGGAGTGACTATTAACACCAAAGGTCTTTCCAGGACANGTATCACCAG
ANATAAAGAGGGTNAATTTATANAGGCAAGAGGTCAGTGATCCAGAAGACACCAATCCCTAAG
TGTATAAGTAACATAATANCAGATCTTCAAAATACGTGATNTAAANGCTAATAGAACTGCAAGGAT
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GTAATCTGAATATTTANNATTTA

SEQ ID NO: 184 ACTTTTTTTTTTTTTTTTTTTTTTTTNNATTTTTTTTTTTTTTTTTTTTTTTT
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CAGCCTGNGANATCCGACCATCCCATTAACCTTTGAAGNTTNTCTNGATTAATAAAAAAAGG
GGNGGGNGAAAAAAGGNGGAACATGCTAAAAACCTAAATGACAATCATCCAAATGNGAGGAAA
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GCCTTCTGGCTNAAAAAGCCTGCAGNCCCANAGAACCCNTGAAAAANAGCCATGGNTCTNCAAAA
GAANTAGGA

SEQ ID NO: 185 ACAGTATTNTGAATGTGAGATGATTGTGTCAGGACTAACTGTCTTTTAAACAAA
ACATTTTCAGTNTTTTAAATAAAATTTTGNAAAAGNAATGTGAATTAAAAATCCTGGAACANATNTG
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SEQ ID NO: 186 ACTTTTTTTTTTTTCTTTTTTTGTTTTTTGGTGATGTGGCTTAAATGCAATAGTT
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SEQ ID NO: 187 ACTTTTTTTTTNTTTTTTTTTTTTTTTNGTAATAAACATGTGGAGNGTCNTGTAN
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SEQ ID NO: 188 ACCACTCACTCCAGCCTGGCGACAGAGTGGAACCTCCGTCTCAAAAAATAAA
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TGATATTCTATGCAAAGATCTNNTCCTGGANGGCACNTNGCGNNACACCACTGNGNACTNTGAT
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SEQ ID NO: 189 ACCTCCAAAGTGTTAAATAAAATTAATTAACCACTGGAAGAGAATAAAAAATT
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SEQ ID NO: 190 ACCCTACCACTGTTGGACCACTGGAGAGCAGTGGATTGAGATCTCGCTACCG
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SEQ ID NO: 191 ACACAATCCTTTATAAAAGTNGTATATATTTTTTTCTGTCAATACCTTCATTAC
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SEQ ID NO: 192 ACTCTGGCTTGTGCTTAATACTGTGGTTAAGAGAATCACCTATATTGTTGCAT
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SEQ ID NO: 193 GGTACAAAATAAACTTTGAGGCAAAAGGCATTGCTGCAGATAAAAAACATGC
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SEQ ID NO: 194 GGTACTTTTTTTTTTTTTTTTTTTTTTTTGACAGGGTCTCACTCTATCACCCAG
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TTTTGTAGCAACAGGGTCTCACTTTGTTGCCAGGCTGATCTCGAATTCCTAGGCTCAAGCATTTNT
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SEQ ID NO: 195 ACTTGATNNGATTCTCAGCTTGGTTGCTGTTGGTGTATAGCANAACTACCGAG
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SEQ ID NO: 196 ACTGCGGGGTCCTTGATGGACCCTAAAAGGGGTTGGAGAGACCGATTACAG
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SEQ ID NO: 197 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCCAAGCATTTTTTAATAAAATAAAAAAC
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AGCCTGCGTATTTCTTTAGCAGGTTTTCTTAGAGACAATAACAACAGCTTATCAATTTCTTTACA
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SEQ ID NO: 198 GGCTGCANAACAAATCAAGCACATCCTTGCTAATTTCAAAAACTACCAAGTTC
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NTGANCCNATTTAATNATTATT

SEQ ID NO: 199 CTAATTTATATGTTGCTCTGCTTATTAATAATCAGCTTAAGGATAATGGGGT
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CCAAGATGANTTAATTTNTANNAGTCCTTATTACACAATAAACANTNNCTTAANNNGNCAACTGT
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SEQ ID NO: 200 ACTTTTTTTTTTTTTTTTTTTTTTTTACAAGGGTAGCAAAAAATATNTGTAA
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SEQ ID NO: 201 CGTACCAGATCCCACTAGGGGCGCNACTTGCTTGCTAACTCCTAAAAANAC
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CCTCAGTTACAATTTTGTAAAGGTGGNTTCAAATGCTTTGCTGACCTCCCATTAACAAGGATGTG
CCGATTGGAACCTNTNTTTTGC

SEQ ID NO: 202 ACTTGCTAGGTATCCTGGGTCAAGTGGCGGTGCAAACTGGTTTCCTCAGCTGCC
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GTGCTTCTACTCCAGCAT

SEQ ID NO: 203 ACAGTCATTTTAATGATGTTGATTCTTCCAAACAATGATCATGGGATATTTT
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TTTGC

SEQ ID NO: 204 ACGTGACAGAGCCAGGCTTAAACGCAGATCATCTGGCTTCAGACTTTCATCA
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SEQ ID NO: 205 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGATGGAGGGCCGCTCTGTTGTCCAGG
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TAGTANAGATGGGGTTTACCAGTGTGGCCAGGCTGGGCTTGACTCTTANCTCAATGNAGGAAAT
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SEQ ID NO: 206 ACCGNATGCTGGCNGGAGGTGGCATATAGCTCACTGGNACTGANGGGCTGG
GCACCAACCTNTTCCACCTGTGCTAATCGCCTGGATCTATCATNANTGCAAAAANCTNCTTTT
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SEQ ID NO: 207 ACAGAGAAACCCCTTAGGCCAAACTTAAAAATGTAAAGGAGGCAGCTTTAGGC
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GCCGGACNCTANGNCNATTCCACNNNTGNGGCGTNATATGGTCNACTCGGACAANTTGNNGNAC
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SEQ ID NO: 208 ACTGNNTGCAACAACTCATGGANTTTGATGGGGAAGACCTGGTCTCAAATAC
CAAGGGGGTCTGGAGCTNCCTGTGGNTTAGNGGNGAAAAAANATNGGGAGANAGCCNGGC
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SEQ ID NO: 209 ACGCGGGGAAACGGAAGTGAGCGCGGGGTGACTGACGGTAACGGGGCA
GAGAGGCTGTTCGAGAGCTGCGGAAGATGAATGCCANAGGACTTGGATCTGAGCTAAAGGACA
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GAATTCAAGGCGTGCNAGGTTTACGGCTTCATTTTAAAGCTCAAATTTTCTGGGATTTTGAG
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ATGNGGNGGCTTTTNTGGGGGANCNANCTTNGGNNAAAGTGGGGGGAAAAANGGGGGANAAA
AGNTTNTCCCGGGGAAAAATTTT

SEQ ID NO: 210 ACTCGGGGAAACGGAGGTGNCCNGGGCGGGGTCNACTGACGGTNACGGGGC
ATATAGGCTGTTCNNANAGCTGCGGATGATGAATGCCANNAGGACTTGGATCTGAGCTAAAGGAC
AGTATNCCANTTACTGAACTTTACCAAGTGGACCTTNTGAAAGCATGATCTTCTCNGAAAGGTT
TTTTCTTGTGTTNAAAAATGAACNTTTNGCCTTANCATCCCTAGAAATTTATCAAGAAAAAATTT
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SEQ ID NO: 211 ACAAATGAAATTTAGGACCAGAGAAAAATGCAAATTAAGTAAAGTTTAA
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AATGGCTAATTTTATTGACTTTCCTGGTAGAAAAACAAAGGAGGTAAGCTATCTATGTAGTGATAT
CTCAGCTAGTGCATGTGAAATGTGTGTGGGCACTTGGGTGGTCACAATGACTGAATGCCTAGCT
GGCATTAAATGTCTGGAAGCCAGGGATTCCAAATGGCTATCCTGGACAGGGGACTGGGTGAGGGG
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SEQ ID NO: 212 ACGCGGCGAGGGGTAGAATGGAAGGAGAGCGGCTGGAGAGGACAGGTGGT
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NAAGGAACCTGTGAAAGCCTTATCAGTCATTTATTGCTGTGANAAGTTCTCTTGGAAATGGGGTA
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SEQ ID NO: 213 ACTTTTAGGAGAGATGGGATTTACCATGTTGGCTAGGATGGTCTCGATCTCT
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GCCATCTTCCCACTTGAACCTCTAAATACTGAGATTAACAGGTATGAGTCACTGTGTCTGACCAT
CATGGAATTAACGACATGCTTCTGAATGACCAAAGAGTTATGAAGAANTTAAGAAGAAAAATA
AANCAAAATCTCAAGACATGAAATAGAACNACCATACCAAAACCCCTGTAATACTGAAAAACC

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TTGNGATCAACCGAATTAACCAAAATTAAGACTTAAAAATCCACNGACCATNGAACCGAAAAGTGGT
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SEQ ID NO: 214 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTAATTAAGTATATAATGTAA
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ACATTTT

SEQ ID NO: 215 ACNCGGGGTCTTTCCCATCTTGCAAGATGGCGGGTGAAAAAGTTGAGAAGCC
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SEQ ID NO: 216 ACCTGTAGTCCCATCTACTAGGGTAGCTAAGGCAGGAGGATCGCTTGAGCCC
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ACCATGTCTCTAAAAAACTAAAAAATATTTTAAAAAATTTTAAATAGACAATACCTAAAAACT
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TGGTCAAGAGCCNTATTTNCACTTNTCAAGAGGGCTGANGGGGGAGGATCACTTGNATCCAAG
AAATCCAGCCTTTAGGCTCATTGAACCTAGCTACCCAACTGNACCCCACTTGGGCAACANA
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SEQ ID NO: 217 ACGCGGGGAGTTCCAAGTAGGTAATCCTTCTGAGAAGTCCCACCTTCTGAG
CAGCTGTGTTTGAAGAAAGCTAGTGGGAAAAGTTCCAGGATTACATGTCAGGAAACTACAAGAGG
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GTNAAAAATG

SEQ ID NO: 218 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGTTTTTTTTTTTTTTTTTTTTT
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GTCCTCATGCAGGGGTNAAAAATNTNCAAAACNCCCTGGGAATGTCCAAGCCCAAAAAANCCAGG
GGCCANTCCCTGAGCAAGNGGAAAATTTGGGTCTGGAGTNNTAGGCTGCCTCCTCTTNTNCTC
CTCTAANTTTTATGANACTGNNGGGNTTGGGGTAACAAACNNGNCAAAATAATTTTTTTGNGCT
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TGGGTTT

SEQ ID NO: 219 ACAGGTTTGGCCAGTCTCTATAGCATGGTATAGTGATAACTGATTTTTTAT
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TTAGATNAGTTTATGTTAANTNTTATAAAATCATNTAACNATTGTTGTANTTGTGGNTCTT

SEQ ID NO: 220 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAAATGTTTATGGTTTTTTT
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SEQ ID NO: 221 ACACTCTATGTCTGCATTGATTATTACCTTAAACAGACTTATTGGGTGACA
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SEQ ID NO: 222 ACGCGGGTAAGAATCCTTGAAATAAATGTTTTTTAAAAATCTCTGGGAAGA
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SEQ ID NO: 223 ACGCGGGACTCTTGAAATGGTATCTTTGTGGATGATTTTTTTTTTAAGCTGA
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GTAAGTTANTTTTAA

SEQ ID NO: 224 ACTATATTTGATTTTTAGTCTAGTAAAAATGTTAGTAACCTGTTAAATGCGTTCT
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SEQ ID NO: 225 GGTACTTTTTTTTTTTTTTTTTTTTTTTTCTTANTATCTGCTTCTGCCTC
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SEQ ID NO: 226 GGTACTCAGAGGAATTTTTTTGTTTTGTTTGTCTTTTAAGAAAGGAAAGAA
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SEQ ID NO: 228 GCGTGGTCCGCGCGGAGGTACTACTTCTCAAGGAGGATTATGGTCTGTCTCT
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SEQ ID NO: 229 GCGAGCGGNCGCCGGGCANGTACAGNGGCCCGGTGAAAGACAGAATTG
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SEQ ID NO: 230 CNCNGGACACTGCGCCATTTCCTGTCCAAAGCTGGGCGAATCAGGGATNCCG
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SEQ ID NO: 231 TAAAGATCCAGCGTTTCCCCTGGAACTTCCTCGTGCCNTCTGTTCCAACTT
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SEQ ID NO: 232 TNNAGAGAGAAAAGACAGGGCTCTGAAAATACTGCCATAGGCTCAAGTTCCAA
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SEQ ID NO: 233 GGTACAACCTTCAAACATTCCAGTTTTTATAAAAAAGGGGCACACAATCGT
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SEQ ID NO: 234 GGTACGCGGGGGATGTGTACAGTCCGCAAGGGGTTTGGGGAAACGGCCGCTGA
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SEQ ID NO: 235 GGTACTCTGGACAAGGACAATCAGCATCTTCTCCAAGGCAGCTCAGGGGCT
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SEQ ID NO: 236 GGTACTTTTTTTTTTTTTTTTTTTTTTTTAAAGACTANGGTAAGTGAAGGTGT
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SEQ ID NO: 237 GGTACAAGTAAAGCCTGTGGTGGGATCAAGGAGCTATCAATATCAAGTTCAA
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SEQ ID NO: 238 CGAGGTACCTGAGCCAGGCGGGGACAAAACTGACAACTGCAGGATGTG
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SEQ ID NO: 240 CGAGGTACAGCAACATGGCGGCGCCCATGGACTCTTAGAAAAGGAGAAAGC
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SEQ ID NO: 242 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGNTTTTTTTTTTTTTTTTTTTC
CAAACTGCAAAATTTGCCCAANTTTTATTTGTAGTCCNTACAAAANGGAAAAAANTTAAGGTTTTN
TAAACNCCACCTACTTGGGGANATGGGGAAATGGNACTGTCCCCCTCACCATCANCTAAACNTTA
TNGGTACGACAGGACTTGNATACATACCAACTGACTGTCCCAANAGGANCTCAGTCT

SEQ ID NO: 243 ACTAGCATTTTCAATTACCAAAAACTATTAGCAGTAACATTGCCATTGGTAG
TATTTTCAGTCAGTCCACTATCACTAAGCTAATGGGAAATCAATAGTAATAAGTGGTAGATTATAA
TGAGCCATGAAAAATGTTGTTTAAATCAAGTCCACAGTCTTTTCAAGAGAGAGGGAGATTGTTT

TGTATGTTCTTGATCTTTCTGAAGTTAAAGTTCATGTATTTTAGGATGCTAAAAAAATATCCTGG
ACNTTAAAAAGGTGCCAACTGTTACACACTCATTAAGAAAACTGCTAGATGAATTATTAATA
CCATGTGAATGCAGNTTATTANCCAANCAATGAATTCNGCATAANACAGTGTATCTTTAANGCA
CTGAAGTAAA

SEQ ID NO: 244 CGTACATNAAANACACGTCCACATCACANTTGGCCCCAACTGCCTGTGCTC
CTCGATGGTGTCTCTCCCTNCATAAAACGCATGCTTATTGACCTTGGTTTGTATNTGCTTGGCCNTG
TCNGTGANGATGAT

SEQ ID NO: 245 ACAGTCACACTGATGAAAGACAGGGAGGCCATGTGGAAACCCAGGGGCCAC
AGAGCCACAGTGAAGCACCAGGCTAAGGCCATGAGTTAACACCACAAACCAGAAAGGCACCAGA
CACTTGGGCTTTTGGTTAAGTAGGTTGGGCTTGCTCATTAAAGGACCTTTCTTGAGACTCATTCTTT
ATAATTTATTCATTTCAAAACACTTCAGTAGACTTCACAAACACTAATATAGTTCTACCATATTA
GTAACCTCTTTAATCCTAACAACTCTATGAGGGAAGGGAAGTATTATTAGCCCCATTTACAGAAAA
GGAAACAGGCNACAGGGAGATTAAACCATTTGCCCAAGATCAGGATGTCTGAAATGTTGATCTGGA
TCAACNCTTCAAGGAATAATGACCTTTGAAAGATGCCCTTTTCTTATAGAAAACTCTTANAATC
CCTAGGAATTCTTAGGAGAGAAATTGTCCAGAAAATCTAGGACCTGCTGATAAAAAGGAAAAAGTA
CACAGATTNTGNCCCTTGCCATACACTGC

SEQ ID NO: 246 ACTTNTTTTTTTTTTTTTTTTTTTTTTTCGACCCATGTGGACCAGGCTGGCC
TNAAACTCNTGCCCTGGAACCCCCGCTCCNNGAGGGCCNAGGGCAGGCNAACCGCCTGAGCC
ACANTGGCTCCCCGCTTACCTNNGCCGANACCANNCTAANGGCGANTTCCTCACACTGGCGGGC
GGTANCTANTG

SEQ ID NO: 247 GTACGCGGGGTTGAAAAATGGCGACTGTGGCAGAGTTGAAGGCTGTTTTAAA
GGACACCTTGGAaaaaaaAGGGGGTATTAGGGCATTTAAAGCAAGGATCCGAGCTGAAGTTTCA
ATGCCCTAAATGATNACCGATAACCCNTANCCCGTGGNCNCCATGGTAGGCACGGCAACTACCN
CAAAAGTTGATAGGGCAAAACNTTCAANTGGGTCGTCCCNCCCCCGCTACTTTTTTTTTNTTTTT
TTTTTAGGGCTTTCAATNTTTTATTNAAATGCCNTGANCCAANATGGNTTTTAAATNTGTTNAAA
AGCAGCCACATCCNTGGNCTGCNNATNTTATTTAAANCAATNGATCNGCTCCTCCAACATATTG
TTCCAACCTTATCNTCTTNAACATACCANTGTTTTTNAAGTTCTTNAATCCGTATCCNCTGNAA
CTTNTTNAAAANACCCCAAACTACCCGTTTNTNNAATGCTTTCTNACCAC

SEQ ID NO: 248 ACGCAGGGGAATGGAATGGAATGGAATGCAATGGAATGGATTTCATCCGGAA
TGGAATCGAAATGGAATGGAATGCAAAAGCAATGGAATCAACTCGATTGCAATGGAATGGAATGGA
ATGGAAAGGAATACATTGGAATCAACCCGAGTGAATGGAATGGAAGGACTGGAATGGAGTGG
AATGGAATGGAATGCAATGGAATGGAATGGAATGGAATCAACTGATTGGAATGGAATGGAATG
GAATGGAATGGAATGGAATGGAATCAACCCGACTGCAGGGGAATGGAATGGAATGGAATGGAAT
GCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT
GGATTGGAATGGAATGGAATGGAATCAACCCGAATACAGGGGAATGGAATGGAATGGAATGCAA
TGGAATGGAATCATCCGTAATGGAATGGAAGGAATGGAATGGAATGGAATGGAATGGAATGGA
ATGGAATGGAATAGAAATCAACTCGATTGCAATCGAATGGAATGGAATGGAATGGAATGGAATGGA
ATGGAATGGAATGGAATGGACCCGGACGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA
AGGAATGGAATGGAATGGAATGGAATGGAAT

SEQ ID NO: 249 ACGCGGGGACGCGCGTCTGTGGAGAAGCGGCTTGGTCGGGGGTGGTCTCGT
GGGGTCTGCCTGTTTAGTCGCTTTCAGGGTTCTTGAGCCCTTCACGACCGTCACCATGGAAGTG
TCACCATGTCAGCCTGTAAATGAAAAATGCAAGTCAGCANAAAAAAAAAAAAAAAAAAAAAN
GTT

SEQ ID NO: 250 ACTCAGGGGAGGCCAGGANGGCCTTGANCTTGGGCCGGGCACTGAGGCGCC
CCACATATGCTGAGAGCAGGGGGAACGCATCCAGNCTGCCANGGGCTAGGACCTCNTGGATCANC
ACNANTNCAGCAGGTTGTATTAGCATAAGGATATNTGGTTTCCACNATTNAAGGINTTGCCTCA
CCTGNTCTGGGACACAGNGGTCTAAAAAGGCTTAATATTNCCCGACAGGGNCTTCACATANTC
ATTNCTTTGCCACCTCTTTNTTT

SEQ ID NO: 251 GAAACANATTAACCACATNCTCCTTCTTTGGGCTAGCAAGGTCCAGGGCTGC
CTGGAGTCTGNCTCTACCATCAGGATANAGNAATCTTCTGCTNGGATATAAAGGAGANGACNNA
CATGTGTTTTCATACTTTNAGAACCATGTGGCCCGNTACCTATTGTGGATAATAACCCNNGTAAGA
TGCTTGTGGAATGNANAAAAAGTGCTGGGCATGAATGGTACTACNTGNGGCGNCTNTCTCAACTC
AGCCAATTATGAGGTNTGTTNATTGCCCATGNAAGATGCTNANTGGNTAAACAANGTCTGGCCTT

NACCTTNCAAGANGGCNTANCCCCATTGNAAGAGCTCCCANTGCCAAATATA

SEQ ID NO: 252 ACTTTTTTTTTTTTTTTTTTTTNTTTCGCGNAGATGTTCTTTCTTTCTTTCTTTCC
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CCACCCACCTTGGCCTCCCAAANNCTGGGATTACNGGCATGAGCCACCNCCTCTGACCANAGTN
ACTTTTGNAANGGGCACTAATNCCACACNTGAGGCTCCACCTTNACNACCTTTTCATTTCCTCAAG
GCTNAACNTCTGCCCNCTCCCAATGAGNCCAGTGGCTTAACCTTTCTNTNATTNTTTTNGNAA
ATNATTGCTCATTTNGGNAACCTCCAAATGCTCCGGTNC

SEQ ID NO: 253 ACCCAACAGGAGGTTTTTTCACTTTTGCTCTTCTCCCTTCTCCACCTCTCA
CATCCCCAGAGCAAATTCAATGTAANTATACANTTTCTTCTTTCTTTTACAAAATATTNTGTTAAN
ACTTACATGAGGTCTTGAAAAATTGGTCTAATATTTCGCTTNTAAAANCTAGATACANAGCCGGGG
TGTGGGTGGCTCAGCTTTGNAATCACAGCACTTTTGGGAGGCCAANACTGGTGGATCACNAGGT
CAGGAGATCGANACCATNCTGCCTAATACCGGNGAAANACTGTCTATACTAATAATTCAAAAATA
TTANC

SEQ ID NO: 254 AGCGGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAAAAANAAAA
AGGAGCATTAACTTGACTATGCTTTTANCTNCAGCCACCTTTTAAAGANTAAATTGCTGGGCAGG
NGGGGGAGGGCTANTCANGNAACGAAACTGTAAGCCGGACNATNTGTGAGGAGGGGAGGTTAT

SEQ ID NO: 255 ACTTACATGTGTGAACACATATAAAGTGTCAAGTTTACAGACCTTGGCTCAA
GGACAGTCTANGATGGGAAAGGAGGTANGGCGAGAAGAAATCACATATTANACTCCCNNGGTGCTT
NAGCCTCACCTATNCAAGGGACATGACNTATGGGGTNTNNTTANTCCATNCCAGGTNCTATNCT
TCANGACTTGAAGTTCCTAATTNGTATGNNGGAACCNCAANANACGTTAACTGGCGGACTCCTG
GNT

SEQ ID NO: 256 ACGCGGGGAGGCCCCAGCCATCTCAGGCTACNCTATCCCAGGATCAGCATGG
CCGCTCCAGTGGATAATCNCCTGGCCTTGGCTGNCCTCCTTGTTGTGGACANGGNAGNGCCTT
AGGCNTCANGAAAGCTCCCTTTNTCATGAATGCCANTNNGTGANCAC

SEQ ID NO: 257 CGCGGGTTTGAAAGTCTTTGGCAATGANATTAAACTANAGAAACCAAAAGGA
ANAGACAGTNANANAGANCGAGATGCGANAACACTTTTGGCTAAAAATCTCCCTTTCAAAGTCAC
TCGCGATGAATCGAAAGAAGTGTGGAAGATGCTGCGGAGATCANATTAGCANNAAGGATGGNA
AAAGTNATAGGGATTGCAT

SEQ ID NO: 258 TCGCGGCGAGGTACACCAAGCTTCATTTTTGTTTTTGCNGGCTGAAGTCATG
GCATGCAATTTTTGCATTTACGATTCTCTTGGGCATGCCCTGTGATCCACCCNCNCNGATTGAGTG
CNTAGCCANTTGTGATCNTACTNTCCANATTGACTTCTTCCNTGGNCTTTCCNAAATTTTACAGA
GTTGACTG

SEQ ID NO: 259 ACGCCNTTCCGGCCAACANATGATATGCAAACCATTTGTGCTGTGGCCGAA
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TTCTGACCTCACCTANTNTNTGCAANAGTGCAANAANCCCCACAATNTCTNTGCTGGGCATCTCAC
TGGAANATGGGGAANTGGTNGNCCCTGATTCCACANCCACCATNTNATGTCTGGGTTTNTGAG
CNAAGGATCAAGCTNNGNCTTAGNGGCCNTTAANCAGCCTGTTTCAAANTGCCATATGGACNAG
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SEQ ID NO: 260 ACTTATTTGNNAATNG
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TGAAANATCCAGCCTTCTNATNTCCTNAAAATCTTNTATGACNTCGGTANTTTCTGAAAAAAT

SEQ ID NO: 261 CGCGGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGANAGAAGGANCCA
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GGGCCTCGCCTTTGNGCACCAAAACCATACAACGCTGGTTTTGTCCTTTANAGAT

SEQ ID NO: 262 ACCCTGGCATTGCTGACAGGATGCAGAAGGAGATCACAGCCCTGGTCCCCAG
CACCATGAAGATCAAGATTATGCTCCCCAGAGCGGANGTACTTTATTTTTTTTTTTTATTTTNTCA
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GATGGGTTTTATTAAGNGGAATTTNCTTGACACNTCTTTGGGAATTCANNTTTTGAATGCT
NGATTACCCNATACCTNTNTNAAATNNTCTNTTTGTTTTAAAGGNTTTTCCAAAAAAATTGNAT
AATACG

SEQ ID NO: 263 ACNCGGGATGTGGAACATCTTTGCATGTTCTGTCCAGCAAGTTCTCTCCCA
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TGAAGGCCTGAATNANACAAAAAAGTGGCTTCTCCCATNCAANAANTGAANATTTGACATATCC
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NAAATTGAAANGTNNCTAGANTNTTAGGACGTATACCGTNTGAAC

SEQ ID NO: 264 ACAACCTTCTCACCTGTGGGTTGGAGCCGAGTCAGGCCACTATGGGGAAG
CAGTTGCCCCACAAAAATGTGGGTTTGCTGACCTATTCTAACTGTTGAATATGCTGCCATTTGCTG
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CNTTNTNNTNTTTTGTNGTNGTACNACCATTTGTGAAAAAATGNNAATTTGGTCTTCCAACT
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CCCA

SEQ ID NO: 265 ACTGTTAAAAATGTTTCCATTGTTTATTCATCCACTGGCATTAGGTATACCTCT
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GACCACTGTACTTTNTTTTNTTTTNTTTTTCGGGGACATTTCCACATGCTTTATCCCNCGCAATC
AAAAATAATNAAANCCATCTCAATTATTATNCACTNCAAAAAATAGGTAACCTNNGNCGGNACC
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SEQ ID NO: 266 ACGAAGAAGTCTGGCAAAAAATCAGCTCCACATCCACAGATCGGCTCACAGT
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SEQ ID NO: 267 GTACGCGGGGGGATACGCCGNGCGCACGGCANTTAGTGGGTAGGCCTGA
ATAGCCGAGGAAAACTGAGCCGTGGGCCTCANAAAGAAAGTTAANGCACCCGCAAGCCGGGCAAC
TGCCCTCCTTCCGCGCCGGCGGAGCGATTNAAAGTGAAGAAACAATGGCCAGCAATCACAAATCTT
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CCTATCAAGGAAAAATATTNAGTTGGCAACTGCNATTTGCCACCTTTGGGACAGGCAAGACCAAGGT
TCTCNTGGGTINGNCCCATAGGGGACTGGTGGGANTTCTGCCTTCTNAAAAATNNAAGNTGCCCC
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GGCANAATTTAGANAATCTTACTTATCTNNGGGCTTTTAAAAAGTAAAAA

SEQ ID NO: 268 ACGCGGGGCTATTGCCTAAGGACTGCTTCCCTCTTCAACAGTGAAAGCTGCA
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ACAGAGCAAGAATCCATCTCAAAAAAANGNNAAAAANNCANTCCTAAAAAATTTGTACA
TGGCATTTGTTTTACAAATTTTCTAANNGGANGAGNGAATATTNATTTTCTGATGGATCCTTCAC
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SEQ ID NO: 269 ACTTTTTTTTTTTTTTTTTTTTGGGATGTTNGNGGTTTAACTTTGTTATGTC
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SEQ ID NO: 276 ACTTTNTTTTTTTTTTTTTTTTTTTTITNGGCCATTCAATTAATATTTATNGAN
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SEQ ID NO: 284 GGTNCGCGGGAGACGGTTTAAACAGAAACAGCGGCAGTGTAGTATGGCCAGG
GATACCCATTCTCCAAGACTCACCATGCTCCTCTAGGTGGCTCTGGCCTTGTGACTCTCATACAC

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CCTTCCAGATGGCAACTGCTATAGCTCCTTCACTGGCAGACTCTGCTAAACAATCAGAGAGCTTCT
CAGAAAGGGGGCCCTGCCAGCATACATCAATCAACAGCCTCTCTNCAACCAATTTAAAAACACAC
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GANAATTCCTGATNC

SEQ ID NO: 285 GGTACAGTGGCGTGATCTTGGCTACTGTAGCTTCTGCCTCTGGGTTC AAGC
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ATTTTAAATTTTGGAGATAATTGTTACCAACATGCTCATCCACAATAATTACCAAAATTCATATAA
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SEQ ID NO: 286 TGTACTGAGGAAGACACCATTCCTTGACGGTGCTAAGAAGCCAGGTGGATG
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AGCCCTGTGAAAGACCATAGCACCAAGCGAGGCCCTTCAGATCCCCCACTGTCCATCGGAAGATG
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SEQ ID NO: 287 ACCGCGGGAAACTATATGCTATCTACAAGAAATTTACTTCACTGTGAAGGAC
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SEQ ID NO: 288 GGTACAATAAGTGCCTTGCACATAAGAGTCCAATAAAATTCTTGAATGATGA
TATGCTGATACATTGTTCAATAATTTATTACATGGAAGTCTACTAAATCCTAAACATCTAAACCA
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SEQ ID NO: 289 GGTACCGAGTGCACCTATGTCTAATCATGTGTGCATGTGAGGAGGTGCTGGC
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AAAAATAATGAAAGTTTTTGCTGATITAAACAAAAATATTACTCTTTTCATTAGCAAAACATTAT
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GCCAAANTGANCNTAGTGTCAAATATGCTNGNTNGGATNTGTCTTCAGCTNATNTTCTTNTT
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SEQ ID NO: 290 CCAGCGTTTCCCTGGAACTCCTTGGGCGCTCTCTGTTCCACCCTTGNCGTT
ACCGGATCCTGGCCGCTTTCTCCTTTNGGAACGTGGCGCTTTTATACTACNCTGAAGATTTTCANTC
GGGNAGNCGTCGTCAACTGGCTGGGGCACAACCCCGTNACCGACGTGNNCTTNTCCGGACTTTG
GT

SEQ ID NO: 291 CCGGGCAGGACGCATACAATGACAAAGCCATTTTGGAGCAGAGGAACATGCT
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AAGTGTTAGAGGTACC

SEQ ID NO: 292 ACTATAAGTAGATCCACGTATAGAGAGAAAAATTGATTTTGGACCAATTTTCAGT
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TCACTGAAAGAAGAAATAAGAATTCATCAGGTAGAGACACCAATTCTATATTGGTATGCACCTAA
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SEQ ID NO: 293 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCNGAAATGAACAAATATTTA
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NTTGTTCAGGACAGTGGAAAAGCTGNTTNTAAATGAGGCCAAAGCACNAGGTAGGTGGAAAGGTT
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SEQ ID NO: 294 ACCATCTCACTCAACTCTTGAAGAACTCTAACGAGACTGGTATTATTATTC
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CCCATTCTACTAAAACAAAATATACAAAATTAGCCAGCCATGGTGGTGTGGGCCTGTAGTCCCA
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SEQ ID NO: 295 ACGCGGGGCTCCTGTCTTGTCTCAGCGGCTGCCAACAGATCATGAGCCATC
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SEQ ID NO: 336 ACAAATGAGACAAAGGCACAGAGGTTAGTTCACATAGCTATGAGGCACAGG
CAGAATTCAAACACAGGCAGTTGGCTTCAGAGACCATGATCTTAACTGCTATGCTCTGATGTCTC
TCCAAAAAGTATAAACATGAGCAGGGTTAATTGTAGCAGCTACTTGGTTTTTACGTCAAGAATCA

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TCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGTGTACACCTGGCTAATTTTTGTATTT
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CTC

SEQ ID NO: 337 ACTTTTTTTTTTTTTTTTTTTTTTGGNCAATCAACAAGTGTATTGATCACC
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AAAATTGTGAATGCTAAGCATCAAAAAGCAATTTATACATTGAGGGTTGGGGAGGGAGGGGT

SEQ ID NO: 338 ACCTAGGGAGTGGCAGAGTAGTGATGTAACTCAGGTCTCTATTACTCCTCG
GTTCCCAGACATCTTCTCTTTGTTCCCTCTGTTTTTCATAGAGAAAGTCTATTCTCTCCACGAGCT
CATTTTTCTTCTGGGACAGAGTCTGGGAAACCTTTCTTCACTCTGTTTCTCTCCCTTTTTATACA
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GAAAGTCATTATACTCATGCTGTATGGAAATGTCTGTATAAATGTCCAATCCTGCATTAACTCTGG
GCTTTCTAAGGCGGGGAAAATACCTTCATAGCCTCAGTANCTGGCATGTGGTAGGTGCTTCGNTCTT
GGTTTTTGNTTGGTTGGTTGGTTTCTGGTTTTTCATTGGCTAGTTTTATACAGGGATTGNAAAACC
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SEQ ID NO: 339 ACATTTGGCATGATCTGGGCCTATGCGGTCTTACAATCCCTGTATAAACTAG
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SEQ ID NO: 340 ACACAGAAAGGGAGGTGTCAACAAAAGAAGATAAGCCCATACAGTGACAC
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TTAATGAAATGTGAATGAGGAAAAATTTTTAATATAGTCTTATCTACCAACATCCCCATAGATT
AAGGATTTTAATA

SEQ ID NO: 341 TCATACAGACCATGGAATACTNTGCAGCCATGAAAAGGAACANGATCACGTT
CTTTGCANAGAGATGGATGGAGCTGGAGGCCATTATCCTTAGCAAACTAATGCANGAAAAAGAAA
CCAAATTCCACATGTNCTCACTTATAAGTGGGAGCTAAATGATGANAACACNTTGACACATGTTGC

SEQ ID NO: 342 ACTTTTTTTTTTTTTTTTTTTTTTGGTAGANACAGGGTCTCACTATGCTGCC
CAGTCTGGTCTTGAGCCTCTGGACTCAAGCAAACTCCTGCTTTGGCTTTCCAAAGTGCTGGAATC
ATAGACATGAGCCCCATCCTTGCCAAATTTTAAATATCATATATAAAAAATTCGGACTTTTGTGTT
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TATAAAGAAAAACTTCCACTCCCTCTCCTTCTCTGCTCAAA

SEQ ID NO: 343 ACCTGGNGGGTCTGTTTCCGAATNTNCCAACCTGTGTGCCATCCACGCTAAGAG
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AGGCAGTTTTATGGCGTTTTGTA

SEQ ID NO: 344 ACTTTTTTTTTTTTTTNGGGNTTTTTTAAAGTANNGGGNGTNGAGCCCCGAAGC
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SEQ ID NO: 345 CGAGGNCNCGGGGGGACCTGGGCTGCAGTCTTTCTATTGTCAATGGCCTAT
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TCTCGCTNGATTAGCNCCTNTGTGCACTNGATTNTCTGTATTGGCCATTTNNATGCCTNNNTGCT
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SEQ ID NO: 346 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACNGGNTTTTTTTTTTTTTTT
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ATTAAANTNTATCCNTTCAAAAAATGCNNAATTGGTTTANTNNNAAAAAATTTNTAAANGGNATCT
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TAAAGGGTNTTANNCATATGNNTACNNTCTGGCCANNNTCTAAATTTTNTATTTCCCTATTNAACT
CTTNTNTNATTTNCNTTTATGNTNAAGATNTGACNNANTANTNNNGNTATNACNTNACTATGTNG
NNNTNTANCTACTTTNACNTATANTTCNNTNAANTTTCNGTACNTTTATNTTGTTCCTTTTATAAA
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SEQ ID NO: 347 ACCGGGGGTAGTGNCCTATTGTCAGATAATTTTNAAGNTAGGGNCTGGGGGT
ANGACGNTTCTCTCTNTTTNAGTCGGAGACCTCTGCNGNATACTNGCTCCNNCANANCAATNTGCN
AGGCCATGAAGCTTCCCAACTTNTTCCNCTTNTTNTANTTATTGAAACTGGGNCNANTCGNAGCA
ANNNTGCATNTCTTGCNTTGNCAATNTGATTACTCCAGATNTATTAC

SEQ ID NO: 348 AATNCGCCCTTAGCNCGGNCCNGGCCGACGNACANCGGTACCGCANCATGG
GCCANAATGTGCATATTACATGCTCTACTNAGTGGAAGAAGATGAANATGCCNACAAGAAACAG
NTCGCTNAAGTCTNTGTGCAACANNANGAGCCCCGAACGTGACTGN

SEQ ID NO: 349 ACTNTTTTTTTTTTTTATTAGANTTNTTNCAGACACACTGTCTNNGNTNCCAA
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TATTTNTATAGAAATGAGGNTTTACCATAATGGCCCGGCTGGCCTNAAATTCCTAGNCTNNANCAA
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TGAANANCNGTTTTNTGATTTCAANNCTTTNNTNGGCCCTGGCGANTTCTCCTTACCCGNATNNAT
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SEQ ID NO: 350 TCGAGNGGCCGNCNGGCANGTACATTCAAAAAANCNTNAGGAAATATTNTG
ANTGCCANGNTGATGAAAACTGGGGTGAATTAACCTCCACACATTTTATTCAAGNNTGNTAAAG
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SEQ ID NO: 351 ACTGCATAGATTAAGAAATCNACTGCNNGNANNCCNCTCGTANGGAANGA
ACGCCATTGCCAATGATAAGNCNTTGCACNTAGGNNNTGANNGCAAACAANTATAGTGNGCTTCC
NAACAGGTNATAACCANCTGATAAACACCATANANNNGCATGCCAAGCATGTNNCNCATNTGG
TGTGACCAANNACTATTATANTGAACAAAAGTTGTGTATANATNCATNCNAAAGGGCAAACCTCCC
TCCNATGATAATACCAGGCTAAGGGCTTCTTAGAACNGNTGTTATGGAATNTNACNNGGAGAAAN
CTGTTGGNTCNGAACTGGGNGTNCATGGTNTCTNTGGTAAACCNAATGTGCCCTAACANACT
CA

SEQ ID NO: 352 ACGGTTCTTCTGTGTACGCTNAATAGCTTGCTGCTTTTTAAGAACCAAGAAG
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SEQ ID NO: 353 ACGCGGGGGCTCAAAGNNGGCGCCATCCGGGACCGGCGGTGTCTGTGGCCG
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ATCCNTTAAACCAANCCACCCGCTTGAGGAAAGTNACCCCTTGNANTGAGCAANCAAAAAA
NCGGCTNAAACCTGANCTAGNAATTCCTTNGAAAAAGGTCTCCAAAAAAATTAATTTNTNACN
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SEQ ID NO: 354 ACAGAAATTTCAAGATGTCAAACACAGTGATGCCATTTGCTATGTTTNAAT
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CATCTTTGCCAGTAAAAATAAANNANCTNNTTTNCAATAANCTTTGANTGGNGGCTNNCNGGATC
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SEQ ID NO: 355 ACTTTCCTACGGCAGCAACCTGCTGACAAAGAGGATCCACCTCCGAAACCC
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SEQ ID NO: 356 ACTCTTTGTTTTGGCACACTTTTCTGACAAACAGCCGGTGTCTNAAACACNT
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SEQ ID NO: 357 ATTCGCCCTTACCGNGGGCCNGNCCGNGCGGCNCCTTGGGTNTGAAGGGTG
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SEQ ID NO: 358 GCGAGGTACTTNTCTTCNCTTTCTTTTTTTTGTTCANGTNGCNCNATAC
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SEQ ID NO: 359 ACTTNTTTTTTTTTTTTTTTTTTTTTTTTNTTGAGCTGGANACTNNCTNTGTTG
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GNTTGGGATA

SEQ ID NO: 360 ACTTTTTTTTTTTTTTTTTTTTTTGGNGCNTTTTTNTTAAAAAGAACNAAATNT
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SEQ ID NO: 361 TCATTTCTACCGAAGACTTNCCNCCGAACNTGTCTGCCAATGAGATAAANTTG
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SEQ ID NO: 362 CCCTTNNCGTAACGGCGCCCGGGCAGGTACTATTANCCATGGNCAACCCCAAC
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SEQ ID NO: 363 ACTCTTGGTTTGTCAATGGGACTTACCAGCNNTCCACCCANNANNTTTINATC
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SEQ ID NO: 364 TNCGNATGCTACTTGNNCANTGATGGTAAAAGGGTAGCTTNTGTTGATCT
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SEQ ID NO: 365 ACGCGGGACAGNCCNGNCCACAGANNANGGCATANTAACTTATTCATTNC
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SEQ ID NO: 366 ACTTTTTTTTTTTTTTTTTTTTTTGTCTGGTGTTCAAATATTTATTTTAAAGTA
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SEQ ID NO: 367 ACATCACAACATGCTTTTAAANTCATTATGCATTGTGCTCACATTCCTTAA
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SEQ ID NO: 368 ACGCGGGGACAGTTCGGCCATGGCCTCCTTGAAGTCAAGTCGATGCTCTCGC
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TTTCNAAAA

SEQ ID NO: 369 ACGCGGGTGGGAATGACAACCTTCGGTCGTGGAGGAACTTCAGTGGGTCGTG
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TNNNGNTGC

SEQ ID NO: 370 ACTGCTGGGCGGCTTCTCGCGCTCGTGGGGTTGGCCAACTCTCGGAANGA
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AAAGGGNTNANACCCTTTTNAAAAAAATTTTAAATNCTNCCCGGNGGCCCTTANAAAGG
GNNAAATTCANNACANTGGCGGNCNNTTATTATNGGATNCCAAC

SEQ ID NO: 371 ACAATTCATCTAACTTCCGGAAGCACTTTCAGTCCAAATGCATAAACCGTCC
CACATGCCCNCCAGAACCACTTNAAAANGTCAANTTNGCTAACTTTAACCAAGNANTTCNAGG
GNTGTTTNTNAAGGCCTNNNTNATNCNNTNNTCCTNNTTNTAANTNATNCNCGGCCCTTGCCTG
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SEQ ID NO: 372 ACGTCGACCACTACAGATCCCTGGAGGAGGACCANGAACCATTGTTTCACA
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ACNCTNNGGNAACCCCATNGGAAAGGGGTTNGGANTCAAAANAAGGANCACNAATTTTCCAN
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CCTNCTTAAAGGCGNTTTNNNAACCCCTNTAAANCCCTAGCCCNAGACCCCTNATAAGCCN
AATTTGGCAAAANCNATCCANGGTTNTGAAAAANCTTTACNANNGNNAANGGNCNGNACCTNT
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GNTATAAAA

SEQ ID NO: 373 ACCTTGGCCAGGTCTCCACAGGCACCACAGTGGGAGGCTGGTAGTTGATGC
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TGGCCCTTNTATTAGNGGTTTATAAANAATGNTATAANGGGCNTTTNTGTNACNNNNAAGGCAN
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SEQ ID NO: 374 CCGCGGCGAGGTACTTTTTTTTTTTTTTTTTTNTGGGAGTTTGAAGCAAACA
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AATTCCCATCATGCATAGTTAACAGGNTNGNNAAAAAANCCGGCCTTTTANGGGGCTAAATGCTTA
AAAATTNTNCAACAANCATNGAAANNTGGGCTTTTTTTTTTTTAAACNCAATTTGTTGGGTTTACCC
CCCTANNGATAAAACNTNTNCANTTTTACNGCAGGNGGANTAAANCTTGGCANCAAAAAATNGCA
CCCCATTCAAAANCTTNAAGNANTACCTNTCCCCCTNTAACNAAAAAACCATTNTTTTNGAA
TTCNAAANATTTNATTTTNGGCTNAGNTTNTAGCCNNGTTTTTGGGATTCNAAAGGGTTTTACCC

AAAAAANGGAAAAATAAANCCTTTTGGGAACCTTTTCNNTTTTTTTTNGATTAAANCCANGGGAAC
NTCCANTTTCCCCCTTTAANATNCAATTTNNTAAAAANAATTTCCCCCANGTGNNTTGNCTANA
ANCCNCACTTTTNCOCACCACTNTTTANNCCCTTNNATTTGAAATTNCCNTAAGGATTAACANC
CNAAAATGGGGGCGGNTNCTT

SEQ ID NO: 375 ACTTTGGCTCTCTGGGATAGAAGTTATTCAGCAGGCACACAACAGAANGCA
GTTCCAGATTTCAACTGCTCATCAGATGGCGGGGAAGATGAAAGACAGNTGGTGNNACCACANTT
TCGTTTGATTTCCACNTTGGTCCCTTGGCCGAACGGTCCACGGGAACACTNTNATNTTGGNTGA
CTNTAATAAACTGCCCACAATCTTNAGCCTGCATGCTGTTTGATGGTNAAAANTNAAANTNTTTT
CCAAAACCCGNTTGGCACTGGAANTCGGTCAAGGGGACCCNCGNATTTCCGGGTAAGATTGCC
NNNAAAATNAATAGTTTNAAGGGNGGCTTGNCCCTGGTTTCTTGGTGATNCCAANCTNATNNANCT
CNTTANTTNTTGGAGGGNGGNTAAAAANACTTTGGNNTNGAACCTNNCNATTNANAGGGNGGGC
CNTCTTGACCANAAAACCAAGTCAGGGGGTTTTNGGA

SEQ ID NO: 376 CGCGGAGGTAAGTGCACATTAAGATCCACGAGACACAGCCNC
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TTGGAAAGACAGTGAAANAGAAACCGGGTTTCGGGGAATTTTACCCAANTCCCGNNNGTTTNGG
AACCGGGTNNACCAACCCNNTTGGGGAANGANCCNANTACTTGNCCAACCTTCNGGCTTNCCT
TTTCANNAAGNTTTGACACTNNTAAGGCCANTACTTTTGGCTTATGATGANCAAGTTNAAANT
GTNCCNTTGAACCGG

SEQ ID NO: 377 CGTNCCTAAANTGAGTATCAACTGNTNNTGCCATANCACTGTGNNAAANTGCA
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AANNTGTGCGCNATATTANTCACNANGTTANTGGCTGCTNCAANCTTATNACANTANCTTGNNTA
ANCCTNNGACTGCTTCTTNANGAAANCCCTGCNNNGCATNTCTNTAAAANGTNTANTNNACAN
TCGACTTTATCTCCTG

SEQ ID NO: 378 ACAGNTGGACCTTNTGNNATTAGAGGCNNTNNNGGTACCAAGGCCCTNCTG
GCCCCACTGGTCTATTTGGNCCTCCTGGACCTCCAGGTGTAATNCGGTNAACTNCTNGACTNAAAGC
AATCATGGACNTTATNCTGGNTGTTACAGGGGAATANCCAACTCTTTACTGTATGCANANNTGT
ATGAAAAAATAATTAATNCTTTNATGACTGNNAAAGGNTTAAANNTGTATCNTCTGAAANG
NAANGNTTANNTAGGNGGNTTNACTNATTCAAATANTTTAA

SEQ ID NO: 379 CATGCCTCGAGCGGCCCGCCATTGTGCGATTGATTTTNGCATTNTTTCNNACTT
TCTTCAGCTTCANCCCTAACAATGTACNTATTCTNCAATNTAAAAANTTCNNGGCGNTCCNCTNCNT
NNCNTCTNNGCTCTCNGGTCCGCTCTCCTCTCTTTTCGATN

SEQ ID NO: 380 GTACTCTTGGTTTGTAATGGGACTTTCCAGCAATCCACCCAAGANCTCTTTA
TCCCCAACATCACTGTNAAATAAATAGNGNGATCCTATACCGTGCCAAAGCCCANCTTCCAGAC
ACTGGGCTCANTANGACCACAGTCCNATACNATCAATNTCTATTCAANTAGCCCNCCCTAAA
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TAACTGGTAANCTTGANATTNAAATAACACAACCCNACCTGTGGGNGGNTNAAATNANANNT
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SEQ ID NO: 381 ACTCCTTGGCCGCTCACTAGCACTCTCCGCTGCTTTTTAAAGGCTTCATTG
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TGCCCCCGGATTGNTCTNGAAGNTNAACTTTTTCGGNAAAAAATTATTNNTTTCCAAATTTTCNCC
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SEQ ID NO: 382 ACCGTTGCACTCCAGCCTGNNCTAGATANTNAGATNCTGTCTCAAANNAATT
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TANTC

- SEQ ID NO: 383 CGTACTACCGANATGCCCGTTCTTACAACCGGTNTCAAATCGNACACTGTCA
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CTATNAACTNGGCT
- SEQ ID NO: 384 ACGCGGGGAATGTCTGAAAGTCCATGAGCTGTCTTTAATAGCGGATTATNAA
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TGCANATTGNAACATTATATCANAGTTGTGNTTNNNTAATTATANATATATTTCNTTATNAAATT
TTAANGTTATNTTCNTATAATNAANTNNTAATNNTTATCNNTAATTTTTTTTCATNTANTATATCTA
ATTTCNTNTT
- SEQ ID NO: 385 ACGCGGGGGACTGGAGACACTGAAGAAGGCAGAGGCCCTTATAGTCTTGGTT
GCCAAACAGATTGCAANATCAANGANAACCCANTGAGTTTCANANAACCGCTAANTANGTTATA
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- SEQ ID NO: 386 ACTTTTTTTTTTTTTTTTTTTTTGNCCTCTTATTTTCAANNNTTGGCTTANTA
ANATTTTTCTTATTTTATAANGCNATTACNACAATTTANGNAACNAAACNATTINAACNAAAAAAT
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- SEQ ID NO: 387 ACTGCNNGGACTTCTCCTTGCTGCTGCCATGTGAAGAAGGATGTGTTTGCTTC
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- SEQ ID NO: 388 TCCNCGAACCCNGCCCGCCAGTGTGATGGATATCCTGCANAATTCAGTCTCT
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- SEQ ID NO: 389 ACTTTGTGGATAAGAAAATGGAGGAACACATCTNATGGANAGTGGGCATTTG
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- SEQ ID NO: 390 ACCNNGGNCCNCTATATCGCNAGNCTNTTCTNCCNAAAGAAGCACACTTTG
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NTG
- SEQ ID NO: 391 CAANTNTAAAGACCCTNAGGAGTTCATGGANCACATATATGTTCCCANAGGA
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SEQ ID NO: 392 TTTTCCGAAGCCGGNCCGCCCGGGGCAAGGGTACACCTTGGTTGGGTGTTT
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CCCAANCATTANATNANTCCATAAACTACCNANTTANAANNCTCCCCCTACTCACACTATCCT
CCTNCTCGGNTGCNAGCCATTCCACACCNCTACCANTCCACAANCTCENNCCATNACTCCCCCTTN
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SEQ ID NO: 393 ACGCGGGGAGTTCGTCGCAGCCGGGATTTGGGTGCGCAAGTTCTTGGTTGTG
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CAAAAGATTCCAAANNNTAAGGGAAGGGCATTCCNTTCTTNGAACCANCNANAANGCTTNATN
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SEQ ID NO: 394 CGTGCACTCTGNTTTGTCAATGGGNCCTTNCANCAATCCACCCCTNGANCTCT
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SEQ ID NO: 395 ACGCGGGTTGAAAAAGAAACAAAGGAATACTTTGAGAGTTGGGGAGAAAGT
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NGGAAGCNAAANAAGGCTNACCCANGCNTCTAAANAANACNGCAN TGCTGCCGCTTAAGGCCCC
TACTAGCGCCCTCCTANCNAAANANGGGNNCTGGGAAAGTTCCATCTCCCGNNTGGTGAAA
CCGCTTAACCTTGCTATTCTNTTCTAATTAT

SEQ ID NO: 396 ATNCAACCTTCAANTTCATANGGTGGGGGAAAAACCCGCGGACTTTTANAT
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CGGATACCTNTCCCCCTTT

SEQ ID NO: 397 ACTTTTTTTTTTTTTTTTTTTTTTTTNTAGCACTTTTTTTTAACTCGGTAANAA
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NNACTTANTA AAAAGGNTGTGTNGGGAANTTNAATTTTNTNATNNCAAAGTTNANTAAATNTANG
TTTTATNTNATGAT

SEQ ID NO: 398 ACGGGGTCCCTCACCAGACATTGAATCTGCCAGTTCCCTTGATCTTGAACCTCT
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SEQ ID NO: 399 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGGACAGTGCAANAANANA
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NAAA

SEQ ID NO: 400 ACTTCACACANGATCCCAACCCCCACNNANNTTCAATGTGACCNCTCTGATC
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SEQ ID NO: 401 ACGCGGGGAGCACGGTTCGTTTTCCTTTANTCAGGAAGGACNTTGGTNTTTA
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- SEQ ID NO: 402 ACTGCATTTTTTTTTTTTTTTNATAAGGCTTATAACTATGGCTGGATCTTTTG
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- SEQ ID NO: 403 ACGGATGCTACTTGTCCTCAATGATGGTAAAAGGGTAGCTTACTGGTTGCTCTCC
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- SEQ ID NO: 404 ACTTCAAGATTAGGANNGTGGGTTTACATAAAATGATTCTCTGGTNANGGT
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- SEQ ID NO: 407 GCNTTTGAAAGATTGGGGCCCTTCTANGATTGCATTTCTTCGANGCCGGCC
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- SEQ ID NO: 408 CGTACCCATCTCAGATGAATGGNTACGGATCATCACCTACCTTTTCCAGACG
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- SEQ ID NO: 409 ACCCGNNGGGTNGCTCNTATNAAAACCTCATNACAAGNCATTTATTCTGT
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- SEQ ID NO: 410 GNNCGNCCGGGCACGAACCNCNGGGGANAGATNNANAATNATTGCCAGNC
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SEQ ID NO: 411 ACCTAACAAACCCACAGGTCCTAAACTACCAAACCTGCATTAAAAATTCGG
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SEQ ID NO: 412 NTGTACTTTTTTTTTTTTTTTTTTTTTTTTNGAGAGGAAAAACCCGGTAATGA
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SEQ ID NO: 413 GGTACTTTTTTTTTTTTTTTTTTTTTTTCCTCCCCACANAACCCATCTCAAAT
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SEQ ID NO: 414 TCNAGCGGCCGNCNCGGGCNCCTTANANATTGGCNCCTATTGGNTGANC
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GNTANG

SEQ ID NO: 415 GGTACTTT
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ANNTTCCNGGGCNGGCTTTNAAANGGNGNATTTANCACANTGGNGGGCGTTANTTTNGANTCC
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ANTTCCCNAAAATTTNANNGAANTTNAAATGTAAACCGNGGGNCCAATATGTNANNNTNTNT

TTANTGGNNNNNTNNATGTCNCTTTTNAATGAAANCTTNNNNCCNNNTTTAAAAANNCCACTN
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SEQ ID NO: 416 TCGCGGGTCTCGTGAGATCTGGTNGTTTAAACGTTTTTGGCACCTCCCCACA
CTGCTTGGATCTGCTCCTGTCACTGTAAGGCACCTGCTCCAGTTTGCCTTCTGCCATGNGGAAAAG
TTACCTGAGGCCTCTTCAGANGCAGAAGCCGTCATGCTCCCTGTACAGCCTGCTTAACATGAGCC
AATTNAGCCTCTTTCCCGTATAAAATTACCCNGTCTCANGTAITTTCTTTATTCAATGCNTGANCAGAC
NACTACTAAGACTTTATTGAANAAATATAGTTGCAAAGACAATATTGCTTGTGNNCANGGATAC
AAAATTGAGCCNTTTGAGAANAAACCGAACTTCAONCATTANACTNGNGTTANTTTGNGGAATC
NACTGATGTTTNTATAAANNCTANTGGTGGAAAGTCATACNNNNTCNAAGTAGNTNNGTTTNGG
GGTGANATTTAACTGNATNCNCTTGGGGTANAAAANGGTTTTTANNGGACAAAANGCATTATAT
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SEQ ID NO: 417 TTGAANCTTCCTTTTGGGCCCTTTCTTTCCNACCTTGCCGTTTACCGGATACCT
GCCGNTTTTCTTTNGGAANGNGGGCTTTNTATAACTAACCTNNAGGNTTAAATTNNGGGG
NGNCTTCTCCAAACNNG

SEQ ID NO: 418 ACACTAANATTTTATTAGNNATCGCTCNGCTTACACACTCCANGCAGGAAG
TTATTTAAATCACCTCANANAAAACCTGNGTGACCTAACCNANTACNTNATATGCAGATCATGAN
TACTTCCANANTANANTCACCNAAGNTNNNANGGNCNTAGGCCCTACGTGNANGANATGTNGCT
TANNTGTCTCANTGTAGGGANANTAAANAGCGTGTCTAGCTCNCNTNTCTACTNNGACAACNCTT
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CATTTCTTNTCACACGATNTCTGCGACCCGCCNGGGATTAATACTCCNGTATGCTTANNNTAAAG
CTCCACAGCTANATTAACAAAATTGCNNGGNAGANCANTACAANNCTCNGNTTACAANTTAAAG
GACCTNGGCGGGGCTTNTATTCCTCTACAGGNANCNNGNCNTNTATTAATAAACCNCGATNC
ACCTTACCNCTTTGTTTNNCTTTTCCGGCTTNTTGTGTCNAANCTGNTGAANGCTCCAAGTTTA
CNCCTTNTCTTCCNGGGCGGGCGGTGAAAGGCGANTTTAAACNNTTGGNGGNGGTTTTTGGGTC
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SEQ ID NO: 419 GCGTGGACGCGGCCGAGGTACTAGAACGGGACTCATCCAGAAGTACTATGCC
CTCCTNNGTTAANGCTCAATCATTTAAGAGTAAACNCAAGGAGAGGCCNTTCTGTATTCATACCCN
TCTATGTGGATTAAGANGANCNNNANTGAGANTGGNCTATGATCTNCCNNGGCTGCTGCTNCTCT
CTACNANTCTGCTGATCCGGAACANTACTATGNCNATAAAAGNNTGNGAGAAAGNCCNCGNC
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NAGTNGGTGACCTATGCTTATNTATGTCATGATTGNGTAGATTGGATTNNGACGNNAATCAANG
AAGAATTNTAGNATCTNCCGTATCTNATATTNAGAAAGAAAAATGGTGTCTCAACNTAACAATT
AATGAGTNCCTCGGCCGCGACNACCCTAATNGGCGATTTCCAGGNCACCTGGCCGGCCNGTGCCT
ANTNGATTCCCAACCTTGGGNCNACCTTGGNGGAATCATGGCNNNAGCCNGTTTNCCTGGGTGA
AATTGGTATTCGGNCNNNTTCCNCAANAATANNANNCCNGTACCATTAGGGTAAACCTGGGG
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SEQ ID NO: 420 ACTTTTTTTTTTTTTTTTTTTTTTAAAGGAAGGGGGNGTNNACCTNNANCCCTT
TTTNAATGGGGGGNNGNTTTAAGNCCNACNNNGGGGTAAATTTTTANCTNTNTANANGGTT
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GGGTTNTGGGNCAAATTNAAAGTTAANNNTAAATTTTNTTNGNANAACCANTTTNACCAGCN
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SEQ ID NO: 421 ACTTTTTTTTTTTTTTTTTTTTTTNGGTTTTTTTTTTTTTTTTTTTTTTTT
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CCATTTTGGAATAAAAAACCTCCTTGTAAATTAANNCCCTTTTNAAGGGCTTATTTTCNAANA

GNCCATTAAAAAATNGGGGGTTGGACCCNCCAAAGAAATGGGGGAACACAGTNACCCANC
CAAGGNCCNTTTTAGGGTTTGGTTAAAACTTGGCCAAACCTCCCCTANGGNAAAAATTTTTTTA
GNAANTNAAATTTTTAAAGGAAACNCCCAATTGAAAAAAAAAAAAATTTTCCTTGNGAA

SEQ ID NO: 422 ACANTATGTNTAATNNTTAAATGTTTTATTATTGGAAAAATAANGCGTGAA
TANNATGCCAGGGACTGNCAAANGACTTGATACAGGATGGNTANNCTTGTCAGCTAAGGNCACAT
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ANAACTGATTNTNAGNNTNACANAAATGTCAGANTTGCAGCTATTGCNGGAATCCAAAGTNATG
GCCNGCTAGCTAGGTTAAAGATTGGTTTAAATCTGGGATNTTGCTTTTNCCTGTNGACATTGCTT
GANGACATTATCTGANAGACAAGTTTGTNGCNCAGTTGCCTGNTANAAAAACCTTTGNNANACT
TNNTTNTNCAANAGCCATTGGNAAAAATCCGAGGAGNTTGGANNGAAAAANCNNNGCTTTAA
ACTNGTTGCCATTTTAAANANNNTTAAATGTATCGTNAANTTTTAAAGCCTCNANTTTACAANTCC
GCTTNGATAANAGACCTATCAANTNTTTTGCTCAAANGCTTNTTACNCTATTA

SEQ ID NO: 423 GGTACTGTNGNNTCATCNNTGGGANNGCCACACCNACANNCCNGCTTTC
TATGCNCNACATNANTGCCNATCNNTGGNNANCNNAGANCNNNGCTCNGCNGCNGCNGC
NTTANNNCCNCCNCCANGANGATCNACANTATGGACNTGCTCCTGCTTNAACGTGGCCAN
CGTCNNGCATCAGATTTGGAGTTGCTGGCCAAAGGTGGCTCTGATAANCAGCCNTGGTGTNTANA
NGATATTTACGAAGACTGGCNTTANNGGACCATACCTGNANTNTTCTANCTACNGNAANCCCA
TTTTATNOCATGGANNTTNTAATCAANGTNTGCTNTGGTCTGAAGCCCTATATGCTGGAGATGG
ACNCCNTAATNAATNATTAAAGGGAANNCCCTATNCTGANGTGGGGTGCNTTTTACNAGACTT
TACNTAANTATAGACGGGCTAACCTGCAACCATNNTGAGAAATGACTCTTNCNTNTTGNCAN
GGTTTTCCAAGATGTCNNTACCANACNCTTTTNTTGAAGGNTTNTTCCCCCTTAATANNNCC
TGTTATCTTCCCTTTTNCNTTGAAGGNGAGATCTGCNTNAGGGTTCCNTAAAAGG

SEQ ID NO: 424 GGTACTTTTTTTTTTNTNTTTTTCTTTGGGAGACTAAAAANTTTATTGCAT
CTTTAAAGCCTTAGGCCGTATGACTAAATGANTAGACTGNANTGACNGCGGGAGGAAGAANCA
NANGAAAGATNTTAAATGAGGNGGTCNGGTTGGGGGAAATAANNCGAANATTCNCTNCCAGGGTG
AGTCCTCACATGGCCTNATGCCCTTGTGANTTGNCCNCCAAACACAGGCTNGNTACTTNCNTT
CTGCACTAGCAGAGAACTTGCNANATTAGGGNNACCTNACATNCCNGTGTAAANTCCTTTCCCC
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NNTTGGGCTNNGGTGNCCTTNTGTGGGTATTGGNACCCAAATTCATACNNAGTTNGNGTAAATTT
ANCCAAATGNNACTNTNATCNNGGGAGNAAACNANAAGGATACCTTCATNTCNCAANNTCACNTNN
NNCTGGTTTCCAAGAGGCTTTTNTGNTGGNNAATNANTGTTTACNCCNTATNTNCGGNGG
ATCACATNCTGGGNTNNTGNTGNNCTAACNCCNTT

SEQ ID NO: 425 TCNAGCGGCCGNNCGGGCGGGNTCTTTTTATGAGAAGCGTATGGCCACANAA
GNTGCTGCTGACGCTATGGGTGAANAATGGAAGGTTATGNGGTCCGAATCAGNGGTGGGAACCA
CAAACATGGGTCCCCCATGATGCAANGGTNTCTTGACCCATGGNGCGTGTCCGTCTGNTTCCGNGC
AAGGGGCTTTCNTGTNNAGACCACGCGANAAACGGNTNANAGANTNNATAATATCTCCCTAGGT
TNCATTTGANAGNTNCATATNAGATCGTNCCTATNNTTNNITNNNGNTAAAAATGGTNAAGTNN
ATTNTCTGNACTGACTGATACGGANNTTGCCTTTGCCNGTCTGGGCCCCNTAACNAGCTTGCANA
ATCCNNNGGATTTTCAATTCNTCTTTAAANAATATNANTGTGCGCCNNTANGNTTGNACNAATNC
CCTTACANTTAAGATNGGGNATTAATTCNTGACCNTATGCNNTCNATCATTTNGANGTTTATTC
ANTTNNNNNNCTNGAACTCATACCNGCTCGGTNATTTTCGNGGANANANTGCNNGAATTTNGTNN
CNNCACNACATATGGCANNANTCTTCCANCTGGTGNCCNACNTAATTGGAANCINACCTCGGAA
NCNTNNTNGGTNAAAGTNNAGTNGTANNTNCTTCTNTGGG

SEQ ID NO: 426 CACTTCAGCAGCGNGGGCGGGAACCTGGGGGTATTGAANAACNGGCAACCNC
AAANTANNAATTATNACAGGGGNCAGAACGNCANGCTAGACTTNNCTTCCACTGGTCACAGNATAA
NGGCAACCTGCAAGACTNAAAAGNAGGAGANGANGNNGAATNGGAAGNATCANCGGACCGACG
GACTGGGAAACCCANGGCNGNNAACGGGNGAAGANNAAAAAAGAAATCCNCCCTGAAGAACCC
GAANGANGGGGACAAGAAGGGGNNACCTGACNACACCCCGGAAGANGNCGAAGGGANGCNC
AAGCNGGAAACCGGAGGANNANANAACCTGGGGAACNGANAACAANAACATACGGGGGCCG
NAAANGNCCCGCAACANNATGCGGGGNAAGAAACCAACGCGCCGNGGGCGGGGAGNAG

SEQ ID NO: 427 ACCGATGATACTGNCNCTTGCNCTGANTATNTAAACACTNCACAGTGTNAT
ATNGGGAANATATNGGGAAGGAAATATNTNNNTNAAANATGAACGCTGNCNTNATGTTTTNTCT
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TATTATGNCNTNGCTTAATTGNNTTNTCCCTGAGCTTTAAATCANTNANAGCTTAAATTGTCATAT
CCGNTCNTTGGCTTTNCAAGGGGATTACNAAANTTTGGTGNATACAAAAANCCTATTTTGGCTCT
CTTCACTACTNGAGGGTCNACCATCCTNATTAAATGTNTGACACCATCAATNAATAACAGNTGCT
GTTTCATGTNTAANAAGANCCNANTATTTTATTTACANGCGGGTNACCTGGGCN

SEQ ID NO: 428 ATTTTGGAAAAAATAATTNCCCCCCCCCNCNTTACNTGTCGGNCCCTG
CCNATGGTGGNCTAATNANGAAGCNGNCAGANTTTANCGANCCTNNANAANGANGGANAAGGC
AGCTGNAGCTATNAAAAACCANCNGGGGATGATNNGATACCATCAGTTTCACANANNGGAGAT
NTGAAGCATTACTNNAAACTGGGAAAAAGGCCNCTTCGGAANGAACTGGTTGACTGGGGCA
CCACAAATTGCACAGNTGGGGGATCTGTGNATNCCNCGAANCACAAACNGAATTTNTNGCTCCNT
GCNANGCCNGGGCNCAGACGCGCNGCGCAAAACCGGCGAANACNACNACCTCCNAAACAAAN
CTANAANAGNNGCAGGCAAAANACAGAAAGCCT

SEQ ID NO: 429 AGCGGNCCGCCCCGGGCANGGACATTCCCTTONGGATCCTGCTTGTCTTCGT
AAAAAGCACCANITGGNACAACCTTACCCCGAGTGGCCNAACCAACCTTTTGGTTATAAGGAAAC
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SEQ ID NO: 430 ACAGAAAGTTTATACTATAAAATTACATCCCTAAGNGATTAGGGTCCTCAGT
AACACANGAATTAAGAAATGAAAAGGONCATTTGCTCGGGAATCCACATAACTACAGANTAGTA
GCGCAAGCTNTTGTTCGTCAGAAAAAGAGACTTTTNAAGAACATTTTACATNTTTCCTAA
CATTATGCCCTCNTANTTAAAGGGNNGCCTANGACNNTNCCNTTNTNATTTTNGGGAANGNC
ANCCCTTTTTTTTNCNCAAAANGGNTTTTTCTGCTNTAAAAAANNGNGTGGTTTC
CCNANGAATGTNCCCTCANTGGANNATTTCTCANNGAAGGTNCCAACNCTTTCCATTTTTT
CANNGGTTTTNTTGANNGTCNCTAGGTGNTTGNAGNANAAATTCNTANNCTTNTTNGNG
ANNNNCCCTTNAAGGANGAANTTNTTTTTACNCCANCNCACANANATATACGNNNTGGNA
NNGGAGCNGNCAANANACCNTTTTANANTNAGTATNTTNGGANTNTAANATATNANNNTCCCG
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SEQ ID NO: 431 ANCCGTGGTCCGCGNCCCGANGTACTTTTGGCCTTTTCTTGGGGATAGNAAGT
TATTTACGCCAGGGCCACAACAAGAAGGCAAGNTTCCAANAATTTTNAACTGGGTTCATTC
AANAATTGGCCGGGNAANAATTAATAAANCAAAATTTGGNCCNACCCCCAAGNTTNGNTTGA
NGGNCCAACCCCTGTTTCTTTTGGGCCNAAAAAGGGGGGAAAAAGGATAAANTNNTAACCTNT
TNTTGAATAATNAATNAATTTNCCAAAAANTTTAAGGGNTTGNAACTNTCTTGTGGGNGGAN
AAGGGGAAATTTTNTNCCAAAAATTCCTGGGGGCTTGAATTTTNTNNGGGCCCTCNCCTTTT
GCNAAAAATGGAAACCCCTTAAATTTTGGGGTTTTTGGGGGCTTCCCTGGGGCTTTTGTGATA
NCCNATTTNCAAACTTNNNGAATAGGGCCNTAACTTTTNCGGCNAAAAAAAGGGNAATCCCN
TTNCCCCAAAAANCCAAAAAGGGGGGGTNGGGAANTTGGGNCACCCNNNTNTTAAATTTT
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SEQ ID NO: 432 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGTTTTTTTTTTTTTTTTTTTT
TTTTTTTTTTTTTTGNANAAATTTTNTTTNTTNAATAGCANINTGANNANNCATGGNCCAA
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NTTNAANAAAAATTTNTTAANTGGNAGNTGTTAAAAANTACCANTNTGANCACTNTTGACTNTTT
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AATACCTNGGCCGGNACCACCTAAGGGNAAATTCANCANANTGGNGGCCGTTANNANGGGAT
CCAAGCTTGTACCAANCTNGGGGAAATAANGGNCANAGNTGTTCTGGGNAAAATGTTNTCN
GCTNAAAAATTNCAANAANATACNANCCGGAAANCANAAAGTNTAAANCTGGGGNGCCNAAAGA
GNGNANCTAACCCNNTAATTTGGGGTTGGNGCANANTGGCCGNTTAAANNGNGNAAAAACNTN

GTN

SEQ ID NO: 433 CATATATACCCAAGNGTGCATCTTGATCTGTATGCTCTTANATGCGCTTTA
TNTACAGCTACNGCACATANNGCNACATANTTTACNCACAANGGTTGAAAACTGTGCAT
GATTNNATATCATCANCNAGCACGNNTGCTGG

SEQ ID NO: 434 GGCCGAAGTACGCGGGCCTGAACCCAAGAGACAGAGGTTGCGNGTGAGCCGA
GATCGCACCAATTGCNCTCCANCTGGGCANCNAGCANAAAACTNTGNCTCAAAGAAAAANNAAA
NANTAGANCNAGACGANAATGGCTTNCNGGACAGGAGCATTTGCTCATTGTGCGGGACNGTTC
NANAATCANNCCNTGGTNTGGTCTTCTNCTTACCTTGGCTNGTTTTNTNCAANCCACGTANNNTN
NTAANACTTTNTTGAAGCNAAATAA

SEQ ID NO: 435 ACTTTTTTTTTTTTTTTTTTTTTTNTGNTTATTTTTTTTTTTTTTTTTTTT
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AAATATCATTCCGNNTTGATNNNGGAANGGGTNTTAAACGGGTTNGGCTAAGGGTTAAAAATTGG
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TAGGGCTTNTANTANTINAANGGCACATNAAATTGAAAGGTAAAAAANNTNGAGGGGGGGANT
GTCTNCTGANTAACTNCTNAAAANTAGTTAAANNAANGNTGACCCAANTTTTTGGGATNGCAGA
NAAATTAATAATNCTAATTACTNNGGCCCANANAATNANATTTTNGCCTNCCGGCGAGNANAA
NNCCTTTA

SEQ ID NO: 436 ACCTTGATACACATAATCAGCCTTTTCAAAAAATGCCTGACAAGAATTAGTCTT
TCCTTTGTGTAAAAAGTCTTCCACCCATGGATGGAAACAGGCTGACTCCTGGAGGGTCAAGCAA
GGGGTGGGGAAAGGGGAACACANTNCTTTTGGGAAGGCNAAAGCAAAAAAGGGTNTTTTGNC
CAAAACCAACNTTGGGCCAGCTCAAANGGGGNCNAAGCNTNCCCNAAAAAAGGNTTCCNTTTT
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CTTTTTCCANANGGAAAAANTTTCCGGGGCCANTCNCCCCAAGGNAANNNGGCCCTTTCCNAAN
CCCNNTTTTGNAAAGNAAGGGCCCGGGGGTCTTNCCAAAAAANNTCNNGGCNCTGGGGGG
AAAAAANCCNTGGGGNAAACCGNCCNCTTANAANTTGGGGCCCTTTGTGGGGGGGCCCN
TTTTATTATGGGGGGGGNNTACT

SEQ ID NO: 437 CNGACGGGCCNCAGGAGCANNACAGGAACACTGCGNTNCTGNNAACCTGN
GGNTGCTNATGTGNCCACTGGGCACCTTATTGCNAACTGAACCAANANACCTCTGNTTACAGC
TTGGGCTGCTGTCCAGCTTCCGAGGTGCAGCAGGTTGTGGGAACAAGAGACGACTTTNAGGAT
NAAANGACCAAAAGGANAAAGCTGCCTTACATGATTGATTGGGGCCTAGGANATGGAANTCANCN
TTATTTNTNAGAGAGTNTTTNACTAATGNNGNAGGCTGAGGNGCANNCCTTNGAATATGCCTT
ANANGGCCGNACGCGTGGNTCCCCCTGCAATCCCNNTACTNNGTGAGGCNAAAGGTGGGCNNGC
CANCCTNNGCTCGAANTCAAAGANCNTCCNTANANTANCNNNGGOTGAANCNNNTTCCNTAN
TNNNNATCCAATNATTTATCNTNNCATCTNNANCTCATNNNNCTNNTAANCNTNANNCTNGTGNA
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SEQ ID NO: 438 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTATTAAATNTNAA
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GGGACCNANAGGGGANCGGCNATNAAAGGGCAATNAAANNCTAAATNCATTGAAACAAGCTTT
ANACAGTNTCNTGCANTCCACATNCTTGTACCTNNGGTCGNAACCCACNCTAAGGGCAAAATTCAN
GGCANNANTGGCGGCCNTTCTAGNGGATCCAAACTGGNTCAAANCTGGGCNAAATCATGGNNAT
ANCTGNTTCCCTGGGTGAAATNGGTATCCANTCACAATCCCCACAACATACCACACCGGANNCT
AACGGGTAAANCTGGGGTNCNNAANGAGTGNNCTAAGNAGATTAAATGCGNTGGNTAANTGG
CCGCTTTC

SEQ ID NO: 439 ACTATGTCGATTGACAGAACANTTTTTANGATTCTCGGCCTTGCCCTTCAC
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TCAAGACCTCTTTATTTNCTATCATCTTTNCTAGACACACACAATCAAGACCTGGCAACTGNT
TTTGAACAAGAGCCATNAGGTANCCNTTANTACTTGGGCCNCTTTCTNAGTTNTGAANTATTCC
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GNCCTTTAAGATCTTTNNNAATNAGTGGATTGNATAGTAANNNTCAACGAAANGGATATNGGAAN
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ANTTANGTTTGNTAAACC

SEQ ID NO: 440 AGCCGTGGTCCGGCCGAGGCACTTTTTTTTTTTTTTTTTTTTTTCGTTTNCN
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CCAAGGCNGATCCTTGAATCNTGANCANAANGATNGACATCCTACANGGTGCTNGCAATACGGC
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NTAAAGGAATNAATNTGCAACATNTTGNNTTANNNGGGACAAAATGNTGNCAATTATTTGNTG
GCCCCCTACTNGTGAACCTGNNANCANAAATGGTCCAGGGACTGTNAANCNNAANGAAGGNTT
TACATTTTTGAAAACCTGCTCTGCAGGATAAAAAANCCNGGNTGCTGCTGNTTAAANCCNG
TGANANAANTTTNCCGGTTGANCCTCNCCTGACTNTTGNNTTGNANGGGCCNCCNCTGGACN
TGNAGGGGGNGGGGATATNTGTACCTNCCCGCCGCGCTTAAAAANGGGNAATTTCAACCCNACTG
NGGTCNNACTTNGGGGNNCCAACCCNGNNTCCANC

SEQ ID NO: 441 ACACGGGGGTGCGTGGCCGGCAGTCATNTCNGGCCGTNTCANAATTATAAG
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CTTGGCTGGGGAATATGTAGATTTCATTTTACNTTGANAATTCNTCTNANNGAAACAAATTTACT
ANATNGCTTGGAACTATATGNTTGNATAAATNATNCNAAAGTCCANTATTGGCAATCATTTGGG
GGATCCCCCTTANTNGTTCAANGAAGCCCTATTATNTCTTAATNCTGNTTACCTGNGNTTTTAAAT
TTNTCANTNATNCTTANTANNAAAAANTTCNANAATTCAA

SEQ ID NO: 442 CGTGGTCCGGNACNAGGNACNAGAATGNTTCATGAAATCCGNTTTTAAAAATGA
ACNTNTNTGNGGCCACANTTCTANGACTGGGGCNAGGNCNCNNTGNCAAGTNTGNTTTGAGG
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CNTGCCANGGATNCTTTGACTTTGGTTTGTCTGCTGNTGCTNNGGATATTGGGAGGGNTATNCTTTN
CANGTTNNAAGAAANGGNTGTGGGTTAANGGCTGTCNTAAAAGANCCCTGGCTGTNACNCCANT
GANTCCNGATTGCGTTTGTACCNTTTGNAACTGACCCGNTAATTTNAAACNNTTTTTCANCTTTT
TTNAAAGCNTNTTANGAAGCCTTCCCGGGANGNAATTTTTTCCAGGTTNATNTNCTTNNCCGGGCN
GGGCCCCGTNAAAAGGGGGAATTTNACCCACTGGNGGGCNTTCTAATGGGANTCC

SEQ ID NO: 443 ACTTNTTANGGCCAN
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NCGAAGAANTNAATCNTNNCNGGGGATCTNGANCTNCAANGACTGTGACGGNAAAGGATGNTN
TTTTTTTACCTGGCTTNNCNAANTTATNNCAAAACAAAATGGGAANCAACCCNCAATTTTTT
GGNAANNAGAAAAACACNACTAGGGNACCCAAAAAAACCCCATTTATTTTCTTTGGAAAAAGG
GNNGGGGNCCANGNTAAAAANTGNANGGGGNAAATTAACNTNANNCAAAAGATGGAAACNT
NCCTAAAAAGNTTNCNNTNGGANGAAAGNGGGTTAAAAANNCTNAAAATCTTTTNTTGGGAAAN
AGGGACTCTAATNGGTCCNTTNGGGCTNCTNAAAAANGGGAAANGGAANNAANANTTTNCTTNA
AAAGGGNGGCNTTNAAAACCCNNAANNGGAAANAAAAAANTTTCCNGTTGAGGTNNGNNAC
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TTAAAAAATAATGGNTTNGGGGGNGNCC

SEQ ID NO: 444 ACCCGGNGCCCNACGGNGCCNACAGATGGCTGGNTNNGACATNGGGCNA
NNCTGCCAGNTGGAGCATTGNCGGCNCCGAGATTTNNTTNCATNTGGGGTGTGATGATTTGTTCA
GAATATNTTGGCCNGAACNAGANCTGGNATTCATGGNTGAGNTGAGGTGACTGNATGTCA
NTGAGAGACTGAACACANATCANCATACATCTTACCCATGCTCTTCAAAGACTGTGCTAAGAGA
GAACCTGTGCNCATTCCCTTCCNTATNGGCAC

SEQ ID NO: 445 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTNTAGGNTT
TTTTTTTTTTTTTTTINCAANCCTTTCANATAANTNNATTTTNTCCTTCNACCANAATAATGGNAT
ATCCAAATTTGTCTTAACCGGGGGGTNNGNAAACACAGGCTTNTCCATCCCACCTTACAGGCAAG
GNAAAGGCTNNTTNTTGAANGGCCCAACCATGGACCTTNNGTAAATCCAANCNAAGCNACCCCC
TNGCCGGGNTTAAATNTAANTANACATGGGCGGCCAGTTAATNAAATCTNNACCCAAATNTTAA
NTTTNCAAGNGGNTTCCNANTATTTGGCATGNTNTTNAANAANAAGGGGANAGACCCCTTA
ANTGNANTTNCNCCCTTTGGGGNCTNAACNNTTTTGGACAAANCCTGNAAATNACAAAAGGG

SEQ ID NO: 446 ACTTNTCTTTTNTTTTTTNTNNTTTTTGNTCAAGATTAATNNCTATNGACAAGG
TTNATAAGAACANATATTTAAANTCGAAGGCCANTTNTAGGTCTCATTTAGCTGCTTATTTNGTT
CACTTGTATTTACCTTNCCTAGNGNGGTGAGNAACTATCAAGAAACAAACCTGTGAAAAATCCT
GNTAACATTCACANATATTTGGTATATATANGGCTCTNGGANGCAANAATTTNTCAACACITA
ANTGGNGNANCAAGNGNGTCATNGGGANATAAACAGGATNGNTTAAANNTTGAGANTTTAATA

NA

SEQ ID NO: 447 GTANTCTTCNTNTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTT
GCAGAAATTCGCCCTTNCGAGCGGCCGCCCGGGCAGGTACNCTTAGAGGTANNTGTNNTNANANAN
AGNNNTGTNNANNTTAAAGANNCTAANGTCNTNATNTNTTATAGNCAANNTACA

SEQ ID NO: 448 GGACNTTTTTTTTTTTTTTTTTTTTTTTGGAGTITTTATTTANTATNGGGAGCAAAT
TGNNTTNTAAAATGNATATTGNGAATAAAACNGCNTTNNNCNTTTAANGGTNTAGGGCTGTNAA
NNGNNNCANGGNGNNGCCGANNNAAACATGANCTGGGCTGGGTTTNTATNTTTGATGAAAAAN
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CNGNCACCTTTNNAAACANTAAATTGCNGGNCNNGGGGGGAGGGCTNTTNNCGGAACTAAACTGT
GAGCCCTTCCATTTTITANGAGGGGANGTGANAAAAAGATTACACNGTGGNTTGAGTGNCCCTNA
GGAAANAATTNGGACCTAACNTGCCCGGAAANGAAGNNATAGGTCTGATNCGTTNGTANAANACG
ACAAANNTCACCTCCCCNTCTGGTGATGCACTGANGGGACAGGTGGAAGNANANTACGNTTA
TTGCNACAGTNTCTGTACCTNCTNNGGANGACCGNGTNTAAAGAAATTTGAAATAAGCTCTTTA
CNTTGCCTTTTNA

SEQ ID NO: 449 GTACTANACACATCNGGGACAACCNCCATTTCCGANATGATGCCGAAAAACNC
AAGGCCANAAGCNAAGCAGGGGATGGANAGTTTGNNGGAAGNTATTTCTTTACCCANNAATGA
CCTGNTGCAAGACTTGATGCNCTGGTANCTGANGAACATCNCACNGTGGACGCCANGGTCTAT
NNCTACGCTNTAGCGCTGAAACATGCNTAAGCAAAGCCATTTGANNGTGCCCTTCTTGANATTTTA
NNCCNAATATGACACTTGGCCATNTATTGTNAACGAAAAGNNCCANGCCTTGTTCNTAAGACNT
TG

SEQ ID NO: 450 CGCGGCGAGGTACTT
TTTTTTTTTTTTTTGGACNCCCAAAACCATCCTTTATNGGANNATNANTTCANGGNANCNCANNA
AAAAACATTTAGGNGGAATTNANAATTNCCGNTNAAAAAACTNGCCCNCCAACANAAACCAATT
TANNAAGNCAATTCATNAAANGGNATAAAACCNNTTGNNGGGCATGANGGCCANGGGACAAAGC
TNNAACTTGGCCCTGGNCCTTTNGAANCCNNGGNAGGNNGANCNTTTNNACCCAAAGAACCCNGAA
NCCCCGGGGCAAAAAAGAAAAATCCNCTNAAAAAATTTTAGCNAGGGGGG

SEQ ID NO: 451 ACGTGCCGAGGAAATACTCCGCTAGCAATCGCATNATCGGTGCCAAGGACC
ACCCATCCTTCCAAATGANCGNGGCCNAGGTTGACATAGGTAACNGGNAGNNATAANGGCCAATT
NANANNTGNNCNTTANGGGGGGCCNTNNCANGNATGGNGAGNNAAATNNNTCCNTTNTCCNA
TNGGCCAAGGCCNANGGCATCNTNTNAAANAACCTTTNGACNGGAAAGAATCAGAAATGTGGAAT
NTTGNNTAANTAANTAATGAAACCCAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT

SEQ ID NO: 452 CNCCTTAACCGTGGCTTNNCCGACGTACANTCCAATCGTCTTCGNGGGGNTTN
CNCTTAGCCGANGAGTTCNCNACNNNTCCACAAATTTTAAAGANGAGGTAGACCCACCTCCAT
CTTAANACTTT

SEQ ID NO: 453 AACTACCATCTTTCACATCAAAATNGGGGANGCTGGAGGTAGTGAAAAAGCTA
TTNGGATTNAAAGTGNNCAGAAATTCNTGTANACCAACAGCAACTGANCCNCTGTGTAATTAANGGC
NNTCCANGGGNAATCANCTANTTCGAGCNTNTTCGCTATTTAGGCT

SEQ ID NO: 454 GACGGAGCAATCGANGAGGCATAACCACACTTGGGGGTGGGCTATAGGGGC
TGGGAAAAACCTGAAAAATGAACTGGCTTTTCACTGGAGGGGCCANGGGTTGGAAATATTGGC
CAGNCTTNGAAANGTNTTTAAAGNCAAAANTTCTTTAAGTGANTCTTTCTCTNAAAAACANCA
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CCTTGATGATNAANAANGGCCCAATTATTGATNGCCCNCAANCCNNANTCNGGGCCANGG
CACNNACANGTCTCTGTAATCTNCTGGGANAAAGGCTTTGGNACNNATAAAATCNCCAATGCNT
TNAGAAANAANGNTNATNCAAGCCCCATGCTCCACCCTGCANTCGTAAACNTCTCAATTNANG
GCNGGAAGGGGAAAAATTTNGGAACCTCGGGAAAAAGGGGNTTCTTGGGCAAGGAAAAANTGTC
TCTGCACTCCTTNGNNGAANGGTTTTNAATTTTAAACCNCTGACNTTNACCNTGGTNGGGNGGA
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CAGTTCTNTNTGAAGNAANTNCC

SEQ ID NO: 455 ANCNTGGCCGCGGNCGAGGTACTNCTNNACTGTGAACGGGCTCCAAAGGA
CATGGNTCTGCANTCAAAATAATNATAAANGGACAGGCNTNGCNAAAAATGCATNGGNCNAC
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ATNTGNGGNTGCTNCNTNTTTTTTATTCANNATCAACNNTCNAGACNTNATNGCCTATCANA

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CNGNANTTGTAGANGTCCATAACTGGTNNAGAACGNCGGTANACATNTCTTTTTNATAGAGGT
CGCTACGNTCTGATTTNCGCNCNAATTCNCNATNCTNNTCNANAANTNNCTTTNANCTTNATTNNAA
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GNAGGTCCG

SEQ ID NO: 456 ACTTTTTTTTTTTTTTNTNATTTTTGNGGGTNTTNGCATCCACAACNGTCCAAN
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CATNGGNCANTTCGGCAGGGCCANTGATNGNAATGCCTNTCANTTTTTNTTGAANACNCACAGTTT
NTTCAAATTNTCTNAATGAATAAAATCTCATCCNCCCTCTTTCCCTTTTNAATAATNTCACNNCCA
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GCCCCCTAANAGAAANGGGGGCAATTTTCTTTNGACCCNATTTCAATNTTCTTTGTCTNAGTTNAA
AATGGNNTNANAAATTTNCCNGGNNANATGNANCAATTTCTTTGANTCTNTGAAAANTTAAAT
CCAANCNTCTTTTTCTTAATNTNTTNTTGTGTCNNNNNNNACTAAANCAAAGTGCTNNTTCNN
AAATTTTATCTNANNGNTNTATGGTGGTAANTCATCAGATCTCTGNANNGNNGNNTCTNTANA
TNG

SEQ ID NO: 457 CGTGGTCGCGGCTCGAGGTACACTGGGAACCTCAAGAAAAAGCTTTGAANAG
AAAATGGAGGAAGCNCGAANCCAGAAACTCTAAATCTTGAGACAAGAAAGACTNTCTATNATGAA
NGAGATCTTTTNGANCAANACCNAACNACAATGTGTGGGAGAAATCTNATGANCTAATACCAT
GGCTGCGAAANNAAAANTGCNAANNNAATNTCTNTCCGGNCGGCCGCTNGAAA

SEQ ID NO: 458 TTNGTACTGATTTNAAAACTAATCACTTAAATGTGCCACNCCGCAAAAGAG
AAAACCAAGAGTGGTCCACAAACACATGCTCCTTTCTCTCNGAAGGTTTTACNANNCATNGTAAT
ACATAACCCANTCTTTTANTANTAACTNAANNGGCCANTNGAAACAAACAGTTTGGAGACCGTT
CTTCCCAACCTNNTNAAAAATNGGGGGGGCAGGGTATNNGGGGATAATATCNNTTATATCCGACNT
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TGATGACTTGCACCGGATTTNGCTGCTCTTTTGNACGNACNNGTNNNTTCCGCCCTAGGGCTGG
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CGGTTTTNACGATACTNTAANATANTTAAAGGGCNCNTTNCANNTTGTITTCANANTNNGT
NAAATANTTTTTCTATNATNTTTNTAAATCTTAAACTTAAATNCTNCCNTGTGTNAACTCCT
NTANNATTGGGNATNNTCNGACCTNTNTATGNNT

SEQ ID NO: 459 GGTACGCGGGGACTGCAAGGCGGCTGCANAGAGAGGTTGTGGCGCTANTTTC
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CCAATATNACCTTTCGTGGCACCCTAAAGGGCCACAAACGGTGGGTAAACCCAAATCNNTANNNCN
CGGATGTTNCGNANATGATCCTTTCCGCNTTTCGANATANAACNTCACANTGNTGGAACNNN
CCAGGGTNGAAACCANCTATGGAATATCCANNNNGTCTTTGCGGGGTNACTCCNACTTGTGNG
AGNNATNTGGATTATTNCCCTNATATGGCNCANATGGCCATCTAAGGGATCCTGGNNATGNAA
CCNTTGGCCTTTGNGTATTTACNAACTTNGATCCCTCENNAANGGGATTTGTGGGCCATACCT
CATGAATTGCTTGAAAGNTGNCNTTTNNNTNTANANTACNNGNNANAATTGTCTNTCTGGAATCTT
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ANACCNATNTAAANGNGTTTTT

SEQ ID NO: 460 ACCGCGGGGCTGNCCTCTCTTTTNGACTCAGCCCGCTGCACCCANGTGAAA
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ACACANTTNAAAAATNGGTAAGCAGCCTTTTTTATTTTTTTTCAAACCTCCTTCATTATCCNTA
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ACATATACCNATTTNATTTTCTNGGTAAGANAAAAAAGAAANANNNNTTTTATCCCGTNGG
GCCCCAAAANTTTCGGNCCNTTTGCTCNAAAGNNTNGNAAANNNGNAANTCTCCCTNNGGNTNCC
TTAAATAAATGGAAGGGANTGCTCTTNTTATTTATACACNCTATGATTATANGGGGTGNTANTAA
CANTCGGGGAAAAANNNGTTTTGGATTTT

SEQ ID NO: 461 GGNACCCCGAGTCCNTGNCTGGCATACTGAGAACNACCAACACACACCCA
AGCTCGGTCTCCTNTTGGTGATTTCTGGGGAGCANATCTTNATNAAGGCGNCCGTCCTCATGAGAG
GGGGAAAAACATCCCTCTCTTGNAAATNTAAGGAAANTTTTNCNATNANTCTGTAAAGNAGAA
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NNGTTCTTACCTTGANANTTATATAAANGAAAGTGTTGATATATTNATTGCANNAGNTTCAANA

AANAAACATCTTATGTTATGTGNANNTNAANTANNCTNANNTGAGGNTTNTTAATNGANNGTTTT
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TNTTGNNAATGTGAGATANTANNGTTTTTTTTTTNGCNTNCTGGNATNTTGGNTATNANTATAAC
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TNTNTATTGATTTTATNCNCAACANTCTTNCCTT

SEQ ID NO: 462 CGAGCGGCCGNC CGGCGCANGNACTTGAGGCATTACCTCCTCTGAGNCACTGA
AGTCATAGGGGNCGTATGAANCCCCATNTTTGGCATNNGGNTGGCGANACTACTNCTCTTGCTA
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TNANTACGGTTANTGTNCTCACNNTAACCTTCNAAAAATAANCANNTNTGNCNGCATCCGNAA
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SEQ ID NO: 463 ACTTTTTTTTTTTTTTTTTTTTTTGNACACATTTNAAAGGGTTNATTTANANA
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GGGNTACAGGCTTTTGTGNGTGAAGTNTACCANTGGGNAACCAAGGGACTNNGGNTCCATGAAAA
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GGGGCG

SEQ ID NO: 464 GGACCTCCGNTCANNGCTNNTCATNNCCNCTCNCNCNGCCTGGTGGANCA
NGCTGACCNNATCCTCTTNTGNATGGAGGCNCTNCTNNGGGANGGGGGAACNNACCATCAANTNA
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CCN

SEQ ID NO: 465 GNGGNGGCCNCGCCGANGNGCACACTTTGGATACACTGGATGCTCATGTCAA
ANGGGGTCAACTCATCTTCACTCTGAGATNCAAAACNTAACNCTTGGCGGCATCAACCAAAAAAAT
CAAACTATCTNTTCCNGAATATTTATAGNCTCCACTNGCTTNNAGGGTTGTTNTGGTTNTTNCNN
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GGTGATGNAAACGACCAACTTGGACANAAACCCCGCGNTCTNCCNGGGCNGNCGNTCGAAA
GGGCTAAATTNCAACTNACTGAAGGNCGTTNCTACCGGATNNGANCTCGGTGCCCCCATCGGCATT
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GCGGGNAGCTAAAAATGTCTAAGCCTTGGGNGCCTAATGANTNAAAGCTTACTTAGATTGAATNGC
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SEQ ID NO: 466 GGTACCAAANCNANTNACAGGANGGGCGGGACTACCGGAACTACAGGCTGT
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ATAACNCATGCCACNGTAGTCCTCACTGGAATTGGAGCANATGAANANCTTGACAGNTATTTTCG
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GGTCCAATTANTTNTCNAAA1NTNGGTNGNGNTGACACAGATATTTNGATCATGGATAAGACNC
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CTTACNCCCAGGATTGGGGAAAAAGGCCTNTCGCTTCCGGGGGGACT

SEQ ID NO: 467 CNGCGGCCNNNCCGNCGGGCTCNCCTNTNCCCAGAAAAAGCGGNACTTGCTG
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TNATNGCTACAGGCATGNCNGCCANNNTTANACCCANAGGAANGCTGNNTNCNCTNTNTNNGAC
CAGCGCCNNANTATCCTTCCACNGATAAGGCGTGCANCTTTTGTCTCTACCAGATNATGANCTGNT
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GATNTGCTNGNGCTCGTCTACTGATGACNNNTGTTACCAAGTGGATNTTGTCAANGATCAAAAG
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CCNNNA

SEQ ID NO: 468 CGCNNNNCCNNNANGACCTATNCATGCNTATGNNGNATGTNGTGTGATNN
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TCGCGANNATANATACCACACTGGNNTCCNTTNTAATATNGCNTCTCGGTGCAANNATGGGTG
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SEQ ID NO: 469 TTTTNTTNTNGNTNCTATNTTTTCTNGGGCNGNCACGTGCACTTTATTGAA
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GCAGGAACATAAGGAACCCNCTTGACCCGTATTATCTNAAACATAGANTTGGTAGGACTGNTNCA
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SEQ ID NO: 470 GGTACNNTNTCANNNNATAAGNGCTGNNGNNNCNCANAATGANGGNGTCA
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GGCGTTCT

SEQ ID NO: 471 GCGAGGTACCACNATACCAACCAATACAAGTTTGAAGTGGACCTGGGGCTC
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NATAITTAANTTCTTTATTTATTTGTTTCTATTTTNTTTTNTTATCNTTTNTTNTTNCCTTCTTNA
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TNTTTTNTTAATTNNINTTCGTTNTAATTTATTTANTTNTATTTTCTACACTTTNTNGTNTNNTATGT
ATCTTANTTTTTNTTGTNTATATATNAAATATNATCTATATTGATTGTTCTATCCNCTTTTTTTNG

SEQ ID NO: 472 GTACGCGGGGGTGGGTGGGATTGAGGTGTGCCCTNCNTCATAAAATACAGACT
CANTTTTGCTTGACACTCTGAATCTTNNACCGCATNCTANCCNACGACTNACACAAAGCACGTGN
GTGAGGAANTCCAGANTTGCCATGGAAAAAATANNATTGTTATCATNATTNCNCCTTGAGGCC
CTTNCCTACACTCTGGCCAAAATTTCCATATTANAAACCTTANCCANAAAGGACAAATATGNCTCT
CNGACNCATTCTGNCCNANACCCNCTNCAGANGTTGNNGTGACCAANTAATCTNGACTCANNACA
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SEQ ID NO: 473 TAGGTCCNGCCGACGTACACTCGAAACCAAATNNCTAAAACTTGGTTNGCNT
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CAGTNTNCTCACACTNNTTCTGGTTTCAAGNCTCAANGCCNGACANNANAAAGGCTTGGAGATT
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ATCTGTNTCTGCAAGG

SEQ ID NO: 474 GGCGNGACGACNCGNNCCAACGTGTGCCCTATNAACTCTCCATGGNAATCC
CCNCGCCTACCATGGTGNCCACCGGTGACGGGGANTAAAGGNTCATTCCCGATANGGAGCCNTA
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GANNTNATTGCCTTTTCTTTTGNAAATAT

SEQ ID NO: 475 CGTGCANTTNANTGCATAAAAAAGGCCTCTCTCCATNANACTCANCACITTTAC
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GCTAGNGAGGGGAAAAAANGTANGAGATNTGGCCCTCAAGGANCAACGAGATNTTAATCTACCT
AACNAAGTCCNNAGNNTNNCCAGGCATGNAAAAATTAGTGNTGCTACATGGAT

SEQ ID NO: 476 ACNTCTTTGACATTTTCAAANTGAANAACCTGNCNNNTTTCATTGTGNAANGG
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GNTACCTCNTTNCACCTNGNGGAATATGGTNGTAACNGTTGCTTGCNNGAAAAANTATCCNCC
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SEQ ID NO: 477 CCGNCGGGCCTGCCAGCANCAGGACCTCANAAGAAANCNCATNACNTCAG
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NNGNCGNA

SEQ ID NO: 478 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCGNTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 479 CGCGGCGAGGTACNCGGGGAGTGAAGGGTCTGCTGCTGAAATTTGGGGGC
AAATAACCGNAGTANGTTGTCTGTGCCTTGGNGAGTNCNCGGCCTACTGGGAACGGGACTTNT
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NNANCNATTTGGAGCACACATCNCNTNTTTAANTGGAAGGNAGTTTTCTCCGAAAAANAACCTTA
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SEQ ID NO: 480 ACTCGGGACTGTGTGANGAATGATGGAAACCAATCATGGAGAGTTTNNNTG
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TTNGTTACACT

SEQ ID NO: 481 ACGNGGTCGAGGTACACANTGGGGGCTCCTCATACATGGCCTCACATTGAGG
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ANATTNGATGATGGGGCAGCCNGTGGGGTANTAATCGTGAA

SEQ ID NO: 482 GTGTGTGTGTGTATGTGTGTGTGTGTGTGTGTGTTTAAGTTTANCCCTTTTGT
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SEQ ID NO: 483 ACNTCCNTCTTCCAACCTGCTTGCCAGCAAAGATCATNCTCTGCTGATCAGGGA
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GGGTGATGGTCTTCCNTANGGTTTTACCANAAATCTGCATTTNGGGGGGGCTCCACCTCAANGG
CCGTATCGAAAGGGCCNNNNANNAACANTTGATACCCCTNCCATCCAAAAATAAGTTTAACT
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SEQ ID NO: 484 ACTTNNTTTTTTTTTTTTTTTTTTTTNTNAAAGGTGATAACGCTTTTCANAN
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TTTG

SEQ ID NO: 485 TGCCTAATNACAACATGGATGACTNGCAAAGGANGGGCTCTTTACTTTAAGC
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TCCACNACATNTTAAAGCCNATTGGTTTGGACCTTGGGCCGGGGACACNNCTTANGGGNGAAT

SEQ ID NO: 486 ACTTTAAGAAAAAAGCAGGGCCTTGGAAAGTTTGGGTCTTNTTCTCCTCC
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ACTGCCACGGTGGGCGGGCTCCTCTCTANTCTAANGGGACCCACCGTNTANATTCTGNAA
CTGGAAGTGTGNAAGGTGAATANGNTCANGNNGNCTTNTNTTTANNTCAANCTNTNCTCTT
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SEQ ID NO: 487 ACTNATNNTGNTNNCCCAATNGATACTGNTTGNACTAACATCCACTCTNGTAT
GTNGCTGAGATAACTTACTTTGACTGNCATTTGGATATCTCTCANACANACCTTGAACNANATAA
AAAGGACANGTTTGTGGACTGTGT

SEQ ID NO: 488 ACCCATGCTCACACNCACACTTCCAGTTTTATACAGAATTTTTTAANGGA
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NTACNNGTTTACCNCAGCTGAAGGTTCTTTTATTCAATTCTNTTTTAAAGTGANCCCATGATTGG
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 NTCNAACTNCATATAGAGAAAAATCGATNACGAAAAATNCNTGNAATAAGACTNAAATNACTTGGC
 CNTAACAAAGGNCCTTAGTAGATATNTAA

SEQ ID NO: 489 CTCNGNGAGGCCCAACGCTGCTNNTGCTACACTATNGNCAGGATNAATCCG
 GTCCNGTGC GG CANATGGNTANTCTCCTTGGCCTTGGCNGCCCTCCTTGTTCTGGACANGGGAN
 ATNTCNNGTGGCANNAGGAAAGCTCCNTTTTTCANGANTGCNCCA

SEQ ID NO: 490 ACACNCGCNNNCTGGNNTNANNACGCAAGCTNANNATAGGTCNGGNNAGCG
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 TNGCTGGATAATGAAATCNAGGATGACGATGCCTTNTTCTGCTGTTCTAGGGCATCCANGACAAT
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 TTTAAANGAGNAACNCTNCNTTATNCCNNCNAAGGACGTCNTNATNAGNTGCNCTCCCNNA
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SEQ ID NO: 491 ACCACAAGGATGTGAAGCATATGAACTCTGCANGANTCCTGNCCCACTGAG
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 CTTTACANANTANNANTANAATTGGGCATCGNGTATGCCCCAG

SEQ ID NO: 492 GTACANAGTAGCCGTGATGTGGTCATTNGTCTGATGCCAGCCTTGAAGATG
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SEQ ID NO: 493 CNGTGGNCGCGGCCGAGGNACAGCATCANTGAAAAACACANTGTATGAAA
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SEQ ID NO: 494 GGNTCNGGGGAANAGGAGTTGGANTATGGGGGACGCGGNAGGCGGCNTAN
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 GGAAACCANTATAANGGCANAANTGAATACNTGANGACGGCTTAGGGGAANTGNACTTNTCTNT
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SEQ ID NO: 495 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCTCAGATAAATTATTTATTATTC
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SEQ ID NO: 496 GCGTGGNCGCGCCGAGGTNCAAGATTACCAGAAAGAGAGTGGTGTGTAN
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SEQ ID NO: 497 GGTACTTTTTTTTTTTTTTTTTTTTTTGGGGTTTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 498 ACGCGGNNNGTNGNAGCCTGNGGGNCCTANTGNNNNATNGATNGNATNAT
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SEQ ID NO: 499 CATTGANCTCCATAGAGACAGNGCCGGGGCAAGTGAGAGCCGGACGGGCAC
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SEQ ID NO: 500 ACCNNGGNCNNNGCCGACGTGCTAACATGCTTNAACNNATCANTATGGAGNCT
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ACTACT

SEQ ID NO: 501 CCGGCCGNCNGCTCAGTCTTNNNTATTACANCNNTCATTGANTATAAAAAAN
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SEQ ID NO: 502 AATAAANACCTTATCCGTGGNCNCGGCCGANGNACATGATNCANATTGGTTT
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SEQ ID NO: 503 ACCCGGGGGGCAATTCGGTGTCTTNCGGTGTCTNGGCAACAAANCCGTCCAAA
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SEQ ID NO: 504 ACGCGGGGGGGTTCGGAAGGGGAAAAACAACACTACGGCTGCGGTGTGGTTGGT
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SEQ ID NO: 505 GGTAATAATTTGTTAATTACTGGAACATTGTAGTAAGAATTTATATCAGGAG
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CCC

SEQ ID NO: 507 CGAGGTACTTTTGTATTTTGATATGGACAGTTTATTCATTTGCATACAGTTAT
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SEQ ID NO: 508 ACTGGTTGGGGATGGGAATCGTGCTTTTCTTTAACTTCAGTTTACGAGATGC
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SEQ ID NO: 509 ACATCAGACTAGATACAACATGCAGAATGTTTTCTGAACTTATCCGAAAT
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CANCCGGC

SEQ ID NO: 510 ACTTGTAATTAGCACTTGGTGAAAGCTGGAAGGAAGATAAATAACACTAAAC
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SEQ ID NO: 511 ACATCAGACTAGATACAACATGCNGAATGTTTCTGAACTTATCCGGAATTC
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SEQ ID NO: 512 ACGCGGGGGGCCACGTTTCAGCGGACACGGGAGCAAGATGGCGATTCCGGGC
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SEQ ID NO: 517 ACTTGGACCATCCACAGCCAGCAAGGCAGAGCAGGATGCTTCTATTCTCTC
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SEQ ID NO: 521 GGTACATACAAAATCTGAAACTGACACTGTCAGTTCTATACTTTGCACACGTG
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SEQ ID NO: 522 ACCTGCCGGCCCACTGTGCACTGCTGTGAGAAAAATGGATTAAAAACTATTCT
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SEQ ID NO: 537 GGNACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACNCNGAAAAATTG
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SEQ ID NO: 573 ACGGTCTCACAGACAACGTTGAGAGAATAGTAGAAAATGAGAAGATTAAATG
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SEQ ID NO: 574 ACGCGGGTGTGCTTCTTCAAGGGTTGGACCTTTAAATTGCTGCAAAAGGT
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SEQ ID NO: 593 ACOCCTAATTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAGTTTCTTTAAG
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SEQ ID NO: 594 ACATACCCAAAAAGAATTAAGCAAGGACITGAACAAACATGGTCCCTAGCA
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SEQ ID NO: 595 ACTCCAGCAGCAGGAGAGCGGATTTACAACATCTCAGGGAATGGCAGCCCTC
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SEQ ID NO: 598 TTCGCCCTTTTCGAGCGGCCGCCGGGCAGGACGCGGGAACGACATTTTGT
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SEQ ID NO: 607 ACATTCTTCAAGCACAGGGGGCCATCAATAGTAAAAATCTGCCCTTCACCATT
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SEQ ID NO: 608 ACATGAGAGTCCTGCCTTAATTTTGCTGTTTGCCCTCGGATCTCTGGGTTTGAT
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SEQ ID NO: 609 ACTTGTTACCAACTTTGCTTTCAAACCATTTTAGGTCCACAAAACTTCACTG
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SEQ ID NO: 613 ACTTCAAATCACATAGCTTAAATATGGAGAAAAGACAGGTAAAAAATTAT
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SEQ ID NO: 614 ACGCGGGGGACCTTTGTAGCACCTCAACATGAAAGGGCATTAGCTATGTTTC
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SEQ ID NO: 615 ACAGCGGGGGTGCACAGACCAAGCAAAGAGACGCAATCAGCAGCTGGTCTCAC
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SEQ ID NO: 617 ACAGGTCTGGCATGGTGGCCACCAGTGCATCTCCTGAATGATGTCAATTTAGG
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GCG

SEQ ID NO: 618 ACTGCGTTTGGGCCTCAAAGGACATCCTTGAAGTCCAGTTTCACATCGTTGT
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SEQ ID NO: 619 ACTAGTAACAGGCAATTAACAACTAATAAGAAAATCAGCATTTTAACAATT
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SEQ ID NO: 624 ACTTTTTTTTTTTTTTTTTTTTTTTNGAATTAATAATCCATTTTATTGCTTGG
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SEQ ID NO: 626 ACAATGATTCTTAAAAATCTTTGGCCTTAGTGGCCTTTTTCTTCACTTACAC
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SEQ ID NO: 627 ACAGAAATAAAATAATGGGAATTATCATTAACTTACCCCTGGTTTTCTAGCTT
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SEQ ID NO: 628 ACGTTCCATTATATTCTTGCTGCTCAATCAATCACAAATTTATATCAGATTAG
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SEQ ID NO: 629 ACATGACCTTTAGTGAAGATTATTTGTCTATCAAATTAACCATATCCAAGTTTC
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SEQ ID NO: 630 ACAGAGTTAACAAGTTTGTAGTTTATATAGGAAAAGCCTAGTCAATTCAG
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SEQ ID NO: 631 ACTAAAGGAGATAAGTGAAGTTCTCCCATGACTTGACTCTGGAGAGAAAAAT
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SEQ ID NO: 634 ACTTTTTTTTTTTTTTTTTTTTCTTTTAAACATTTAATAGAACTNTATNCA
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SEQ ID NO: 635 ACGGCAGGGAAGAACTGAAACTCAGAGAAAGAACTGCCCTTCCATCTAC
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SEQ ID NO: 636 ACGCGGGGGGGTTTCTGGGCTACTACGATGGCGATGAGTTTCGAGTGGCCG
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SEQ ID NO: 638 ACNTNNTTTTTTTTTTTTTTTTTTTTACATTCTCANCCATGCTGCTTATT
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SEQ ID NO: 640 ACGCGGGGACCTACCTGGGATAACGGCGGCGAGCGGACGGCTGCATTTACG
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SEQ ID NO: 642 ACTTGAGTGCTGCTGAGCTTCAGCCCACTGAGAGTTTACCTCTGGAGTTGACT
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SEQ ID NO: 643 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTNCACTTATTATTTATTTAT
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SEQ ID NO: 644 ACTCTAATTTCACTAACTGCCAAAAGGTTTTCCAGAATAATCTCAGTTGCTTC
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SEQ ID NO: 646 CTTTTGTNGCGGCCGAGGTACACAAGTAAATACTACAGAAATTAATTTCTT
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SEQ ID NO: 648 ACTGGATTCTATAGGTCCACCATTAAAAAGCTGGTATGGGACACCAATTATAC
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SEQ ID NO: 649 ACCGGAAGAAGCAGCTGGCAAAGCAGCTCCCTGCACATGACCAGGACCCCTTC
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SEQ ID NO: 650 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGANAACCAACGCCAGTNTTT
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SEQ ID NO: 651 ACTGATATAATCTAACAAATGAAGGTGCACCTTTACTTCCTGGAACATAGAC
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SEQ ID NO: 652 ACTGCCAAGGACAAGTTGATTCTGGCCAGGCAAAGTTAACTCAGTTTTTTAG
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SEQ ID NO: 653 ACITTTTTTTTTTTTTTTTTTTTITNGGCTTCAATCTTTTATTAAATGCCATG
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CCGACC

SEQ ID NO: 655 ACCCTAAGGCAGGCCCACTGGCTCTTTTGTCAAGGATTCTGAGAAAAGCT
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SEQ ID NO: 656 ACACTTCAAATGCTGATTCTGTTGAATCTTCTTATTTTTTTTCCCCCAATGAAC
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SEQ ID NO: 657 ACTGTAGAATGTGATGGAAAAGCATTGATGAGAATTTATTGGCAGTTCAGAT
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SEQ ID NO: 658 ACTGCTTTTATTTGAGTTTATGAACAGAAATAGAAAAGTATGGTGCTTGGGTTT
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SEQ ID NO: 659 ACTTCTATATATAAATTTGGACGAATAGAAGTAAATATGTTTATTGGTGAAAA
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SEQ ID NO: 660 AGCAAACCTTCTGGATGCCAACATGATTTTCAGTAACCACCCTTTAGAGTAT
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SEQ ID NO: 661 ACTGGATTCTATAGGTCCACCATTAAAGCTGGTATGGGACACCAATTTATAC
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SEQ ID NO: 662 ACTTTTTTTTTTAAAGATTACTAAACATACAGGAAGTGATAAGAAGTATCAT
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SEQ ID NO: 663 ACATTAATGTTACTTTGGCATTCTATTTCTAGGCTTACAGGAATTATTA
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SEQ ID NO: 664 ACAGTCCGGCCCGTGGGGAGGAGGGAGGGAAGGCAGGCACACGAAGACAC
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SEQ ID NO: 665 CGTCAAGTTCTTCTAGCAGGGACCTGTCTCCCTTTACTTCTTACCTCCCACCTT
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SEQ ID NO: 666 ACTTTTTTTTTTTTTTTTTTTTTTAAATTAATTCAAATAAAATTTTAAATGAT
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SEQ ID NO: 672 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGNGANATTATTTACTAAATAATTGATAT
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SEQ ID NO: 673 ACACCATTACTCTTCTGAAGAGCCTGGTAAACAGCAGATGCTTTATTCAGAA
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SEQ ID NO: 674 ACCTCAACATAACCTGTAAAAGTATTTCTAGATAAACTTTACAAGTGAAGA
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NGGCC

SEQ ID NO: 675 ACCAGGCTGGCGACAGGTGCTACCAGGAGTGGGCTGAGGGGAGAAAACTA
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SEQ ID NO: 676 ACAAATTTAAGACTAGACAATTAACAAAAAACAACAAATATAGCCGC
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SEQ ID NO: 677 ACGCGGGGGAGGCCGCTNTNTCTCATCGAAGATGGCGGCGCATCTGTGTCG
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SEQ ID NO: 678 ACTTTNTTTTTTTTTTTTTTGGCTTTATAAGAGAAATTTTATTGTTAATTATT
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SEQ ID NO: 679 ACCTGGGTGTATCCTGTGTTTGCCAACTCAGCCTCTTGGGTCTAGCAGCTTT
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SEQ ID NO: 680 ACAAGATATTGCGGTTTTGTTTTTATAACCCACTAAGCCAAGATTGTATC
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SEQ ID NO: 681 ACAAATATCATCATTTATTTTTGATTTTTTTACCAGCCCTGAATTTTCAA
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SEQ ID NO: 682 ACACATGCACATCAAAACACTTCAACTGAATATAGATGCCATTACATTATTTA
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SEQ ID NO: 683 ACTTTTTCTTTTTCTTCTTTTTTTTTGGAATTTATTTCTGAGCCTTTTGTGTT
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SEQ ID NO: 685 ACTTTTGGAGGCCAAGGCAGGTGGATCACTTGAGCTCAGGAGTTTGAGACCA
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SEQ ID NO: 689 ACGCGGGGTGAAGATATTATGGCTGCTGCCACGGAGCATAATCGCCCGAGCA
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SEQ ID NO: 691 ACGCGGGGGGATGCGCTTGGGCTCCCTGTTCGTTCCCATGACAGGGCAGC
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SEQ ID NO: 692 ACCCCACACCTGAAGGTGTCTATGAGTTCACATGGCTCAGGAATGGAGTTT
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SEQ ID NO: 693 ACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA
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SEQ ID NO: 694 ACGCGGGTAGGCAGAGAACAAAAATGTTAAGCATGGTGTGTCTATCTTATT
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SEQ ID NO: 695 ACTAAAGGCTTTTGCATGAATTAAGGAAGGAGAGTCTTGGGGCAGAAOCAA
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SEQ ID NO: 696 ACGCGGGTATTGAAGAAGATTTTAATATTGCACTAGGAGTTTTGCTTTAGCT
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SEQ ID NO: 697 ACTACAATGTTCTATGCAATTTCTTCATCCTAGACATTAATAAAACACATCCCT
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SEQ ID NO: 698 ACTAGGGATACAAAGACTTGGTTATTCTTGTGGAGTAATGATTCTCCTCTAT
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SEQ ID NO: 701 GTACGCCTGTAATCCAGTGACTTGGGAGGCTGAGGCAGGAGAATCGCTTGA
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NTTNGAAC

SEQ ID NO: 702 ACCTGACAAATTATTGGATTCCAGCAGTGACTCACTTATTCAAGATAACTG
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SEQ ID NO: 703 ACATGACCTTTAGTGAAGATTATTTGTATCAAAATTACCCATATCCAAGTTTC
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SEQ ID NO: 704 ACAGACTGAACAGATTAGGTCTTTGTCTGAAGCTATGTCAGTGGAAAAAATT
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SEQ ID NO: 707 ACTTGCTTACAGGAAGAGTAATTCCTAGCAAAGGTCATTAGCTCCTAAGGC
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SEQ ID NO: 708 ACTTTTTTTTTTTTTTTTTTTTNGGTATCTATCTAATAAAAGTTTATTGTGTAT
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SEQ ID NO: 709 ACGCGGGAAGCATATGTTACTTACCTTGTATTAAATATTTCTTGAAAAGCAA
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SEQ ID NO: 710 ACTATACTCAGTATTTAAATATGTCCAGTATAGAANCATAACTTCAATTAAT
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SEQ ID NO: 711 ACATGGCCTTTTAAAAACGGAGACAACTGGAAATTCATTGGACCTGATCAA
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SEQ ID NO: 712 ACGCGGGGACCTGGGATAACGGCGGCGAGCGGACGGCTGCAATTACGGGT
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SEQ ID NO: 713 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNAANAACCTTTTATTCATCATCTA
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SEQ ID NO: 714 ACTTTCATAATTTGCTCCTGCTATCTAAAAGGCAGAGCCAGGTATACAGGAT
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SEQ ID NO: 715 ACGCGGGGTGAGAAGGAGAAGGAGCGGCTGGGAGGCGGTTTGGGAGTGGCG
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SEQ ID NO: 717 ACGCGGGGCGAGATCAGGGATCGCGATTGCGAATCCTCCGCTGAGGTGATTT
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- SEQ ID NO: 718 GCTTTTTTTTTTTTTTTTTTTTTTTTACTTTGGGAGGANATAAACCAGTCTC
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- SEQ ID NO: 719 ACGCGGGATGGGAATGAGGNTCTACCACTCTGGAAATTCATGCCTGCAGGT
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- SEQ ID NO: 720 ACAAATAAAAGTGATGGTGAGAACCTGGCTCAGGAAATGCAGTAGCAGGGCC
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- SEQ ID NO: 721 ACTTTTTTTTTTTTTTCTTTTGATTTCTCAGGACCTTAGAGGGAAAAACAAAC
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- SEQ ID NO: 722 ACCGGAAGAAGCAGCTGGCAAAGCAGCTCCCTGCACATGACCAGGACCCCTTC
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- SEQ ID NO: 723 ACAGCGTTCACAATGCTGGTATTAATCAGCTACATATTTTGAACATCTACTGT
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- SEQ ID NO: 724 ACGCGGGGAGTGCCTGCCGCTCCGCCGACCGAANAGGCTGGACATGACACC
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- SEQ ID NO: 725 ACCTCATCGGTATCCAAGGCCCGACTATGTTCTTGTGCGCTCCGACCGGGTG
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SEQ ID NO: 730 ACCTCCTNTTCTTCTATTTTTAGGAANAAGTTATAACAAGTTTTAAATATCT
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SEQ ID NO: 731 ACCTCCTCTTCTTCTATTTTTAGGAAGAAGTTATAACAAGTTTTAAATATCT
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SEQ ID NO: 733 ACCAGGCTGGCGACAGGTGCTACCAGGAGTGGGCTGAGGGGAGAAAACTA
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SEQ ID NO: 734 CAGCAGAGATATATGCCTATCGAGAAGAACAGGATTTTGAATTGAGATAGT
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SEQ ID NO: 736 ACGCGGGATAGACGGAAATGGAGAGCTGGATTTCTCCACTTTTCTGACCATT
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SEQ ID NO: 743 ACTGGGATTATATAGGCATGAGCCACTGAGCCTGGCCANAAAGCGTTTTCTC
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SEQ ID NO: 744 ACTTTCTTTCTGCTGGTAATTTATGGAGCAGGTTAAGAAGGCTGCTCTGT
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SEQ ID NO: 745 GGTACTGCTATAAACTCATTCTGTGTGGTGGCTGTGCTATAGAGTCTGTGT
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SEQ ID NO: 746 ACTTTTTTTTTTTTTTTTTTNGCCTGGAAATGTTTTAATANAATGGTCTAG
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SEQ ID NO: 747 ACTGTGATGTGAAGCTGTTGCTGGTAAAAATTAGCATTTGGCCTCCTGAAAGGT
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SEQ ID NO: 748 CGAGGTACGGGGGCTTGTAGCGCAGAAACACTTACTTTTCCCCCTACCCCTGCT
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GGAATTA

SEQ ID NO: 749 ACGCGGGATTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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SEQ ID NO: 750 GGTACGGGGGCTTGTAGCGCAGAAACACTTACTTTTCCCCCTACCCCTGCTCCT
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SEQ ID NO: 751 GGTACGGCGGAACCTTTGTAAGATGCAAGAGGTTGGATCAAGTTTAAATGAC
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SEQ ID NO: 752 CGAGGTACTGGATGTGGTTGCCCCATTTGTGTGTGTGGTTGTGTGTGTGG
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SEQ ID NO: 753 ACGCGGGGGTCTCATTGAATCGCTGCAGCTCTTGGGTTTTTGTGGCTTC
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CAGGGAAACCGAACCCTCCAAGCTATGTCGCCCTTACGGCACTGAACGGTTGATCGGTGATGC
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SEQ ID NO: 754 GGTACCGACCATAGAGCAAGAATCAAGATTCTGTAACTCTGCACAGCCCC
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ACGGTTTTTTA

SEQ ID NO: 755 ACGCGGGGGACGAACACGTGACGCGGTGGGGCGGACCACTGCAGACTGAGC
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ANGGGA

SEQ ID NO: 756 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTTTCAAAGATTTTACTAAATCAT
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SEQ ID NO: 757 GGTACTATAATGGTCCCCATCTTAATTTGAAAGCGTTTGAAGATCTTTTAGGA
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SEQ ID NO: 758 GGTACTATAATGGTCCCCATCTTAATTTGAAAGCGTTTGAAGATCTTTTAGGA
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SEQ ID NO: 759 GGTACTTTTTTTTTTTTTTTTTTTTTTTAGNTATTCTTGCTTAATCATTTTTAA
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SEQ ID NO: 760 GGTACTTTTAATGGTGGGAATTTACAGTAGAAGCATCCTTTGCTGAGTTATAC
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SEQ ID NO: 761 GGTACTGGGATTATATAGGCATGAGCCACTGAGCCTGGCCAGAAAGCGTTTT
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SEQ ID NO: 762 ACTTTTTTGTATTATTCTTCTAGCTTATCCCTGCACAATTATTAGAGTGAA
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SEQ ID NO: 763 GGTACCATAGTCCAGCACTTGGCCAGGGTCTAGACTGCTGGGTAGGTCC
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SEQ ID NO: 764 ACAATAGATGCAACGCCAAAAATGAGATGAAAGAGAATTCAGAATAAAATTC
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CNNT

SEQ ID NO: 765 ACITTTTTTTTTTTTTTTTTTTTTTTTINACTNGTTTGGTTGGATGCTCTTCCA
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SEQ ID NO: 766 CGAGGTACTGTACCCGGACATACCTATTCTTCAAGTTCTGGTTCTTCAG
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SEQ ID NO: 767 ACTCTATAAATCTAGTGGAACATTTCTGCACAACTAGATTCTGGACACCA
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SEQ ID NO: 768 GGTACGCGGGGATTTGTGGTGAGATTCTCTCCAGGCCACANGACATTTCTCG
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SEQ ID NO: 769 CGAGGTACTTTTAAGAAAAAGTCCAATGTTACAAAAATCAAAATGCTTATATCA
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SEQ ID NO: 770 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGGTNGNCTGATTTTAA
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SEQ ID NO: 771 GGTACCGCTGAAGACACCCAGAATGAAGGAAAAAGACAAAAAGAATAAA
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SEQ ID NO: 772 ACTGTATATCCATATGGCACATTTATGACTTTGTAATATGTAATTCATAATAC
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SEQ ID NO: 773 GGTACGCGGGATCTGGGAGAATTTAATGGAAAAATCGCTTGGTTAAACCT
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SEQ ID NO: 791 ACTAAAGGCTTTTGCATGAATTAGGAAGGAGAGTCTTGGGGCAGAAAGCAATA
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- SEQ ID NO: 801 ACTTCTTTTTTACAGTTTTTTTTTTTTTACACACATATTATACAACTTTT
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- SEQ ID NO: 802 ACTGGATTCTATAGGTCACCATTAAAGCTGGTATGGGACCAATTTATAC
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- SEQ ID NO: 803 ACCTCACAACCAAAAGCAGTTAACTATGCCTGGCATAACCCCTGTCTATGTG
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- SEQ ID NO: 804 ACTGGGAACAGGTGCTTGCTTGCTATGGCCACGGTTTGAACGTATCTGGGA
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- SEQ ID NO: 806 ACTATTGCTATTAGGGGTTCTGTTTTATAAATTTTCTTATCATACTTTATT
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SEQ ID NO: 808 ACTTTTTTTTTTTTTTTTTTTTTTGGNTTTTTTTTTTTTTTTTTTTTTNA
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GTTCCGAAAAA

SEQ ID NO: 810 ACCGCGGGATTTAAAGCATTGTTCCTCAATAAAATAAATAGAGGGGAACTTG
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CTANTG

SEQ ID NO: 811 ACAGAATGGTATTTGTGTATGTGTGTGGGCTTANAGATTACAAGTAAATATT
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SEQ ID NO: 812 ACTGAAAAGTTGCCACTTTTTATTAGTAAGAAAAACAACATTTGGCTCACT
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SEQ ID NO: 813 ACAAATATGTATCTGAAACACTTCTATTTGGCAATTTTATAACAAATCAAAT
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SEQ ID NO: 815 ACATTTTGAATAGACCTCAAAAACTTCATTCTGCTGCTGTTCAAGTTGGCT
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SEQ ID NO: 817 ACCCAACTTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAGTTTCTTTAAG
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SEQ ID NO: 818 ACAGAATGGTATTTGTGTATGTGTGGGCTTAGAGATTACAAAGTAAATATT
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SEQ ID NO: 819 ACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGCAGGGCAGGA
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SEQ ID NO: 820 ACTCAGGGGCATCATGTTGCTGCAGAGGCCACACTTCCAGAAAGTTTCTCCT
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SEQ ID NO: 821 ACAAATCTTTGGCCTTTCTCTTGACATTTTCGTATGTCAAAAAGCAAAAAACC
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SEQ ID NO: 830 GGTNCAAGTGATTGTGACAAATGACGTAAAAATGGCATTCTATGATGTCGAA
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SEQ ID NO: 831 GGTACCTCTTTAGTAGAGACTGGGTTTACCATTGTTGGCCAGGATGGTCTCT
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SEQ ID NO: 832 GGTACCGGAAGAAGCAGCTGGCAAAGCAGCTCCCTGCACATGACCAGGACC
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SEQ ID NO: 833 GGTACGCGGGGGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGC
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SEQ ID NO: 834 ACAAAGATTGGTAGCTTTATATTTTAAAAAATGCTATACTAAGAGAAAAA
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SEQ ID NO: 838 ACCAAGCACTGGGTAAGGCACCTTTGTGGAGCATTAGACAGTAACCCCTCAAG
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SEQ ID NO: 839 ACGCGGGGCTGTGACTTAAATCCATTTTCACTTAGAGAAATAGAAACACAAG
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SEQ ID NO: 840 ACTATTTATTTCTCAAGTCTTCCATGGGGGAAAAAATAAAGTCTAATATG
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SEQ ID NO: 841 ACTGTACAGAACTTTTACATACATTTCTCAGTCTAGTTGTGAAAGGCCTAAA
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SEQ ID NO: 843 ACTTTTTTTTTTTTTTTTTTTTTTTTTTANAAAGGATGACTTTTATTTCCATCC
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SEQ ID NO: 844 ACTTTTTTTTTTTTTTTTTTTTANATTGCCTGCTGCTAGGAGGAGGCC
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SEQ ID NO: 845 CGCGTCGAGGTACCCCTGGCAGAGCATTTGCAGATTAAAGAAGCATTTGAGA
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SEQ ID NO: 846 ACGCGGGGGAGTTGCTCTGCGCGGTGTTCCACGTGCGGCTGAACCTGAG
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SEQ ID NO: 847 ACCCTGACCCATGAACACCTGGCCATGACCTTTGACTGCTGTTACTGTCCACC
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SEQ ID NO: 848 TCGCGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGTCTTTTATAGG
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SEQ ID NO: 849 CCGCGCGAGGTNCCCTTNNGAATTGAAAGTGAANGATCCTGAGCTGGAGG
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SEQ ID NO: 850 ACTGTGAAACCACTTCAAGTTGCTCAGACTCCAGTAATACAACGGTCA
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SEQ ID NO: 851 CCGCGGCGAGGTNCCCTTNGNGAATATGAGGAGTATATTACTAAACTTTTCA
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SEQ ID NO: 852 CCGCGGCGAGGTNCCCTTNNNGAATTTGAAGTGAANGATCCTGAGCTGGAGG
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SEQ ID NO: 853 ACGCGGGAGGATTGTCCACTAAAAATTTATTTTCAAAAAATTTACTTCACAT
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SEQ ID NO: 854 ACTATTTATTTCTCAAGTGCTTCCATGGGGGAAAAATAAAAGTCTAATATG
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SEQ ID NO: 855 ACTACTGTTAATATCTCTAAGAACAAAAACACATTGAACATCCTTCCAGAAAG
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SEQ ID NO: 858 ACTTGAAGGAGAACAGTTTACATCGGGCGTTAGCCACCTTGCAGGAGGAGAC
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SEQ ID NO: 863 ACAAAGGCTGCTTAAGGCAGTGCAGCCCTTCTCAAAGTCAGCATGTCAATG
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TGAAACCTTTTGCCTTGAATCATGGATAGTTGAGGAGATCTTAAACCCANCAAGCTGATGTCCACTA
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SEQ ID NO: 864 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATTAATCCAAATTTTATTA
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SEQ ID NO: 865 ACCATGAAGAAGAAATAATGAGGGTAAGGGGCTAGTGTGATAGGGAGAGGG
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SEQ ID NO: 866 ACTTTTTTTTTTTTTTTTTTTTTTTTTNAAATAAGGNCTCACTCTGTCATCCAG
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SEQ ID NO: 867 ACATAGGGTCTGTACACCAGTTTATAGGATAAAGAACTGGAAGAATTCCT
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SEQ ID NO: 868 ACCTGTCCCATTCCTAAAAGGATTTGTGGGCAATGCTGGCACTTGGTGGCCAG
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SEQ ID NO: 869 ACCCACTGCTATTGCCTAAGGGTGTAGTCTGAAACTGAAGCCAGTTGCCGA
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SEQ ID NO: 870 ACAGGCTTAAATCTATGTCATTTACACTCACTGAATCATCAACCTNATCACCA
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SEQ ID NO: 871 ACTTACCTTCACTGAAGAGCGTAACATGAATTTCTGCAGTGGTATAAGGAT
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SEQ ID NO: 872 ACTTATGAACCTTATGTTGCTGTTTACTTCCCTTTTCTGATTTTTTAAGTTCATC
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SEQ ID NO: 873 ACGCGGGGGGACAACCTGGCCATCCAGACCCGGGTGGCCAGAAAAGCAT
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SEQ ID NO: 874 ACGCGGGGGGTTCTTGGCTTTGACAGCTTCAAAGAATGGACAGTGATAAGTT
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CTGTTGTACC

SEQ ID NO: 875 ACTGTCCATATCTTTTGTATTTACTTCAAAGGATTTGGATCAGCAGTATAAA
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SEQ ID NO: 876 ACGCTGGATAGCCTCCAGGCCAGAAAGAGAGAGTAGCGCGAGCACAGCTAA
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SEQ ID NO: 877 ACGCGGGGAGTGTCTTCTGGGATGGGAACCAAGCCGCTTCCCACTCTGTGTC
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SEQ ID NO: 878 ACAACCAACCACTCCTGTCTCCTTCCATTTTTCTGGCCTAGTGTCACTGCCAGGT
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SEQ ID NO: 879 ACCTTTTCTAGCATAGCCTGGGAAGAGTCACTGAAGGAGATTTAACTGAA
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SEQ ID NO: 880 GGTACTAATCTCTGAATTTGTCTATGCGGAAAATTTGGAGACTTGGCTTGTGC
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SEQ ID NO: 881 ACTGAGGAAGACACCACTTCTTGACGGTGTCTAAGAAGCCAGGTGGATGTGT
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SEQ ID NO: 882 CCGGGCAGGACTTTTTTTTTTTTTTTTTTTTTTTTNGGNTAAAAGGANAATTG
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SEQ ID NO: 883 ACAGACAAGGTCTATAGAATGTGGTAAAACTTGACTGCAACACAAGGCTTA
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SEQ ID NO: 884 GGTACCTCCAAACAGAGATGGAAGCTACACTGCAGTTCCCAATACTACTTCA
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SEQ ID NO: 885 ACCCTTTTTCTTTTCTTTTTTTTTTTTTTTAAGTATTGTTAACAATCCTTTGG
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SEQ ID NO: 887 ACCAAGGAGCTCTTCTTATTATTTCATATGGCCCTCAGCAGCTTTCATCTG
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SEQ ID NO: 888 ACTTATTTTTTTTTTTTTTTTTTTTTTNGNNGTTAATTCATTTTAATAGTAT
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SEQ ID NO: 889 ACTTTTTTTTTTTTTTTTTTTTTTTGGNGACAGTTGATTTTATTTTTTAAAGTTA
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SEQ ID NO: 890 GAAGAAGCCAAAAGAAACGAAATAGATGCGGAGCCGCCAGCTAAGCGGCA
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TTC

SEQ ID NO: 891 GGTACCAGCACCAGCCCCTCTGAAAGGAAAAAGTGTAGTCATGACTGTCCAT
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SEQ ID NO: 892 GGTACTACGTACGCAATTTCTCCAAACAGCTGCTCGACAGCATATGGCACCA
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SEQ ID NO: 893 GGTACCGGGGGCATGCGCGTTTCTCTGATGGTGTGCGTTCTCGTTCTAGCT
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SEQ ID NO: 894 ACACAATCAGATAACAAGGTTTCAAGCTCTAGTCAAAGACAAGATGATATTA
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SEQ ID NO: 895 GGTACCTTGCAGCCAAGGAAAACTGAAGAGCCAAAACACCAAGCCTTATCT
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SEQ ID NO: 896 CGAGGTACTNCTTCCAAATGACGAATTTCTGTCTCCAAATAATGGGACAAAG
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SEQ ID NO: 900 GGTACGCGGGGGGGTTCGGTTTCCGCGGTGGCCATGACTGCGGCCGTGTCTT
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SEQ ID NO: 901 CGAGGTACAGCAGCTTGGGAGTTCATTGCTGGTCTGGGACTATTGCTTGGGC
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SEQ ID NO: 902 ACCACATGTCCACCAGGAAGGAGCTGAGGTGATGCTGAGTTTTAGGCAACGC
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SEQ ID NO: 903 ACTGCTGACATCCAAACTATGTCCCTTTTAGGGTCTACTCGGAGAAAAATTGC
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SEQ ID NO: 904 ACTTTCTGTCTTGGGCACATTTTCCCCAGCGGATGCAACTTCTATCCTCAGTC
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SEQ ID NO: 905 ACAAAGTGACATACAATTGGAATCCATTTTGTGTGTAAGACATTGTTTTTC
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SEQ ID NO: 906 ACTGAAGATTATTGCTTCTAGGGCATTTTAAACAGCACCATTTGTATTGTTGA
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SEQ ID NO: 907 ACTTTTTTTTTTTTTTTTTTTTTTTTGAACGGANTCCCACTCTGTGCGCCAA
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SEQ ID NO: 908 ACAAAGGCTGCTTAAGGCACTGCAGCCCTTCTCAAAGTCAGCATGTCAATG
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SEQ ID NO: 909 ATCCACCTCCGAAACCCCTCGGCGGCGTCTCTGTGTGGCCCGCCTGCNGGA
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SEQ ID NO: 910 GTACTGACTTAAATTTGGAATTTACTAATTAAGTGGGATCTTTAGNGAGTCT
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SEQ ID NO: 911 ACGCGGGGTGGGGGGGCTCGTGTCTTTGGCTTCTCGACTCGGTCTGTTTCG
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SEQ ID NO: 912 ACATAGAGAAGAAAAATTTGGTTTTAGCAAATGACAGAGCCTTCAAAAAATATT
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SEQ ID NO: 913 ACGCGGGCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAAACACC
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SEQ ID NO: 918 ACAACCTTCAAACTTCCAGTTTTTATAAAAAAGGGGCACACAATCGTGGTTT
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SEQ ID NO: 920 ACAAAGAGCCCTCTACGAGAAGGACAGCTCTGTTGCAGCCAGATTTGAGC
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SEQ ID NO: 922 ACATAAGCCTTGATATCCATTTTGTGGCTGGTCCAAGGGGAGCCTAACTCA
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SEQ ID NO: 923 ACCTTTTCATGACAGGATTTCTGCTTAATATAACAAGCAAAAAACAACACTG
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SEQ ID NO: 924 ACTGCCGAATGTGTTTCCATGACATACCTCGTAAGTCCAATAAGACTCAATT
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SEQ ID NO: 925 ACGCGGGGCGAGTCACGGGGGAGCGAGGCTGCTGGGCTTGGCAACGAGGG
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SEQ ID NO: 927 ACCTAGCTTCTGATGTATGCAAAACACTGCAGGAAGAGAGAATGAAAGAAA
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SEQ ID NO: 928 ACTTTTTTTTTTTTTTTTTTTTNGGAACACAAGGGTCAGTTTCTCAATTCATG
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SEQ ID NO: 929 ACTGGTGACCTCTACATATCAAGGAAAAGCAAAACACAGAATAATTTAAT
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SEQ ID NO: 930 ACTCGATGTGAATGAAACCTGAAATAATAAGATAATAAGAAAAGCAATAAT
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SEQ ID NO: 931 ACATTAGAAAACACTTGTGACATTATTTCTAAGTGCAGGAGAGAGCTCCT
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SEQ ID NO: 933 ACTTTTTTTTTTTTTTTTTTTTTTTTNGAACCCAGTTACAAGAAACAGGCTGA
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SEQ ID NO: 935 ACCCTGGCATTGTGACAGGATGCAGAAGGAGATCACAGCCCTGGTCCCCAG
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SEQ ID NO: 939 CGCGGCGAGGTACAGTGACCTGCAGAACTTAGCCAAGAGTCTGGGTCTCCGG
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SEQ ID NO: 940 ACTGTCTCTCCCCAGAAGGCCTTCAAGGTTAACACACAACANTGCCCTGCC
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SEQ ID NO: 941 ACTCATCACTCTGTCCATACGCGATCACAATATCTCTAGTTCTTCCATCACA
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 TTAATAT

SEQ ID NO: 943 TTAATAAACTTCGAAAGTCACAGACACAGAAATTTAGGAAGCTGAAGGCTGAO
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 ATCCA

SEQ ID NO: 944 ACCTCTCTCTGTTGGAATGGGTTATCCAGTAAAAAGGGCGTGCCCATGCAA
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SEQ ID NO: 945 ACTGGAACATAAATCATATTTCTTCCCTCAAAATTTACCCATTCTGACTTTG
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SEQ ID NO: 948 ACTTTTTTTTTTTTTTTTTTTTTTTTGGATATTACACCATAGGTTTATTAA
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GCGT

SEQ ID NO: 950 ACTTCCAGCCAACCTCGTAGCCAGGCGCCAGATAGGCAAACTTTCTTGT
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SEQ ID NO: 951 ACGCGGGGCGCTTACAGTTGCTGAGAGGAGGCGAGAGGCGGGGGCGCTAGG
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SEQ ID NO: 952 ACITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATGGCCANGCTGCCTTCCT
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SEQ ID NO: 953 ACAGTTGAAAGCAGAGTGTAAACAAGGGATATGTCAAGGTAAAGCAGGTAGG
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SEQ ID NO: 956 TGCTGAAGCTTCACAGGGCGGCCAACTAACTCGCTGATTTTGAAGACCA
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SEQ ID NO: 957 ACCAGCAGATGAAGCCCTTCTACAAAATCTCTGACGGACTGGGAATAAAAAAT
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SEQ ID NO: 958 ACCACAAAGGGACCCAAATTCAGCGGTCTGTGCCTACAACTTCATTAATAA
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SEQ ID NO: 960 ACGCGGGATTAAAAATTTCTGTATTTCTGTGCATTAACTGACGATAATTT
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SEQ ID NO: 972 GGTACAAGCAACAAATAAAAAATAGATAAATTGGAATTTATGGAAGTTAGA
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SEQ ID NO: 973 ACGGGGAACAGGACAAAAGAAAGGAACGAGAAAAAGACAGATCCAAAGAG
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SEQ ID NO: 975 GGTACGCGGGGTGCCCCGTTTCATCCAAGGCGCAAGATGGCGCTGCTTTTTC
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SEQ ID NO: 977 ACAGATACGCTGTCCCATACATCAGGATCAAAATTATTAGTTTCAGTTTCACAT
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SEQ ID NO: 979 GGTACATCTTTGGCTTGTGAAAAACCAACATCTTTCTCTGGGCAATAGTAG
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SEQ ID NO: 989 GGTACTGGCTGGAACAAAATTTGTTTGTGTGTGTTAGAGTTATAAATCAATTAATCTTTATTTTCGGGTGGTTTACCTTTATGCGCACTCCCTTATATTTAAATTTCTGTGTTTATATATTTTGAATGTCCTTTATAGATTCTTTTAAATTTCCCTATAGAACAATTAAGAAAAATCAATACATTTTAAATATACCTTTCACAGCAAAAAGCTCCAAAATGAAGTATAGGGTTTATGCTCTATTTTCCTTCAGCTGAATACGAATGAACACAGTGGTGGAAATTTCTGAAGGGAAGTGATGAAAATATATATTTTTCAGTGGGCACTTTTCCATTTTACCACCTGACAAGATGTCCAAATTTGGCGAAGATCTATTTGGGCAATCTCTGTGTGAAAAACAGCACTTGAATGCATCCACTGAAACAGGCAGGGCTTGGCCATCCCGCAATGACCTCAAAAGAAAAAATCATGATAAAAAACAAGCNGCTGAAACCTGAAGTTGAAAAAAAACAGCTGGGAAGCTTTGGAACATGATGGAACCTGGAGAATTTGCCTCCACAACATTTAAAGGCGATATGAAAAAGAGATCGAAG

SEQ ID NO: 990 GGTACAAAGTTGTCCAGTCTTAGTGTCTGAGGCCAGTATGGGTGCGAAGGGGC
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ACACTGTATAGATAGACTGCATAATCGNAATTTTGCTCTCTAAAGGGGACCTTTTTTTTTTG
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GNNGGNACATTTTAAATAAACNGGNGAAGCTTTCTNTTA

SEQ ID NO: 991 GGTACTACAGCTGTGGAGTAGGGGTTATGAGCTCCAGTATTTTCAGCCGCAG CAGCCACATCCATAAAGAGCAGCTGCCCAACTCTCCCGGATGTTTCAAGGCCAACCTCCACT GGAGACAGCAGCAGCAACAATTCCTTCGTGGTCCACAACCAGCGCCTACCGTGTCCAAAGTGC CTGAGCATTTTCTCTCACTCTGATGTCCTCTCTTCTTGTGTCATAAACTCTGTGTCCACCTT CTGGCAGCTCTAGTTTCTCTGTGTTCTTTAAATGCAGCTAAACTGAATCTGTGGTCATGATGT TAGGAGGGCAAAAGGGGTATTCATGATCTACTGCCCATCTGTAGGCTCTTTTCCCAATAAAAG CAGGGAGGAAATTTGCCAGCCGAGAGTCTGCCCTTTGGCCCTTCACATAAAAGTCTGTGGGC AATCCGANACTGGGTTTGTGATTTCCCTCAGTGGCTCCAACCTGGTTCNAAAATTAANGGATTTTC CTCTCTATGCTNGNGTACAOCCTCAATTTTACATCAANAATTTAAA

SEQ ID NO: 992 ACAACTCTTGCTAATGGAATGCTATAAGCAACAGGTGCAGGAATTTAATAATA
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TTCCTATTATAAAGTCCCGACGAAGTTGAAATCTAACTAGAAAAAAGTANCAGCCCAANGCAAA
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SEQ ID NO: 993 GGTACTTTTTTTTTTTTTTTTTTTNGAGGTTTCAACTTAACATTTATTGCACAA
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SEQ ID NO: 994 ACNAGCATGTTTTTATAGAACAATGTGCTCACTTTGAGAAATGAGAAACATG
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SEQ ID NO: 995 ACGCGGGGGCCAGGGACTCGGGTGCTGGGGCAGACGAGGCGGCTTCTCC
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SEQ ID NO: 996 ACGCGGGGTTGGCAACGAGGGACTCGGCCTCGGAGGCGACCCAGACCAC
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GAGAATGTCAGGATGAAGGTTTNGGAAGAGAGCTCTGCCTTTTCTCTGTGAAGCATGCTTGTCA
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SEQ ID NO: 997 ACTAGTGCTGCAATGCAAGGGTATGACAAAACCTGTCTGTAATGTAGGA
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SEQ ID NO: 998 GCGTGGNCGCGGCGAGGTACTTCNCAAGCAAGCCCTATGATTTGCTACTAT
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ACCTCCACCAATGTGCCTCAGCCCTGTGTGCTGTGGCAACAGCATTCGTGTCCCATCGCCAAAG
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SEQ ID NO: 999 ACNTGGCTTGCAGTTTCTTCAAAAAACATTGCATCACAGAACACATAGATT
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SEQ ID NO: 1000 ACTATTTAAATATATTTCTCCATGAACCTTTTGTGAAATTCAGATCGCAGTGTGT
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SEQ ID NO: 1001 ACGCGGGGGATCAAGTTTAAATGACTGTGCTGCCCTTTACATCAAAGAAC
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SEQ ID NO: 1002 CGCGGCCGAGGTCAGTTGTTTGTGTTTGTATTTTTTTCTTTGAAGGGGT
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GCCCTTCAAAAGNA

SEQ ID NO: 1003 ACTGACACATCCAAGCATGAGTGTGCAGAAATCCCTTGTCTATTCTGTCT
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SEQ ID NO: 1004 ACGCGGGGGTGC CGCGGTGGCGGGACTCTGGGGAATAATGGCTGCGTCTTCGA
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SEQ ID NO: 1005 GGTACACAAGCCATCAATTACCACTCTCTGCTCGCCCTCCATGAAAAATCCAA
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SEQ ID NO: 1006 ACGCGGGGGTGC CGCGGTGGCGGGACTCTGGGGAATAATGGCTGCGTCTTCGA
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SEQ ID NO: 1007 ACATCCGGCGAGTAGCTGGCGGTCCCGGGTGTCTGCTGGTTAGTGTCTGTA
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SEQ ID NO: 1008 GCGTGGGNCGCGGGCCGAGGTACTACTTTCTNACTTTTCTGTTAGCCAGA
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CNC

SEQ ID NO: 1009 ACACTCTCATAGAGATAGAGAAGATCTAAAAAGTTGAGACTACTCAATCCAG
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SEQ ID NO: 1010 CGAGGTACTACTTTAGGAACAGTGTGTAGATCCATTAGAAAAAGGAGAA
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SEQ ID NO: 1011 ACAAATGTGCATTAAACAATTCAGTGACGTAGCTGTGGATCTCTGGATGGCTAT
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SEQ ID NO: 1012 GGTACTTTTTTTTTTTTTTTTTTTTTTTGTCAATATTTATGGGCGCCTATTA
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SEQ ID NO: 1013 CGAGGTACTCCTTGACAGTTGATAGATTATATTTCTTCCATCCCTCAAACCT
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SEQ ID NO: 1014 CGAGGTACTTTGATTCCGTGCTCTGGCCTTTGAAACCTGCTGTTCTGACG
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ANATTCCAAACCCAAGGAGACTGGCCTGGGCTGGNATTCACACNCTCACTTTTTTTATNGGANGG
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SEQ ID NO: 1015 GGTACAGCAGAGACCTTCCTGCTTTTACTGGGGACTCCAGATTTCCCCAAA
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CCATCAAA

SEQ ID NO: 1016 ACTTCTGTCTTTGGCACATTTGCCAGCGGATGCAACTTCTATCCTCAGTC
CAGTTCATATATCTCAGGCAGTGATCCATTTTGTATCAGCCAGTTTCCCTTGTAGGGCCGCTACCC
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TAAAGCAGTAGGCAGCTTCCATCAGCAATGGAAGTGTCCCCACTCCAGTGGTGGAGGTGCAGT
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AGGATCTTCTCTCGCAGGCTGTGGCCCACTCCTTTTCTGTGTATGAGGGGCATCTTAGTTTTT
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SEQ ID NO: 1017 GGTACTCAAAGACGAATCATGAAAAAGAAAAAACTTTATTTCAAACAGGT
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CACCCCTGAGGTCAAGGAGAGACCGGCTAGCCAACATGCTGAAACCCGCTCTACTAATAATACA
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SEQ ID NO: 1018 ACTTTTTTTTTTTTTTTTTTTTAAATCAATATTATTTGGGCGCTATTATGTG
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SEQ ID NO: 1019 ACATATATCAATCTCCCTGCTTGTCTTTAAGAAAGGGCCGTTTATAGCATT
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GTGCNCC

SEQ ID NO: 1020 ACTTANCITGATTTCAAATAAGTAATCTTCCCCCTTTTGTAGGACTTTAAA
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GGCAACACTGGTCTTGGGCTATNATGACCCACAGATGACTCATTATAGAGTTCATTGTCTGATTT
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SEQ ID NO: 1021 AAAAAACCCATACTTGGGGCTATATGCGATTTCAAGTTGGATAAACGAGTC
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GGTGGT

SEQ ID NO: 1022 ACATTCCACAAGCATTGCCTTCTTATTTTACTTCTTTTAGCTGTTAACTTTGT
AAGATGCAAAGAGGTTGGATCAAGTTTAAATGACTGTGCTGCCCCCTTCACATCAAAGAACTACT
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ATATAAACCA

SEQ ID NO: 1023 ACTACACCACTTTTCTCACCAACCCCATCTCTATTCTTGAGTTGCAGGATAC
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SEQ ID NO: 1024 ACAAATTTGCCACAGGTTGAACACTTAATTTGTGTTCTTAAAAATAATGCT
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TCTGGAGGTTGAAATGTCCACGATCAGAGTTCTGTCATGGTCTGGTTCTCGTGACGACTCTTCTCTG
GCTTGCAAGATTGGGGCCTTGTCTGATCCTCACGTGGCATAAAGAGAGCTCTTGTCTCTTATTCCT
TGNAAGGCTCCAATTCATCATGAGTTCCCCCGCGT

SEQ ID NO: 1025 GTACTCTATTCTGATTANGAAAGAGAGGCTAGATACCAAACATCACGAGATC
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TAGT

SEQ ID NO: 1026 ACGCGGGTTCCTCGGCTGGATTTAAGGTTGCCCTAGCCGCTGGGAATTTA
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SEQ ID NO: 1027 ACATACACAAAAAGTTACTGGAATGCTCGGAATAAGATTGTTTTCTGTGT
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SEQ ID NO: 1028 ACAGTCCCTCTCCTATAAGCAAGAAGCTCTCGTGTGCTAGTGTCAAAAGCCA
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CCGCTGCTGCCACCTGACCTGACAGGGAAGGCTGAGAACTCACTTTTGTGACCATGACAGTAA
TGAAACCAAGGTCCCAACCAAGAAATCTAACTCAAACATCCCACTTCATTGTTCCATTCTGATT
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SEQ ID NO: 1029 ACAGGAAATGACTTAGCACTTCCCTGTTTTCTATTGCATAATTTTTTTTT
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SEQ ID NO: 1030 ACACATGCACCTTTGTGCTTTTACACACAAAAAGTATACTGTAATCCACTGAG
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SEQ ID NO: 1031 ACTGTATAACATCTTGTTTATTATTTAATGTTTCTAAAAATAAAAAATGTTAGT
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NGGCTGATCACCCCTGAGGTGAGGANAGACCGGCTACCAACNTGCTGAAACCCCNNTTTACTTA
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SEQ ID NO: 1032 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGNGAAAAATACTTAITTCATGT
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SEQ ID NO: 1033 ACGCGGGGAGGCTTGAGGGAAGCATGGAGGTCCATGGCAAGCCCCAGGCTA
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SEQ ID NO: 1034 ACTGAAGCAGCATATCAATCCCAATAAGACATTGGACCCCTTTGAAACCATG
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SEQ ID NO: 1035 ACTAGGCCATCAAGAAAAGCTGTGAACAGCAACATCATAGACACAAAAGG
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SEQ ID NO: 1042 ACGCGAATTGGAGAAAAAGTTCAGTGGAAGCATGTCGTCTTTATCGCTCAG
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GGCCAT

SEQ ID NO: 1043 ACGAGCGGCGCGCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCT
CAAAATTTATCAAGAAAAGGTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTAGAC
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SEQ ID NO: 1044 ACTTCTGTCTTTGGCACATTTGCCAGCGGATGCAACTTCTATCCTCAGTC
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GCAC

SEQ ID NO: 1045 ACAGCTTCTTCGTCTCCATGCTAAGAGATGTAAGGCTTAAGGGTCAAAC
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ATCGCAACTGCTGCAATTAATTGCCTAGGACCTCAACAGCTTCATGAAAGTCTGGGAAATGTTTCATG
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SEQ ID NO: 1046 ACCAGTAAAACTTAAAGGCACAAATTTCTCTTGAAGACCTTCTCCCTTTAT
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SEQ ID NO: 1047 ACCCCACAGCTCCACACTGTATCCCCAGCCAAGGGCCATCCCTAGAAAA
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SEQ ID NO: 1048 ACGCGGGGGGCAACGAGGAGGGCTGCGAGGCCATCAGCTTCTCTCTGCTCCT
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TGCTATGACTGTCTGGT

SEQ ID NO: 1049 ACAGATGTGTATGGGAAACCCCAACCCCTATATATTGTAATAGATGGGCTG
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SEQ ID NO: 1050 ACTACTTGATTGTTTATATCCAAATTCCTTTCCATCATTTGATTGAATCTTTTGG
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SEQ ID NO: 1051 ACTCTGTTGTAATGGGAAACATTAATATCTGCTTCTTCTGACACGACAGTAA
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SEQ ID NO: 1052 ACAAAGAATACAAATATGATTTGTCAAAAACATATAAAAGACAGCTGCTC
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ATTCCA

SEQ ID NO: 1053 ACTTTTTTTTTTTTTTTTTTNGGGNNCCATNAAAAGCTTTATTTCCATTGG
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AGNG

SEQ ID NO: 1054 ACTTTTTTTTTTTTTTTTTTCTTCTACTTTTCTTTATTGTCTGGCTAAC
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TTNC

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SEQ ID NO: 1057 ACGCGGGGCAACCGTGGAGAGCAGAGCGCGGCGGTGGAAGCTGCTAAGTCA
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SEQ ID NO: 1058 ACGCGGGACTCTAAACTGGTGGTTTCTTACTGAAGGTGTTCTCCATTGAAA
TTTTATCTTCAAAGTATTTATAAGTANTATCTTTAAGACATGACTTGTTAGTAAATAAAGTGTACT
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GAAATTTTAAACCAC

SEQ ID NO: 1059 ACAGAGAAACCAAGGTTGCCCTTTCCACAGCTGGATAGACTTATCCAAAAC
GGCAGGATGGTTCTGTATTAATCTTTTGGAAAGCATGTCTGTATTAAGATTGCAAAACATACAGA
TAGCTACCACAAATAGGTCAAACGACTGATCAAGTTGTAACATCTGTGAGGTCAAATTCAGTTA
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TATGGGCATGTAAAATTGACTCTGCATTTCTGCATGTGTGCATTACATTAAGAGAGACCACTGCG
ACTGAGTCATATATACTCCAACTGAAAAAGTAAGTGTAACAACTGGTTAATCATGCAAGTCTGT
TGTAATATAACAATGACTGGTAAACATGAATTTCTCGCACAGTAGTAATAGGTGCACTCATTA
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SEQ ID NO: 1060 ACATACTGCTGAATTTAACTCAAAATATTTCAAGGTAAGTGAAGTGGTGCTA
ATGTAGACTATAGAATGACTTTCAAGGTGTTTCAACTGAAAGTATATATCCAGAACTGCATCCTTA
TAGAAATACAAAGTAAGACTTAGGATAATTTGCCCTTCAAAACAGTTTCTTAATCTCAGCAGTATCC
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SEQ ID NO: 1061 ACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCC
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CCAGTCTCTCGCTTCTTTATTTCTCCCATATTTCACTCTGTCTCTCACCCCAACCCCTCCCTTC
TGTTTCTCTCCCTCTCTTTCCACCCCTGCTGGCCTTCCATATATCAAGCAGAGTTTATCA
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GCCATGTCACAAAGTCCAGGACAGCATCAAAAAATAGCCCTGATGTCTAAACCACTTCAGCTATCTT
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SEQ ID NO: 1062 ACAGACCAGTGAGTCTGGGGAATTGCGGTCTCCACCAAGATCTGTGGGTGCA
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TCATCCCTTTTGGACCAAGGCTCTTGAGAGCAAGCATGTGTTGATATTCCTTTGTCTACCCCTC
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GCCAAGACGGGCAGATCACGAGGTCAGGANATAGAAACCATCCTGGTTAACACCGGTGAAACCCCT
GTCTNTTCCAAA

SEQ ID NO: 1063 ACNCTAAACAGTGGATTGAGTTCANCNGNTTATCTTTTNCITTTTTTCANA
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GCTTCAACGGCTTGTGCTCACTGTCTGCCAGGTATGAGAAGAACACGTAAGACCGCCACAC
ACTCACCTCCCTCAAGGCCCTTGTCCATAGGGTGGCCACCCGACCTGCCCCANAACCTTTGG
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SEQ ID NO: 1071 ACTGCAACTGCCAGAACTTGGTATTGTAGCTGCTGCCCGCTGACTAGCAGCTC
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SEQ ID NO: 1077 ACGCGGATTGTGACAAAGATGGTGATGGAACATAACAACAAAGGAATTGG
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TTGT

SEQ ID NO: 1078 ACTGTCACTTAACCCCTATTAACATACGGTGTTCAGCCTTCCAGTATCAGCG
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GCTGAATATTTAGTAGAAATGATGCTTCTGCTCAGGAATGGCCACAAATCTGTAATTTGAAATTT
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ANTAAAAAA

SEQ ID NO: 1079 ACTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATGTCCAGGCTGCCTTCTGTG
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SEQ ID NO: 1080 ACTGTGAAGTCAAAGGCCAACATTACAGAGCGCACTCTGCCTGAAATACA
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TCAATGTATGGATGTAATTTGTTATCCATTGCTGTTGGTGGANGAAGNCNCGGGGCATTGGA
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SEQ ID NO: 1081 ACCTTTGTGCATGTTGCCTTCATTCCTGAGCAGGTATCATCCTCAGGGAACCA
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TTCCAAACTCAGTTCCAGACTAGATTGATACCTGGAGCCAGCTGCCTACTCAGCATTTCCACT
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SEQ ID NO: 1082 ACTTTTTTTTTTTTTTTTTTTTTTGGTAAGGACCAGTATTGATTTGACTTT
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SEQ ID NO: 1083 ACTGTAAAAGTTCTGACACAAGACAGTGTNGTGGTTACTTTTCATCGACTTT
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CTACAACTAACT

SEQ ID NO: 1084 ACTGCTGCCGAAGTTGCCCGAGTCCATGGGGTTCGTGCTTTGGCATCAACA
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SEQ ID NO: 1085 ACAACCTTCAAACTTCCAGTTTATAAAAAAGGGGCACACAATCGTGGT
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GCTTTGAAATTCACATCAAAATGACTTTTCCATAAAGCTCAATTGGACAGTCAAGGAACCTTTTGGC
TGNTACGATTCCGGCA

SEQ ID NO: 1086 CGAGGTACAAATGTTCTGTAAAGTTGTAAACAGAAATGAACCCCACTCTT
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SEQ ID NO: 1087 GGTACTNCANCTANNGGCTCAITGGNATGCTATCNTGAANNACNTGGTNATN
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SEQ ID NO: 1088 ACTTCTGTGAGATTACGGNCGCTATGACATGGCTCAGCTTCGGTTAAAAA
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SEQ ID NO: 1089 ACTAAGGAGATAAGTGTAAAGTTTCCATGACTTGACTCTGGAGAGAAAA
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TGGGATGAGAAAAAGCTCTGAAGAGTATNGAACAANAAGCACNGTGAGGCGGAAAAATAAAAA
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SEQ ID NO: 1090 ACAACCTGTGACTGTGATTGGGTIATTCACAGCGTAATTCAGATTCACTC
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TTTTNT

SEQ ID NO: 1091 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTTAAAAATCCATCTGACTGGG
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SEQ ID NO: 1092 ACTTTTTTTTTTTTTTTTTTTTNGNTNTTTTGGGGCAGTCAAGTTAATACAA
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ACANAAAAGGTTTTNTNTNAAATGGTGGCNAACGNCANCTTGANCTAAANANCCNAACTTA
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SEQ ID NO: 1093 CATCCTTACAAAGATTCTGCNGTGATTTGTGTGAAGAAGAAACGTTGTCT
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SEQ ID NO: 1094 ACCTGGTNAANCACTGTGGCAACATACCTGTCTCNTTATTAATTATCCATTA
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SEQ ID NO: 1095 GGTACGCGGGGATTCTTCCCCTCTCTACAACCTCTCTCCTCAGCGCTTCTTCT
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CCACCTCCACAAGTACT

SEQ ID NO: 1096 ACTGCCCTTTCACATCAAAGAACTACTGACAAAGGCGCGCGCTGCCCTT
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GTCCTGCAGGCTGTAATGCAGTTAATCAGAGTGCCATTTTTTTTTTGTCAAATGAATTTAATTA
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SEQ ID NO: 1097 NGTACCACCATTTGNACCTTAACGAAGAANAANATCTTCAAGTNGACCOCTAN
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NTG

SEQ ID NO: 1098 GGTACGCGGGATGGACTCTGCCACTGCCCGGACAAGATCAGAAAGCTGTAT
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SEQ ID NO: 1099 ACTTGTNCCTAGTTTTTCAAGGTATGGCTGTTCTATAGATGCANTGATTGTC
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SEQ ID NO: 1100 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCTNNTNTTTTTTTTTTTTTTTGA
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TGNAAAACATTAATTTCTTAAAAAANGNTGCCACATGTCCCTNTAANATGCCCAAN
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TGCAACCAATC

SEQ ID NO: 1101 GTTCNCGGGGAGAANCTTGGACCGCATNCTAGCCGNCGACTCNCACAAGGCA
GAGTTGCCATGGNGAANANTNCACTGGNNNCATTNTTGTCTCTTGTGGCCCTTCTCTNCACTCATG
GCCAGAGANACCACAGNCANACTGGAGCCATGAAGGACACAAAGGACTNNTGACCNAACTGN
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GNTNAANTTTANANAAAGAGNNTGCTGATAAAAAATTAATTCAGANAATTGGCNATNCNT
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SEQ ID NO: 1102 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCTTAATGGGGG
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AATTCCTGCAAGGNAAGGACGTNATCATGTCTCGNCCCTTGGCNTTNACTNAACTGGGNAAG
NAAANCGGGTTCNTGCTTNTATAAAAAANNAANACCT

SEQ ID NO: 1103 ACACTTGAAACCAAAATTTCTAAACTTGTTTTCTTAAAAATAGTTGTGTA
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NGTCTTTNANGCAACNTTGAANCCCTTCTTNTATNTTGNCAAGCAACCAGANCCCTTNTATNTGN

SEQ ID NO: 1109 ACGCGGGGATGCCAAGGTTCATGAAGGATGCAAGAGCAAGAAAGGTTANTAGA
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ATTTCATAATTN

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GACACATTTGGCCGCTGTGATTGTTGCCTACAAGAAAAATCTGGTANAACAGCACATTCAGGAC
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SEQ ID NO: 4323 ACTCTCTGCAGATGGTCCAAAATTGTAATGGAGTCTGTATTAGAAGAAAAATA
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SEQ ID NO: 4324 ACCAGGTGGGGAGAAGGTAGCAAAATCTCAGTGCCAATTTGAGGGGAAGCC
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SEQ ID NO: 4325 ACTATCCCTGTAACCTGCCAAGAGCTCAGGAGCCAGGCTAGTGATCACACCAG
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SEQ ID NO: 4326 ACAGAGTCTTTTGCTTCTCCACCCCTAGGGGGAAAAACTGCTTTGTGCTTT
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SEQ ID NO: 4327 ACATAAGCATAATCAGTTATGGACAGCTTCTTGATAAAATTGCTATTCAGCAA
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SEQ ID NO: 4329 ACGCGGGGAAAGGAGAGACAAATTATGTTCTGAGGTCTCAGCCTTGGATCAG
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SEQ ID NO: 4330 ACATCTTTAGAAACATCACTTTTAGCTCTGTGATCAGTCTTTGAACAATCATC
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SEQ ID NO: 4331 ACGCGGGGCTTTTCGCAACGGGTTTGCCGCCAGAACACAGGTGTCGTGAAA
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ACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGT
CTTGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGA
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SEQ ID NO: 4332 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAACACANTCTTGCTCTGTTG
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TTNGTATTTTNANTAAAAACGGGGTTTACCCGTGTTANCCAGGATGGTCTCAATCTCCTGACCTG
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SEQ ID NO: 4333 ACGCGGGGGATGAGGTTTTNAAGATTATGCCATTNCANAANCAGACCCNTGC
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SEQ ID NO: 4334 ACTTGGGTCGCTGTCTACTGCTCCTTCATCAGCTTGCCAACTCTCGGAGCTC
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GTCTATCCACTAGGCCCTGGGCTTTGGCTGCTAAACCTGCTGCCTTCAGCTGCCATCCTGGACTCCCT
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SEQ ID NO: 4335 ACTGCTACTTGAATAACTCAGTTAACGCTGTTTTGAAGCTTACATGGACAAAT
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SEQ ID NO: 4336 ACAGAGGGTGCCAGCAGGGTCTTCTACAGTGGCTGTTGAAGAGGCTGAAGG
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SEQ ID NO: 4337 ACTACCAGAGCGAGGAGCAGGCAGAGGAGGAGCTCCTGGACATGGCGGTGC
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SEQ ID NO: 4347 ACGCGGGCGCTCCTAATTTCAATATTGTTGCGTTTCAGGGAATAGGGAAGCC
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SEQ ID NO: 4350 ACCAAGTAAAAATGCAGTCATTTGGATGAAAAATGTATAACATGGTCACAT
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SEQ ID NO: 4359 ACCAGCAGCTGCAGGATGCTTCCATGCAGTGTGTGTGACCTTGGAGGCGCTG
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SEQ ID NO: 4361 ACTACCAGATAGAAATTCTGAAATTGGAATTGGAGGCCAAAGCCTTAATCT
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SEQ ID NO: 4375 ACTTGAAGCTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTC
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SEQ ID NO: 4415 GGTACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTTGCTTNT
GTCACCTTTGAAAGCCAGCANACGCTAAGGATGCAGCCAGAGACATGAATGGAAAGTCATTANA
TGGAAAAGCCATCAAGGTGGANCAAGCNTCCANACCATCATTTGAAAGTGGTATNACGTGGACCG
TCTTTANCTCCAAGAGTATAGGCCCTCCAANAGGTNTTATNNGTNGAATAAGANGTGTNNAGN
ANCCNGGGANTTTTNTCTTCTGNNANGTCTCTTTGTAATTACCTTTTCTATNTTTATNTTTTAN
NNTTNTNTATTTTNTTNTTGGATTTACTTTCTNTTNTATAGTNTGTCTCNTTTATNTTTATATGNT

NTNTAGATNTCNTGGTANNNTTTNTTTTTNTGNTTTCGTTCTTTNTTCTTTTTTCTNTNGTNATA
 TTTTTTATCTTTTTNNATNNNTTTNTNATNTTACTATATTTNTAATNTTTNTTACTTTNTTN
 GTTCTTTTTTTNTTANTNTATNTNTTTTTTTTTTTNTTTTTTTNG

SEQ ID NO: 4416 GCGTGGTGGCGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTGGAGCAGAA
 GGAACCTCTTTATGGAAAGTGGATGANAGAGGCNCCTCCAGCCGTGGGCATCCTGAATGGGAGGA
 AGAATGGACAGTGTGGGAAGGGGAAGGGCANCAGGGACTTAGGACCAGATGGGGCCTGTAGCTC
 TGNNGGACGGCACAGGTTTCATNANGGACCGCTCCNTNTCNNTGGGGAACNAATCNGGCCATCCCN
 CTAGANCCCTTCNCANNANTTCTTGATTCTGNNCAGTTTANTNTTTTTTCATTCATTNNTTAGGGN
 NATTCANCCCTTNGCTTCANCTGNTTNNNTGTTNATGTTGCNATTGANCNAGGNTTNTGNNCATCT
 GNACCTTTTATCTTNGCNCNTTTCTTNACTTNTTTNTTNNCTTTTCCNCTTNTCTTTTTNTTAT
 TTGNATNTNTTNTANTNTTCTTTNTTNTTANTTTNTTTTTTTTTCTCNTTGTTTTTTATGTATNIC
 TCNTTATTNTNTNCTTTATNTANTNGTTATNATTTTNCINTCTTTTANTTAAATNTTCTTATNTGTT
 TTGTANCTTTTATTTNTCNTTCTATTTATCTGNATNTTNTANTNNNTANTTTATNTNTNNNTNTAN
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SEQ ID NO: 4417 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNNAAAAATNAAATTTT
 ATTCNCATTGATANAAANCCATGAAAAACNTTNCCTTTCCCATGTTNCAGCNCATNTTTCAAN
 GGAANATTTNTNGCCATAAANAANATCTNGCTGATTNGNAAAAAGNAAAAANACGTTTATGTTNT
 TCAGGGNAAAAAANGACNTAGTAAANGATNGTTTAAATTTTAAANCCAAACATAANCATAN
 GGCTTNTTATNAACANCCNGTNTAGCCCATTTCTAAATTTTCCNTTATCAATTANCCCCNTTT
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 AAATTTTCAGCCAACTTTTGCACAAAAAACNGGGNGGGGACCACCTTTATGGGATAGGGGT
 TTGGACNACCTTTATACCCAAAAANTNGGTTTNNAAAAATTTTACCNAATTTNGGGA

SEQ ID NO: 4418 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTNGCTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTTNANCCAAANGNTTATTGAAANGGNTTCCNCTCATNTTGACTIONAAANGG
 CTTTTAGGGCTGCTTCCNCTGAAAGGAANATCCTTTTGNAAACCTTGCTTTTCCNCTGTAGGCTGG
 CAAAGGANANNGGANCACCCAACNCNNAAACTACCGTTTGGGCATGGNTAAAAACNNGGGGA
 TTTTANANCATCCTGGGCNTTTCACATCCATGAANTAGGAATGGGGCTNTGCACCANGCGTTCT
 TTTTGGGNTNCCNCTTCCNCTTNTGGAGAGGGATGAAGGAAATCCTTTGCGANAAGNATTTTN
 CNNGGCCNAGGGNCAACCCCGAAAAAGGCCCNNTTCTTGCCCGNGGGCCNTTTAAANGGG
 GAAATTCACCCCTNNGGGGCGGTTNTAANGGATCCAACNNGGNCCAANTTTNGGGTNAN

SEQ ID NO: 4419 GCGTGGNCNCGGCCGACGTNCGCNGGTAAGATAGTTAANCCTGCNTAANN
 AACTNCCAATNTACATACTCNGCTTAAAAATTTGGGGGAAAAATTTAGAAATNTNATTGACAGGAT
 ATNGGAAANTTGGTATAATGAATGAAACATTTTGNATATAAGATTTCATATNNACTTCTTATACNT
 TTGATAAAGNNAGGCNTGGTTGTGGTTAATCTGGNTTATTTTGNCCACNNGTTAANTNTNTCNT
 ATNACTGNNNNNANCCCTCATGACTTANGAAAAANNGGAAANANCTTTGTGACCTAAAGACGAT
 GCCATGCTNNTAAAAAGNAANAGNNGNCAAGGCTCNANATTTGAAAAACGINTTCCNNAATNTT
 TTNCNCTTTNGATGNATCNAACNGTGTGTTNGTCATNGGNNNATNTNGAATGAAACNNGTTTN
 AAACNTNTCCTATNGANTTNNCTTCTCNTANAGTTTNTAGNGNNNTNTNNCTNGTTAAAAATGNT
 TTTATNTTTGTTNGNGTNTANNGNTTCCCTTTTCTNCTANCNAGCNGTGNNGTC

SEQ ID NO: 4420 ACTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTAGGGTTTCATTATTTATTTATGACAAANNTTCCNCTATNTGGGATNTNTCCANTCA
 AAANTNTTTGAAANNANGCCNTNGGCCTTGGCCAATCGGANAATGGAATCATTGACTNACCCA
 TNCACNAANGGNCCCCAAATNGCNTAAGTTTAAACTGGNCNTTAAACCTGCCTGNGACCTTNT
 NAACCTCGGCCNCGTTNATTTGGAAGGANGCCTGGNCCTTGGCNCCTATNANGCNANTGGTTNCN
 GANATTTCCNNGGGACGTNCCCTTGGNCNGNANACCCNAAGGGNNAATTCAGCNCACNTNGNGG
 NCCGNTACTNATGGANNCCAACCTTCGGNNCCCACTTTNGNGGNANCAAGGGGNANAANNNGTT
 CCCNGGNGNAAANTNGTTTCCCTCACAATTTCCACAANATANCAACCCGNANCTTNAAGGG
 TAAACCCNNGGGGGGCC

SEQ ID NO: 4421 NCCAGCGGCCGNCNCGNCNGGCNCTTTTTTTTTTTTTTTTTTTGGTTGGNN
 CNNTATNGNNNACATNNCTACTGNGCATACNATATATACNNTGTATTTNAAAAANGGNCNTTAC
 AATATGNACNTTGACTGNGGNTNACAACGTAATATATGNGAACAATTGTCTGTCTACAACA
 GTTAAAAAGAAATGAATNCTTGGAGGAAACACANTNTANTAAACNATCTTGTGTGGGACATTGAG
 GCATAATTTNTTTCTAAGGAGGCTTAATNTTTTNAACAANGNCTTTGGGAAAAAAGGGGNGTT
 CTNGTCTTATATNGCTTNTATANANGATGGAAACNTGCCCTTCCATTTAGCCTTTTACTNGCTTC
 TNTACCAGACCTAATCACCATCAAGTTACCCATTTTGGTTTAAACCNCTCTATTTGGCTT
 CCGNTTCTACCCAATNTTCTGGGGAACNCCNAAGGGNCTTCATTCTTGGNACTTTNGGTT

CCTACCCTTAAAGAAGGNACCTTTCCTTTTAAANAA

SEQ ID NO: 4422 GGTACTNTCNTNTTCTNCITTTTTTNNTTTTTGNNTTTTNNAACTTNNCACTTT
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ANCTCTTNTATNTGAAACCAAANCTGGATTCTGGACNCTTTGCATTGATTGCTAAAGCAAGTTTT
TGATTGGTANCATAACCTGGGTAAGGTTACNNGAGTGAAGGTATTGANGAAGATNCNCAATTGAT
CTTCTGTGAATTTGGTGCAANTGCACCTATGATTTGNTGCNACCATCTTGTGGGAAGAGGGGGCNT
NAACTATGCAAAAAAGAGAGTTCTNGAAGGCCTGAACTACTGNCNGGAGACTGCTTACACCTCA
TTTTTAAAAAAGAAAGGTACATNTTATACAATATAAAAAATNCACAAAGCTNAAGCTTA

SEQ ID NO: 4423 ACAGGAGAGAATCAATAAGGAGATAGTTAATTCACCACTACAGCTTTGTGCA
TTAAAGACAAGTTTGCAGAAAGCTATGTCTTACAATCCTCTTTAGTTGCATCAAACTGGCAGN
TCAATGACTTTCTACTTCTTATAGGCATTTTATGCNTTTNTTCCCACTGNAATGNTTTTTNANANGA
TCNAACNCCNACCNAGATGCGNCAAAACCAATCATNCNAACTGAAAGATGAATGNTATTAGTGAA
TNACATTGGNTNTTAAATGNNNGNATTGGTTCAAAACAAACATNNAAATNCNTCATATTNAACTGAA
ANTTTGNCNAGGCGCNTGACTNCCCCCTNTGATNCCACACTTTTGGNGGGCGAGGNNNGCNGA
TCNCAAGNNNGGATCTATACCTTTTCTTNNATNGNGGGAANGCTGNTTTCTTAAAAAAN
AAAAAAT

SEQ ID NO: 4424 ACTTTTTTTTTTTTTTTTTTTTTTTTATTAATTTGGGNCCTACAAATGA
TCACTTTTAAATGGACTTTCTGTAAATAATGTAACCTCAAAAAATTTGCCAAGNNTNTATNTGATC
CNCNCAAAATCCCCAAAAGGGTTTNTGGGTNGTCTTNTATTAACGCAAAATNTTTGGGAANGTTTAC
TNTTACTGNAGGATCTTGAATATGTTTTACAATAANGAANCTNCAAAGTTTTATGCGNGGCGNTTC
ATTGNNAACTATAAATAACATTTGTATTAAGAAAGAACTGGGNAATACAAAAATNGNGANACTCT
GNGGGCNGCAATTGNGANGCCAGAATATTTNTTGGCTTTGGGAGCNGGTGCATCCTTCAAAAGC
ACCCNCAATGNGGNTGNAATCATCTGGCTGGNACCCNNTATTTAAAAANTGGTGTCCGAAAACTG
GNNATTTCAAACTTTTTGNTATTACCGAAGTTTGTNAACTTTTGTGNGGTTNACAATGCGGA
GNGGCTTNAAAAAATGGTTTGNANCTGCACCCTTAANTTTGGCT

SEQ ID NO: 4425 ACGCGGGGTATTGAACTGGGGGTGGTCTGGCCTACTGGGCTGACATTAAT
ACAATTATGGGAAATGCAAAAGTTGTTTGGATATGGTAAGTGTGTGGTTCTCTTTTGGAATTTTT
TCAGGTGATTNAATAATAATTAACAACTACTATAGAAACTGCAAAANCAAGGGAATTTCTCTG
ANGGGAACCTTTTGATTTATNAANTAAATCCTNTTTTAAAGTTGNNNGNAANCCAAAGTTTTTTTAA
GTGGAAGAAAAAACCTTCCATTTGTAACTGNAAAAACAAAAAGNTAAGGGATTCCTCAAAAT
TTTGGNAANTNTTATTTTAAACTATCTGTTNAAANTTGGNANCGGTTAAANAATTTGGGATA
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AAAAAANCTNNCTTGAAANTGNNNAATAAAAGGNNAAAAAANTNTTNCNATNCCTNNAT
GGGGGAANANCNTANNCCNTNANANTINTNCNTCTANNAAAANCATTNTCTGCNTNTGCCAAAAA
TTAANCATAA

SEQ ID NO: 4426 ACACAAGCTTTGAGGAAGTGCAAAGGACTGACCTCTAGGCCAGAACAAAGAT
GGAAAACTACCAGGCCCATCAGGCTATAACCCAGACACCAGCATGGACAAAACTCAGTTNTACT
GAATTCANAGACAAAAATCAGTGACACTTNTACCANTTTTTANGGNTTTTACANCAATTGACTG
ANCAAACTTANTTTTTNGTCTGGTGTANNAACCTTTANTNNAANGNTATTANTTAATTNANTA
CTTTGATTNAATTTNTNTNCTNATTTNTATTTATTNTNCNANCTTTNANTGGCT

SEQ ID NO: 4427 ACTTCCAGCCACTAATTGAGATGTAGTTATGAAAGATTAGAATTGCCTTAA
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CNTTTNTTTCTTGACTTTCCCATTTCTTCATNTNAAAGCAATNATTGGCTTTGNTGACNGAAGGGN
NGNCTNAATNTTTTTTCCAGCCTTTTTTNGTGGNATTANTTCTNNCANNTNTTTTTCCCTTTTA
AGAACTTGGTCAATNNNAATCTTANTNTCCGNCCAAAAAGANAAACNAAAGANCNTTTGGCTTNC
CATNCATGGNCTTGGTCCATNCNTGAAGGGTNTTGAATCTTGGAAANCCATCATNAAAAATTT
NTTCTTNGANCNTTGGNCCGNTTGNNTNAGACCANTTNCCTTTTNAATAACCNATGGGNTT
TNNACTGGNACCTTNNCNGCGGGGCCCTTAAAAANGGNCAATTNCAACCCNTGGGGGGCGGTTT
TTTGGGANTCCAGCTCGGGNCCACNTGGGGGNATNTNNGGNATATACNGGTTCCCGTGGGAAAT
GNTGTT

SEQ ID NO: 4428 ACAAGTCATTTTAGGAATAATAGAAATAGGAATGTGGGAAGGCCAGGTGGT
TCTGTAGAAATTTGAACAAGGCTTTTCCAAGAACTCCTCCNTCCGCCCATCCTCCATATGGAN
AGTTGGTGANCTGAAGTGATTGACAGNTGANTCCTTCTNTTTCAGGGNTTANCCGCCAGTCTT

NNCTCNTGTNCAANATTTTNTCCAGGGTCCGGATTCATCANATCACCTCANATTTGGNTCACCTNN
TGTTCNACTNGATTTTANCAATTCCTTNCNAGGCTGNNGAACNTTTGGCAGGTNGGANCACCT
TGGNTAACTAAGNANACTTTTAAANGGGGGCTTTTAAATGAGTGGNNNAATTTTAAACCTGGAAAA
ANACTTTATCCAANTNCCNTNNTTTTAAAGTAAGGCTTAAAAAATANAGGGGNGNCCTTCTTTTA
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GCNGGNGNANATAGGGGGTNAAGCCCTTTGGCTAGGGTTATGGNNTTGGCTNTNCTGGGAGGNAN
GGGGCCCTTCNACTCCCAATTTTATNTGAAANTANTTTGGCNANCCGGGGGNCNCCCNCTTGGN
NGNCCNC

SEQ ID NO: 4429 ACTCTGGATGCCAGCACCAAGATCTATGCTGTGCGCGTGGATGCCGNCCATG
CCGATGTATACAGAGTCCCTTGGGGGGCTGGGCAAGATGCACCGTCTTTGGAAGAGTAGANNGC
CATGTTGCTGATGGAAGNGCTACTGAAATGGNAAACCAAAAAANGGNTGTAAANCCAAAGAAAG
ANGNACTTACACAGACCTATTGAGCAGAACATAAACCAACCTCAATGCTCCAANGCANATCGGAAT
TGTGAGATTGTCTTGTTCATAGACANNAGCNTCAATTTGATGANTNCACTACAGCANGGGTGT
CATGTCNCTTCTNCNCTGCCATANCNTACATAAGTNAACTGTTGTTCCNCTNAGGNNCAAACNT
TNTCCAAGGNGAAACCTNTAGGGTTGCAACAGTAAGGNTGGNNANAANGTTNNCNATTTTNAAT
NGCCTTTGGCCCCNNTTTNGCAAGANTANCNAAAAATNTTGCCTTACTTGGANGGGGTAAAAAC
CTANCAGGA

SEQ ID NO: 4430 CGTGCCCNACGATTNCNCGCTTTGAAAAGTGAACCTATGGNTACCAAAACAN
CTATTNTNATTATAGCATNTACAGTGTCTGGAAAANGATNTAAACAATAANTAAGTGGACGCAT
CACNAGACATCCATTTACTTAATCACAGAAGTGGATCCTGCTACATANNTTCTGAANGTCTNCAT
TCTACAAATTCTCCAGGCTNACGAATGTCAACANTNNAAAATNATTCTANCNATNTNTGTNGNA
AGAGATATCTTGCNGCTTTT

SEQ ID NO: 4431 ACTTTTTTTTTTTTTTTTTTTTTTGTNTNTAACCCTGAANCANTTGATTCCAGT
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NTGTTTCCCCCTCCTTNTNNAANAANGNAGCTGGTAATGGCAAANANTTCTTCAGNNNAACTT
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TTTTNTNGTGNANTTTAAAAACCCCCNTCCTTNCNGGGCGGNCCGTTAAAANGGNCAAATTCCT
AACANCTTGCCGGCCTT

SEQ ID NO: 4432 GNCTCGNCGCCTTTNNNGTCTCNCAACCAANCCCATNGNNGCNCNGTAACTCT
AACACANTTCCCTAAGGAATNAGCATGGGTTCGTAGGAAGCAAAACNNAGCTCTCCATAGAGAAAC
CACTTTCACAGGATGATTAGGTGGACCTGCAATGAANANAATACATTTCAAAGATGGGTCTGA
CTTACACCAAGTTTCACTGATNTACTTAAANAAAAANCGACCCCTTCTCTGTATCAAAAGAAATTAN
AAAAAATTCATNACGATAAAATANATCTCAGGAAAAGGTCCAAGTCTCTCANAGACATACATT
TGCTAATTAATATNAATTTAAAGTTTGACAACAAAATTNCTATTGGGANCTACCTTANAATAGGCC
ATNCTNAGTTCNTGNTCTNNTTTACNTGCNTTNCNTNGANATGAATNCNNNNNTCTNCTATAANN
ATTTNTCTTNTNTATNATNCAACATNGGTGTCTCTTA

SEQ ID NO: 4433 ACGCGGGGGCGTCTTGTCTTGCCTGGTGTGGTGGTTAGTTTCTGCGACTTG
TGTTGGGACTGCTGATAGGAAGATGTCTTCAGGAAATGCTAAAAATTGGGCACCCCTGCCCCCACTT
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ACTTTTNNCAANTAACCATGGGTAATTACACCTAAAAAAAAGGGAGGACTNGGACCCATNAAC
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TTCNATTACTNANAAANNTGGGGAATNTTNCACCTTGGNTNGANACNTGGNANTATACCNTN
AACC

SEQ ID NO: 4434 ACGCGGGGGCTGCGCGCCGCTAGGTGTCTGGGCGATCTATGGGCAAGAGCA
AGGGCCACNATNACAGATTACGGCGAGGAGCANCTCAACGAGCTGGAGGCCCTGGAGTCCATCT
ACCCGACTCCTTCACAGAATTATCANAAAAATCCACCCAGCTTCACCATTAAGTGTACGTTCTGAGG
CTGGAAAAAATGATGAAACTGTCCAGACTACCTNAAAGTTTANATACAGTGANAATAATCCAGATG
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TTAAAAATTAATNCAATTTATGCTNANNAAAATCTNGGTATNATGATGATTTATACTATANTNACT
CNGGANCAATAAAAAANTAANGGATATAANTTTTAAATANAATTTNTATTTATAANATATTAAN

NATTATAANNNTGAATCTNNAAANTTTANTTANANTTTATTACNTTTTTNATCTAATAANNAACATN
ANAANTATNNATAAAAANTAATAATNGNAGNANTTTATTNANATNANCTANATNANTANCANTNAA
ATNNNTANTAGTNAAANANTNNNTGAAATGTGAATTCAGATGTAATTNGGTTATTATTTTNTTAA
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SEQ ID NO: 4435 ACGCGGGGCGAGTCAGCGAGCCACGTGCTTGTGTTGACTGGACAACCTTCCT
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CCGGAGCCANAGCCANCTACTCAACACCTCTAANTAAAAAGCANAAAAACATNTTTCGATATTT
CGGTNAGGAGCATNCCANTATAANANNGGTTTINATAATNGGATNNTTATCNATNAGATTNGTN
NCCTNAAAAATANTNTNANCATCTNNAAANTANAACATCTGCTTATAANNITCAACNTAAACT
TATTNNGGTTATNNATNANAACCTACTTATNTATTATCTNNTATTAGATTNATACTAAAT

SEQ ID NO: 4436 ACCGCCGGGTTGAAAAAGAAACAAAGGAATACTTTGAGAGTTGGGGAGAAA
GTGGAGAAAAAATGTGTTGAAGCTCTTCTGAGCTCATAATTTTAACAGCTAGCCATTGTTTGC
ATGGAAAGGAAATCAGAAATCNACTCANTGAAAAGGTACCACAGCTGTATGCATATTTGGATGGA
GGTTTCACCCATCCAGCCTGTCTCTTACCNGTGGCTGCCTTCTAGTTNCAANCCGATGGNCAN
ACCTNCTCNGCANNANCCNGNTCTTTCCCTNANGCCANCCCCGNNCCTCCCCNGCCTNCCNANNT
CTTNGTNGACATTCTCCTNCTGTNCTTNTTGTCTNTTAATGGGATTGCCNCCCCCTTINACTCTTGN
TNTCCTCNGNCCGTNNNTCTNGATNCCNCTGGCCGCCNCCNNTTCTNNACTNCTNACCCNTN
CNCNCCNTTCCNTTTNCCCCNCTCNCCTNCCCTCTCCNACCTCCTTNCCTCNCNCCNCTCNCCTCG
CCANGACCTACTNTTCTCCTCTT

SEQ ID NO: 4437 ACTTTTTTTTTTTTTTTTTTTCAGNGNAAAAATACTTTTATTGAAACCCNACC
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CATNAATGCTTCTTNTCCTCNATGGTNGTNAANCGNNATGGNCAAACTTGNANGTGTGTCAAT
AAACTNAAAGGTAAATTTTTNAANANACC

SEQ ID NO: 4438 ACCCTNCAGANNATNGTGTNTTTTACNCCATTTTCTACAACCTCTGGATTGCTT
GATACCTTTATAGGANAANGCAAANATTATATTTTTGTGTCTAACATATATAATCTGGGTGCCACA
GTNGATCTGTATATTCTTAATCATCTAATNAACCCACCAATTTGAAAAACNCTNTTAAATTTGTCATN
GAANTCAGAAATANAACACNTCATATGTAAANGGCTGGACACTCACTCAATATNAANGCAAACNTN
ATACTNGTTNAAANTTGTNAAGTNCCAAAAATGCACATTTAAANCNATTTTCAAATCTNGTTNCA
AANTTCAAAAAATTTTAAACANACAANCNANTTGATTTNTTTTTNNACATNTAAAAAACTTCAA

SEQ ID NO: 4439 ACANGNGGAACAATCNGGNTTTTTTAATCAAAGAAGGNGGTGTTCAAGTTGCT
GCTCACAATANTTGATACCCACNATTTGGAATGCAATGGATAATATTAATTGNTGGCANCTGT
TATCAACTACATTGATAGTAAATTTGAGGACTACCTAAATGCAAAATCANCNANTNAACANACTTC
ATATGGCTGATAACAGGGTGCANTGTTGTTTATACTTCAATGCTCCTTNAGGACATNGACTTAAAC
CATTNNGAATATTGATTTATTGAANNGTGNTATAAAAAANTGANTATCATTCCANTNTTNNCNA
AGTAANATNCNNTTACNCCNAAATGAAATNCNATCATNTTAAAAATCANTNTTTTAAATNAATTCN
AGAACATTATATTANAATTATTNCNAATTTCCNNANAANGTATTAATAATCATNATNTTACANCTT
CNTTANAAAAANTAACGGNCCCNNTNACTNTATNCNTGGAGNANGCNANTTAATGTTATCTTCTAA
ATAANTG

SEQ ID NO: 4440 ACCATAGCCAAATCTGGGACAAGCGAGTGTTTAAACAAAAATGACTGAAGCAC
AGGAAGATGGCCAGTCAACTTCTGAATTGATTGNCCAGTTTGGTGTGGTTCATTCCGCCTTCCT
TGTAAGCAGATAAGGTTATTGTCACTTCAAAACACAACAACGATACCCAGCACATCTGGGAGTCTG
ACTCCAATGAATTTCTGTAATTGCTGACCCAAGAGGAAACACTTAGGACGGGGAACGACAATT
ACCCTTGTCTTAAAAAGAAAGCATCTGATTACCTTGAATTGGATACAAATAAAAATCTCGTCAAA
AAATATTACAGTTCATAAACTTTCCTATTTATGTATGGAGCACAAGACTGAAACTGGTTGAGGGA
CCCATGGAGGAANAANAACNCCCNNGAANAAGANAATTTTGTGATTAACTGCNNTNNNN
NNNNNNNNNNNNNNNNNNNGTCCCTGGNCNNNACNCTTANGNGAANTCNCCNCTGGG
GGGNCGNTNTTNTGNANCCANTTNGNCCANNTNGGNNNT

SEQ ID NO: 4441 GGTACTGGATCCAGGTGAGGTTGTGGGCTGNGNCCCGAAGGTGCTTGGCTCC
TTTATGGCGCATGACAAACTCAATCCAGAAGACTGCTCGATCCAGGGGCTTACCGGTTGATCATG
ATGAATCTTGATAATTTGATGATTTCTCTTATAGATAGGGTCATTAATGACTGACTTCAATGCA
TTGAGCAAAATCTCTACTTGACATGGTCTGATGTCCACACTGAGGGCTGCTCCCTTGGCTTTCATGT
GAGCAATGTTATCATGTTGATCCGCAAAACAAGGGAATGCCACCATAAGGGATCCCATGGTANAT
CGCCTCATAAATGCCCATTTGGTTCCCATGAAGTTATAAANGGTTGGTTTGGGATGACCAANAA
GGNCATCTGGGGTAACCCCGCGTACCTNCCNGGCGGNCGNTNAAANGGGCNAATTCACNC
NCTNGNNGGCGGTNANNANNGGNCCNANCTNGNCCNANCTTGGNNNAATNATGGNNTAANN

NNNNCTNNNNAAAATTNNTTNCNTTNNANNNNNCCNNNNNNNNCC

SEQ ID NO: 4442 GGTACGCGGGGAGGAGATCGCCATTATCCCCAGCAAAAAGCTCCGCAACAA
GATAGCAGGTTATGTACGCATCTGATGAAGCGAATTCAGAGAGGCCAGTAAGAGGTATCTCCA
TCAAGCTGCAGGAGGAGAGAGAGAAAGGAGAGACAATTATGTTCTGAGGTCTCAGCCTTGGAT
CAGGAGATTATTGAAGTAGATCCTGACACTAAGGAAATGCTGAAGCTTTGGACTTCGGCAGTCT
GTCCAACCTTCAGGTCACTCAGCCTACAGTTGGGATGAATTTCAAAACGCCTCGGGACCTGTTTG
AATTTTTCTGTAGTGTGNATTATTTCAATAAATCTGGGACANCCCCNNTNNAAAAAATNTTN
NNATTTACNCCNTNNTNGCCTNNNNCNNNCCATTNTNTAANNNTNNANNTNNNNNNNNNN
NNTTTNCCGGTNGGNCNTTCNAAAGGGGGGAATTNNNNCCCTCCCCGGNCCCTTTTAAAGGGG
TTTTTCCNNCTTNGGGGNNNNNTNTAAAAANCCNCTGNCNCAANTTTTGTNNCCNTNN

SEQ ID NO: 4443 ACCTATTAGTAGTCACCGCCTTTTCCCTTCTCTCCAGCCCCCTAACAACTA
ATCTACTTCTGTCTCTACGGATTGTCCTACTCTGGACATTTATATAAATAGGTTAATACGATGCG
TCCTTTTATACAAAAATGTTTCATAGCAGCATTACTATAAAAGCCCCAAAGCGAAACACCTCAAGT
GTCCATCAACCGATGAATGGATAAAACAAAATGTAATATATCCACACAATAGAATCTTATTCGTCA
ATAAAAAGGAATGAAGTACTTTTTTTTTTTTTTTTGGGATTTTTAGGTAGNGGGGTGTGAGCT
TGAACGCTTTCTTAATTGGGGGCTGCTTTTANGCCTACTATGGGTGGTAAAT

SEQ ID NO: 4444 GGTACGAUTGNTAGTGATGAGTTTGCTAATACAATGCCNGTCAGGCCACCT
ACGGTGAAGAAGATGATGAATCCTAGGGCTCANAGCACTGCAGNAGATCATNNATATCGCTNCC
GTGNAGTGTGGNGAGCCAGCTAANTACTTTGACGCGGTGGGGATAGCGATGATTATGGTNGCGG
AGGTGAAATATGCTCGTGTGTCTACGTCTATTCCTCTGNAATATATGGNGTGTCTACACNATANA
ACCCTATGAAGCCAATTGATNTCATAGCTCAGACCACTTCTATGTATCCAAATGGTTCTTTTTTCC
GGANTNTAATGTACAATATGGGGANATTATTCGNAAGCCTGGTAGGGATNAGAANTNTAAGCTT
TCANGNGAGCCNAAAAATCNTAATNNGTGTCTGGTTAAAGAAATGGGGGTCTNCTNCCNCGNCGG
GGTCTANNAAGGGGGTGTGAGNGGTTGCGNCGTGTGTANTANTNTNATTCNCCATCTTNN
CACTGGNAAAAANNTTGNATAATTCTGGNCTCTCNCCNNTATNGACCGGCNCAACCNATANGGTN
TTTNGTTTGGGNNTTGGCNGGGGTTTTATTTAAATTTTGGGGGNNAANTNTGCG

SEQ ID NO: 4445 ACNCGGTGCAAGAGTCTCGCTCAGCNNAAATANGNTNGCTTTCTTTAAT
TACANTGCCATTTTGAATTTGCCTATACAGNCTTAGNGACCATTTAAACCGGACGAACTACGTGN
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TGAATGGTTTTGTATTAAATTTGCTTTGAAATAGATTTTATTCTTGTGCACACAGCCAAGATTTCTT
CAATGGGNCGTGAGCTAGTTGAGGGNTAACCTTGTANGTTGCANAGTGCAATNGCTTGTNTGNTTG
ATCTTCTGTGATGAGGTCAAGTCTGTATNTTGAAGGAGGATATTCACTGAAGCTCATAGTTTA
TAAACAAGGAAATCACTGATAANAATGGGAATNNGTNTCTGNGTTCTGGGAAAAACNTAAANAGA
GCNACTGATTTTCAAGCCAGCCTTTGCCACTACCCCTATAATTAANTGCCAGTCTTATGTTATANAAG
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TGCATGTGCAGAGCCTTTTANTGCCACAGCTTTTCAAGAAAAANGCCCTATCTAAGNACCTTGG
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ANTCCNGCCTCGGGGTTCCCAANCCCTTNNGGGGGAATCCNATGGGGCCATAGGCNTGNNTTCCC
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SEQ ID NO: 4446 ACAAATGTTTTTTATTCAAAAATACAAAATAAATTATCTGTAGGCATGGACA
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CAGCCAGCCTTTTCTTCATTTCTNCAANTGACTTGINTGAANTTATATGGNGAGGAACACTGCN
TNGGGCTTCTGNCACAGNNCANTNCTAGTAGGGCCAGCTGNATTANNGAANTNNGGNAANNCN
CGGGGAGNNTANNCCCTCCCATTTNACCCATTGCACCCATTCCAGGGNCCTTCTCTTTTAGGAA
TTTCTGTGACTACAATTTCTGCTGTAGTTAACANAAGAGGCCNCACNAANCAGCAATCCAATAA
AGCAGGGTCTTCACANACCTTTGTTNNGGGCCCAATGGATTCCCTTTTNTCCACCAATAATTACAAA
ATCTCCANCCATTAGNANNNTANCCCACTTTNTGAANGAANCTTTGGCNTANNTTTNTCAACTNT
TCAAAAGATCCTTCCACAACCTGCATTCTTAACCAATGGGCCANTNGGNGGNATTTNANGNGTCC
TTTAATAANTNTNNACCAATTTT

SEQ ID NO: 4447 ACTTTGGGAGAATCGTGGTGTCTGGATGGCCTGATCAATGTATTAATAATCA
AGCAGTATGTCTTCTTAAATACTCTTAAATCCATACAAATGTGCTTGGGTTGTGGAGCTGAGAT
TTCTCTACTGGCATGATAAAATTTGAACATGTGTTATGAAAAGTTACACCAATTTTGGTTTGGT
CCTTCTTCATTAANCCCGGTGGGCTTCCCTTTTCCATTTTCTTCTTGGTGGTCCGGCTGGTNTTT
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NCTTGNGGGAATTAAAGGGCANAANTTGGGGGACCGGCAAATCNACNAANAAAAACCCNNGCCC
 CCCNTTGNNGGGAANGCCAAAANTAAAGGGGNTNNNTTNTTATTAATAAANCAATTTTCNNGGNTTT
 TNCANAANAGGNGGGGNGCGGGGCCNNNAANATAGNNGNGNCCCAAGNGGGTCCAAAAAAA
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SEQ ID NO: 4448 ACCTACTGGTAGTTGGGTTCAGGGAATGGGATTGACTTGGCCTTCAGGCTCC
 TTTGGTCATAATTTTAAATATGGGAGTAGAAAAACAACAAAGAATGGAATGGAATCTTAAACAA
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 ACCCC

SEQ ID NO: 4449 ACGCGGTGCACACTTTGGGAAGCATCACCATGAAGGTGAGGGACAGAGCTC
 TGGAGCTTTCACGCGCTTGAGTGTCTTCTCCAGTGATCTTAGACCTTGGGAGGAAAGAAAAAGC
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 NATAAGTTTTTTTTTTTNTTTGAAAGGA

SEQ ID NO: 4450 GCGTNGNCCCGCCGTTTNTCTGGCNGAGCTGAGGCTCNAATTCNNNAGG
 NCAACGTGGTGGGACTCACCGNTNNGGCCAGGGTGCTTATGGAAACANGTGNCGAGGACGCCGA
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 NCCCCATCTGTTNTGCCCTGGNTGCNTCANCCCTACCATCACTGGGCANGNCTANNGGGCCTCGTA
 NNGAGGAANNNCCTGAACCTTNCNTTGGANAAGTGAAGATAAAGGATGAAGGCTACNAGGATGCA
 AGGAAGCTONTTNGCTCCNNAAGAAAACNTAAANCCTGGNATGATATCNAAAGGCCTATGNCNCT
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 NGCATCATCTAANGAGGATAATGGTATCATCAAGGCCTCAGAAACATNCTGGAANTACTGTC
 TTAATGNAAGCCCNCTGGACATTTTGNAAACGTGCCCTGGTNGCTAGTNGGACCTTTTTTAANTT
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SEQ ID NO: 4451 ACTTTTTTTTTTTTTTTTTTTTTTTTATTAGGGCAAGTGCATGTTCTGTA
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 GTTAAAGGACCACCANONGGNGTTTCCCTCTGCAGCTGCTTAACCTTTNGTTCCAGTTTCCCTCC
 GNAGTTTTTTCACTGTNTCTCTTGGCAAAGNAATCAGNGATACNTTGCCTTNTCANAAGGATGC
 CNGTTATTTAAGCACCATTNTGGGGACCTTGGTANCNNTCAGTGTNTTTNATNGGAAGNNGCCCCA
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 CAANCTCGNTTTCATGAACAGNACACTATTACAGTAACCAAGTTTTNTNCCATTAAAGTNGGNG
 TCTCCACNCTTNCNTTTGTAAGGNCATTAAGATATCCNCANATTCANTGTTTTTTTACCCCTCAA
 AAATNCANNAAGAAATGNCCTGAAAAAATGGAAANACTAAACNNGNGANTGCNTGNATCCTCT
 GTAATTTAGNNGCAAAAANCCTGNNNTTTTTGNGGGAAAAATTANTNTATTTGTTGGNCGGAGA
 TTTTTTTTA

SEQ ID NO: 4452 GGTACAATGCCTATCGCTTCTTAATCCAAAACGTTCTGNGGCTCCAGANGGA
 GGAAGAAATAGAATTTCTCTACANTGAAAACNCGGNTAGAGAAAGCCCCAACATTNCANACCGG
 GGGATCCTGTCTTCAATGCANNTCTTTTCTTGGCTCTTTTGAGACTGAAATGGCAGCTTATANGCTT
 TNTACNGTGGTGCCTCGCCTGGNCAAGNCTTGTNNATATTCTNACCAAANGGTATGNTAATAATG
 NACCGCANAAANATTAAAGGGNGAAATATGGNATGGATGATTGTTGATATNGCCCTATAAACCTTG
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 CCNANCACTNGTACCCNAGCTTTGGCGTNTTNCATGGGNCATAGCTTTNTTCCCTGANNNAAATT
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GNGNCGCNATANAAT

SEQ ID NO: 4453 ACNGCGGGGCTCACTGAGCACCGTCCCAGCATCCGGACACCACAGCGGNCCT
TCGTTCCACGCANAAAAACCACTTCTCAAACCTTNACTCANCACTTCCTTCCCCAAAGCCTGAAN
ATGCACAAGGAGGAACATGAGGGGGCTGTGCTGGGGGCACCCCCAGCACCATNCTTCCAAGTC
CACCGTGATCAACATCCACAGNGANACCTCCGNGCCCGACCATGTCGTNTGGTCCCTTGTTTNAAC
ACCCNTTCTTGAACCTGGTGCTTGTCTGGGCTTAATANCNTTTNGCCTACTCCGGGAANNTCTANG
GACAGGAAGATGGTTGGCGANTTGACCGNGGCCANNNCTATCNTTATCCGNCAATGTGCCTTGA
ACATNTGGGCCNTGNTTNTGGCCTTCCATANTGACCATTTGATTAATNCTGTGACTNGGTATTTN
TGNTCTTNNACANNTTCCNTTATTTGNTTTNTNATANTACAGGGAAAAANCGGGGTTANTATT
AGNACCCCATTCCTCGGNAATCTTTTGNANTTATNTNTTAAAGCTGGTCTAGANNNTGGNGCNT

SEQ ID NO: 4454 GCGTGGCCGCGGNCGATGTNCANCACAGGCTACATGTAGGCAAGCTAAAGCT
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ATGATACNCTNTCANGCAACNTNCCATNTNTTCTAACAGNTNGAATTACATTNCAATATATGATN
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TACNANGNTTATCNCAAAGCTTTGGANTACAANTGGGAAAAANCTNATTNANNNTTCCCAATANT
CTTCTTTGATGNNAAATATNNAANNCTTNTTNGCGCNTCCTT

SEQ ID NO: 4455 ATNTNCCATGAAATATCCATGAACATACTTATANGTNAAGTATTATTTATTTG
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ATACANNAATAGCTANATTGANGCCAAGGCCAANAGAATATCCGNACTTAAATTTCANGANTTGA
ATGGGTTNGCTAGAATGTGATTTTNNANCAATCACAATAATATGATGGGACAATAAATTTTNCN
TATTAGTCAAATTTANCTTGGAAATCCNGNANCTTTTTCTGTNAANATCGGCTACCCCTAAGNT
GCTNTTNCATGATCCACAAAGTCTTNTTCCNNGCGCCCTCNGGTTNCCNTCTTANTNTCTAANG
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AGCANATNTTAAGTNNNTTGCNTCANAACAATAAATTTTNTCAANNNGGNNACNTATNNACCC
NTCTGNATATNTTCGGGNTAGAATGNAANCAANCNTATATTTNGNGCCTNNATTTGCGATANTCTT
NNTTAANNCTTTTNTATT

SEQ ID NO: 4456 ACGCGGGGAGGGCGGTGGCTCAGGCTCCTGGAAAGGACCGTCCACCCCTCC
GCGCTGGCGGTGTGGACGCGGAACCTCAGCGGAGAAACGCGATTGAGAAATGGAAAGAAAAATGA
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NANTNCCNNAACATTNCAACCCGAANCNTTAANGGNAANCCNNGGTTGNCNTATNNNNNGAC
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TNTCTTNGCNTGGCNTTNGGTTGGGGAACCGGTTTAACTTATTTAAAGGCGGANNACGGTTTCCNA
NATTAGGGTTACCCNGAAA

SEQ ID NO: 4457 GGTACTTNAATTG
NCCAAATTTTTATTTAATGCNCAAGNATGANAATGAACTTTTTAAATCAACTGATTNTATGGA
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GATNTAATGGGCNCCGATAAACAATTCACAGTCNTTTTTAATANAGTATNTTTCAAACACAACCT
TTGNTAAAAAATGGTCCAAANATNGACAGCNCGTGGGAATGCTTAACAGGGGNGGNGATCAGGG
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TGCACTCAAAAAAACCCTGTNGCTTCAATTTAGAAAACNTTCTGNGTATNCCCAGGONTTGCCTTT
TNTNCCATGGGNCCTNCCCTTATTNCAATTNCCACTANNGGGGTTTGCCTTTACTTGTGAGCAA
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NCNNTTCTTNGGNTTTCNATAANACTNCTTGCN

SEQ ID NO: 4458 GCGNGGGCNGGCCGANGNNCACNGGCTGCTNCCNNGTNTTATNNNNGT
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TGAAACANAAACACTTTCTGGAGCATATGGCTTCTANGGGCCCNNAACAGATNCCANGTGGAT
CTGGAACCTTGAGATTGAAATATGGGTGCTCNTNTNAATGNNNATACTTNCANANAGCAGACTGN

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AANGTTNAATCCTATTTTACAAGAAAATGTTTTGATNATNTNTNTGCCNCANCTTATCAAAAAA
GCGCNTGGACAGGACAAATTTGNGNCCACNGNTAAAATTCAAATTTTTAGTCTTNACGGANTTT
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SEQ ID NO: 4459 GGTACTTTTTTTTTTTTTTTTTTTTTTTTATGGGCCAGGTTTATCCCTCACAT
GGGTGGTTTACATACACAGCACANAGGCACGGGCACCATGGGANAGGGCAGCACTCCTGCCTTNT
GAGGGGATCTTGGCCTCACGGTGTAAANAAGGGANAGGATGGTTTCTCTTCTGCCCTCACTAGGGC
CTAGGGAACCCAGGAGCAAAATCCCACCAACGCTTNCATNTCTNANCCAAGGAGAAGCCACCTTGG
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SEQ ID NO: 4460 GGTANTTTNGGGAGCTACAGATAGTAAAGATGATGATGACATTGACCTCTTT
GGATCTGATGATGAGGAGGAAAGTGAANAAGCAAANAGGCTAAGGGAAGAACGCTCTTGACAAAT
ATGAATCAAAGAAAGCCAAAAACCTGCACTTGTGCAAGTCTTCCATCTTACTAGATGTGAAA
CCTCGGGATGATGAGACAGATATGGCNAAATAGAGGAGTGGCTCANAAGCATTCAAGCANACG
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GTGTGATGTCGAAGATGATNANNTTGAACAGANNTGCTGGAGGAGCCAGGATCACTGCTTTGA
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TTTNAATNNNAANATTNTCNGGATTTTGTCTCGNGCTGGGCTGTATNNCANNGNCCTANTTTGNG
ATNTCTTTGCTGGCTNCNTTTGGGNGTATCTCATNTNTGATCCANNANAGNNGTNTCTCTTNCGG
GGNNGGCCNGTTAAATGGGAAATTTNTNAANNNNNGGNCNTTTNTTANGNAANCCNACCTTGN
ACCAANTGGGNTAANNNTGGG

SEQ ID NO: 4461 NCNAGCGGCCGCNCNGNCGGGNACGCGGGGCTCTTCTGCNCTACATNATGG
CNCANGATCAANGTGAAGAGGATAACCCCATGCNCGGAACCTTACATNNGCGAACTCTGTCTNANC
ATNTGTGTTGNGNANAGTGGACACAGACTGACGCNANCNNCANGGTGNNGGAGCAGNTNACAG
GGCNTACCCNTGTGTTTTCCAAAGCTAGATCACTGTGATGATNCTTTGGCATCCGGAAAAATGAAAN
GATNGTGNNACTGNACANTTNGAGGGGCCNANGCAGAAGANATNTTNGANAANGTCTAAAG
GTNCGGANTNTGAGTTAAGAAAAAAACAACTTCTCAGATCTGGAAACTTTGGNTTTGGGATCCNG
GAANACATCGNTCTGGGGATNAAATATNACCCAAGCATNGGTNTCTACAGCCTGTACTNTTATNT
NNGGCTNNGTACGNACNTTTTACGNTCTCAAAACANGAAACTCACGACACGCTGGATNGNGGCC
NTACACGAAATCAGCTNAGAAGAAAGNCCTGCCTGTTCAGCCANAAAGTTTGATNNGGTCATACTT
CTGGCAAAATAATCCGTTCTATCCAAAAAACNTAACATNTTTGGCCAAACNAANAAACNAAAAA
AANTCCGGGNTCNTTTGTGCCCGACCGCC

SEQ ID NO: 4462 GGTACTTGCATGTAGGACAACTCAGTTAGAAAAAGTATAGTGAATGGATGGAA
TCTACTGTATGATAAAAAATGCTACAAACACCATTTAGTTGCCATNAATAAGAAATATACTTGT
AAAAAAATCCAAATGCTGGCATTGTCCAGAAAAATTAACANGTTTATTTATNATTATNATNAG
CTGAACCGTGGNAACTTGTCTCTNGAAACNAATTANCTTGCAATTNATGCCNTACGNTTCTCTTTC
ATTGCNATTATACTCNCACAGATGAAATTTGGTTTACTTTNAAATTNANTGNTTCTNTCCNNNTCN
TTTCCNCATGNTATTGCTTCTCNNTTNTCTNTGCTNTCTNTCTANCCTTTTTNTCTNTTACCT
TNTTCTGNCTTNTTTATCNATCTNTTATNNTNTNANNTTATTTTTNTNTTATTTCTTGTNT
TGCCNTTTTGCNTNTTANCNTTTAAATNNCTTCTACANCTTTTNTTNTNNTNATAATTTATATC
TNTTATNTCGGNNNNCTTTTATTNGTCTTNTTTNTTNTGATTCTATNTTTCATACNTNTACN
NTTTTANTTATGNATCTCNTCTCTATCATAATANCTTCCATNTATGGANTCCTTNTCTTNTCTA
TNGTTNNNTTNNNTTNG

SEQ ID NO: 4463 ACANAGTNTTTTCAACAACCTGAATTTTAAAGTTTCTTCTNCAATGTCTGCCCT
CTACATGGACCTTCCATAATCTTCTGCAATGTGATCATGCTCTGANATGATGGCATAAAGGAGGC
NTTGGGGTGGGATGANGCANGCTGGGCTGGGGCTTCTNTTCCAGNNNNCTTNNNGANGCTGAT
NCANCNCANTNTTNTAATNNTATATTCTAANGCNTNCTGAATNTNAAATCAAAATGCCACACCTCC
ANATCTGAACTATGAAGACTTNTCTTTNGGAAAGAAATCATTAATTGANAGTGTGNAANAGTN
GCTNCTCGTGGTNTAAATCACTATAGCNATATNACCNTATNGATCTCCTCCACCAACCAANT
CTAAAGAACTTATGGGCTCNCCTCGGNAANNTATNAAATTTNTCTCACTCCANTTAAAGACCTTAG
AATGAGGGCTNAAATGNNNAAAAAAAAAAATNTCNCNTGACCATNTTAGGGGNTACCTGAA

NCTCTNNAANGATAAAATTGNCATTTGCTTCCAAAAAATCTN

SEQ ID NO: 4464 ACCACCCTGAGTTCCTGTCCAGGCCTATCAAGCCCTCCCCACCATACTTTGGC
CTCCTCTGGCCTCTGTGGGGCGGCTCTCACATTACCTNCAGAAAGGCTTGACGGCTCTCACCNAG
GGACACCTATAGNTGACAGGAGTGGAAGCAGCTCCCCTGACTCTGAAATCACCGAACTGAANTTT
CCATCAATAAAATCATGACTGATCTTGTAGCGGATGATTCTTCAAGATACCCCTCNAACCTGGGTN
NAGTTTACAGCTCTGACTTTACACTTCGGNTTNGGANACTTCTTAAATATGTTNNATTAAAAAT
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CNGCNGNNGAANCACTCTAANGCGGCGAATTNCAAGTNNANTGGCCTGCCGAACTANTNGGNT
CNNGANCTACGGTACCNGGCTTNGNNNNANNATANGNNATANNCTTGATTCATGANTGAAANTT
ATTATNNATTNNCNNTNACGNNANTNNATTNNATCCGGGAAAGNATNNAAGGNGAAAAAGCCCTG
GGGAGNCTNAAATNANTNATGNNTANTCANNTNNNTNTATTTNGCTTAATCTNNNTTATCTG
GT

SEQ ID NO: 4465 GTACGCGGGGATTTCNATGCGGGGAANANGTGGTTTTGACANAATGCCTC
CTGNTCNGGGTGGGCGTNCCTATGCCTCCATNTATAANANATTATGATNATATGAGCCCTNGTNGA
GGACACCTTCCCCTCTCCCGGACGAGGCGGCGGGGTGGTANCAGAACTCGGANTCTTNCNT
TCCTCTNACNACCACCTATAGGGGGAGACCTCATNNCCTTNTGACATAACAGGGAGACCTGNA
AACNNNNCAACTGCNTGGTTTGGTTTC

SEQ ID NO: 4466 ACNAGAAAAGGGTCCGAGCACAAGCCAAGAAGTTTGGCCCTCATAAGCAG
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AAATCTAAAGTTGCTCCATACAATGACTACCTGGGGGGGTGGGCGGGCGCCATCTTNCATT
GCCGNCNCTNGGTGTGCGGACATTGANTTNCNTGAATTGCCCGTATACNTACANGGTATNNNTCTT
CCGTCTTTTNGGATTTTAGAATGGNTNINTAANAACCTNNNTTTTATTTTAAATNTNAGNTGGCC
AGTATTCTCAAACTGCTGNNAANAATATAAACTTTTAAACTTTGGGGTAAANNCCCCCATNG
GCCGAANTTCCCNCTCCTNGGGAATGCCAGNCCATGCTTTTNNACCCGANNCCNAACCTTGGCNC
NTTGGNCCTNNAGCTGGGCTGTANTAGAAAATNGNTACCTCTCCCTCTGGCCTGNTNCCTTTTTT
TAAAACTTTTATATAAACNNGCGNGTCTGGNNCTGTCTTTTCNNACCTCNANACTCNNNTGGNAT
NNATTTTCGGGNNCTTGCG

SEQ ID NO: 4467 GGTACTTTTTTTTTTTTTTTTTTTTAAATCATCACANGCNCGTGCACTTTATT
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GGGGCAACAGCCCCAGCGTGCNNGGGCCAACATTGCACANTGGAGTGCAAAGGTGTCATGCTANG
GGCGGCTACTAATAACCCCGTTTTCNNGTATTATCTGNAACATAATATGGTAGACTTGGCNCANAG
CCGAATACCACTAACAGGAGGAATCCAANTGGTCATNGAGGATGCCNNAAATCAAGGGCCCAN
ATNTTNAATGCCCTTTNNCGCTGANGCATANGCCTGGGCCCCNGGTTANTTCTCCATCNTNTNT
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TTATATNTAAANANNNNGNTTGNACAATGGGCTCNTTACNTNANTGNGTNTGGTCCCGGNATGGT
NTNTCCTNTGGATNTTTGATCACCTCTCTCAACCNTNNNAAAGAAATGGTNTNTNGGGGNNCCTCC
ANGANAACNCTNATTTTNTNCCTGGNNNTNTATTGGCNTTGGGCANGGAAATTN

SEQ ID NO: 4468 ANATTTGGCCCTGGTTGATTCTCTCTGAATAGTTTCCATCCCNATGAAGAG
GACCTCTCAAGTATTAGTGCAGACCACTTCCAGAGGAGTTTGAATTANAAGGATTTTGGCATTTG
AGANCTTCTTTTCAAGGAACCTGGATTNTNNAAAGGTCACCANGGTATTACAGGGGACAAAANAAGG
TNAGCNCAGCAATACNACNGCAANGCTNGATCTNTATNGGNAAATGGATTGTTGATAATCATC
CTAGGCTNATTCAGTGTGAAANTGANGNAGGGAAATTTGTTGGGTATCACGANANATCCNGAATT
AATACTGGAAGACNCCAGNGTAGCNAAGAGAACCGATTCTACAAGAACAACTCGANATAGAGT
CGCTTGTNTAANTGGGANTCCANGGTNTAAAANCAGGGTGNNTNTACAAANCNCGAAAAANNA
NNATATNTTTTNNCNCNNGANANGAATNCANTTNGGNCCTTNCANANGATNTTTTGGGNACCAN
GGNTTGGNCCTTNCCTAAAATCTTGGNGGCCTTNAATATTAACTTNAAGGGGANTTTNGGNGGTT
TANTNTCTTT

SEQ ID NO: 4469 GGTACCTGCAGGCCTCTACACCTACCTCTCTCTGGGCTTCTATTTTCGACCGC
GATGATGTGGCTCTGGAAGGCGTGAGCCACTTCTTCCGNGAACTGGCCGAGGAGAGCGCGAGGG
CTACGAGCGTCTCNTGAAGATGCAAAACAGCGTGGCGGGCGCGCTCTCTTCCAGGACATCANAG
AANCCAGCTGAAGATGAGTGGGGTAAAACCNAGACGCCATGAAAGCTGCNATGGCCCTGNANA
NAAAGNTGANCCAGNCCCTTTTGGAACTTAATGCCCTGGGNGNNTGTNGCGCNCCTGGCNCNCAAT
NTTGTANANTNTTCTGGANNNTTANCTTCTNTATNANGTGGGAANTTGANACTGTATNAGNAN
NATTGTTNGATNANTNTNANCTAANNNTNTATNTGTTGNGGGTGCNCANGTTGCTTTGGCTNGTC
TGAAATNTTCTNTAGATNGGATAANCANTTTCAGCTATGTATTTAAGATTATCTNCNNNAATTCT
NNNGNTGACCNNTGGGATANGGCTNTCTTCTTATTTAAAAATNGGTTATGTATATCNTNTATNTCTT

TNTNTCATGAGGNTTGCTNTTTNAATNNTCANACANCTCNOCCCTTG

SEQ ID NO: 4470 GTACGAGATGGCACCCCTCCAGAGCCCNCTTCTATGGAGATNAGATGAATCTT
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NAAGTNACCANAACNGTCAGCATGTNCAATNTGCCNTGACCCCACCANATAOCTGANATCENNAT
ACGTGCACCAGGTGGCCAAGCAGATNCACATATNGATGTCCAGCACCTGAGCATGNATGCACCNG
TCCTATCAAANNCANGCACCCTTTGCCTTACTTGAGTCGTCTCTNTTCAAGTGGCCACCTGGTA
GCCTANACAGATAANACCCAGGGNTCAGNANGTTCCCCAAANGCTGCNCAACCTTACANCANAT
GCTTNAGGCATANNNACTGANGGAGGGGCGCTGGCCACAATGTGNACTGATGGNTAGATTNCA
AANTTCCTTTNTTTATACTGTGTGNAGCANNTCTAAANTTGGTCAANTAANGCAAGGGGNGGTCA
ACNCAGC

Figure 3.

SEQ ID NO: 4471

MASRSMRLLLLSCLAKTGVLDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELEC
 QSYGNGAHLASILSLKEASTIAEYISGYQRSQPTWIGLHDPQKRQQWQWIDGAMYLIRS
 WSGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP

SEQ ID NO: 4473

MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYE
 EALYKSKTSNKPLMIHHLDECPSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHL
 PDGQYVPRIMFVPSLTVRADITGRYSNRLYAYEPADTALLDNMCKALKLLKTEL

SEQ ID NO: 4475

MRAWIFLLCLAGRALAAPQQEALPDETEVVEETVAEVTEVSVGANPVQVEVGEFDDG
 AEETEEVVVAENPCQNHCKHGKVCULDENNTPMCVCQDPTSCPAIGEFKVCSDN
 KTFDSSCHFFATKCTLEGTKKGKHLHDYIGPCKYIPCLDSELTEFPLMRDWLKNVL
 VTLYERDEDNNLLTEKQKL RVKKIHENEKRL EAGDHPVELLARDFEKNYNMYIFPVHW
 QFGQLDQHPIDGYLSHTELAPLRAPLIPMEHCTTRFFETCDLDNDKYIALDEWAGCFGIK
 QKDIDKDLVI

SEQ ID NO: 4477

MEKLVQLKESFGGSSEIVDQLEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKE
 CEASKDQNTPVVHPPTPGSCGHGGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPQHP
 NKGLYWVAPLNTDGRLLLEYILYNTLDDLLYNARELRITYGQGSGTAVYNNNMVYN
 MYNTGNIRVNLTTNTIAVTQTLPNAAYNRRFSYANVAWQAY

SEQ ID NO: 4479

MTERRVPFSLLRGPSWDPF RDWYPHSRLFDQAFGLPRLPEEWSQWLGGSSWPGYVRPL
 PPAAIESPAVAAPAYSRAISRQLSSGVSEIRHTADRWVSLDVNHFAPDELTVKTKDGV
 VEITGKHEERQDEHGYISRCFTRKYTLPPGVDPTQVSSSLSPGTLTVEAPMPKLATQSN
 EITIPVTFESRAQLGGPEAAKSDETAAK

SEQ ID NO: 4481

MSSTSPNLQKAIDLASKAAQEDKAGNYEALQLYQHAVQYFLHVVKYEAQGDKAKQS
 IRAKCTEYLDRAEKLKEYLKNKEKKAQKPVKEGQPSADEKGNDSDGEGESDDPEKRR
 LQNQLQGAVIDRPNVKWSDVAGLEGAKEALKEAVILPIKFPFLFTGKRTPWRGILLFGP
 PGTGKSYLAKAVATEANNSTFFSISSDLVSKWLGESEKLVKNLFQLARENKPSIIFIDEID
 SLCGSRSENESEAARRIKTEFLVQMGGVGVNDGILVLGATNIPWVLDSAIRRRFEKRIY
 IPLPEPHARAAMFKLHLGTTQNSLTEADFRELGRKTDGYSGADIGIIVRDALMQPVRKV
 QSATHFKKVRGPSRADPNHLVDDLLTPCSPGDPGAIEMTWMDVPGDKLLEPVVMSMDM
 LRLSNTKPTVNEHDLLKLKKFTEDFGQEG

SEQ ID NO: 4483

MHKEEHEVAVLGAPPSTILPRSTVINIHSETSVDPDHVVWSLFNTLFLNWCCLGFIAFAYS
 VKSRDRKMVGDTVGAQAYASTAKCLNIWALILGILMTIGFILLVFGSVTVYHIMLQIIQ
 EKRGY

SEQ ID NO: 4485

MRTIALAAILLVALQAQAESLQERADEATTQKQSGEDNQDLAISFAGNGLSALRTSGSQ
ARATCYCRTGRCATRESLSGVCEISGRLYRLCCR

SEQ ID NO: 4487

MPAPEQASLVEEGQPQTRQEAASTGPGMEPETTATTLASVKEQELQFQRLTRELEVER
QIVASQLERCRLGAESPSIASTSSTEKSFPWRSTDVPNTGVSKPRVSDAVQPNNYLIRTEP
EQGTLYSPEQTSLHESEGLGNSRSSTQMNSYSDSGYQEAGSFHNSQNVSKADNRQQHS
FIGSTNNHVVRNSRAEGQTLVQPSVANRAMRRVSSVPSRAQSPSYVISTGVSPSRGSLRT
SLGSGFGSPSVTDPRPLNPSAYSSITLPAARAASPYSQRPASPTAIRRIGSVTSRQTSNPNG
PTPQYQTTARVGSPLTLTDAQTRVASPSQGVGSSSPKRSGMTAVPQHLGPSLQRTVHD
MEQFGQQQYDIYERMVPPRPSLTGLRSSYASQHSQGLQDLRSAVSPDLHITPIYEGRTY
YSPVYRSPNHGTVELQGSQTALYRTGVSGIGNLQRTSSQRSTLTQYRNNYALNTTATYA
EPYRPIQYRVQECNYNRLQHAVPADDGTTSPSIDSIQKDPREFAWRDPPELPEVIHMLEH
QFPSVQANAAAYLQHLCFGDNKVKMEVCRLGGIKHLVDLLDHRVLEVQKNACGALRN
LVFGKSTDENKIAMKNVGGIPALLRLLRKSIDAEVRELVTGVLWNLSSCDAVKMTIIRD
ALSTLTNTVIVPHSGWNNSSFDDHKKIKFQTSVLNNTTGCLRNLTSAGEEARKQMRSC
EGLVDSLLYVIHTCVNTSDYDSKTVENCVCTLRNLSYRLELEVQPQARLLGLNELDDLLG
KESPSKDSEPCWGKKKKKKKRTQEDQWDGVGPIGLSKSPKGVEMLWHPVVKPYL
TLAESSNPATLEGSAGSLQNLASNWKFAAYIRGGRPKRKGLPILVELLRMDNDRVVS
SGATALRNMALDVRNKEKIGKYAMRDLVNRLPGNGGPSVLSDETMAAICCALHEVTSK
NMENAKALADSGGIEKLVNITKGRGDRSSLKVVKAAAQVLNLTWQYRDLRSIYKKDG
WNQNHFITPVSTLERDRFKSHPSLSTTNQMSPIQSVGSTSSSPALLGIRDPRSEYDRTQP
PMQYYNSQGDATHKGLYPGSSKPSPIYISSYSSPAREQNRRLLQHQQLYYSQDDSNRKNF
DAYRLYLQSPHSYEDPYFDDRHHFPASTDYSTQYGLKSTTNYVDFYSTKRPSYRAEQYP
GSPDSWVYDQDAQQRNSFFLTFLRLR

SEQ ID NO: 4489

MSGIALSRLAQERKAWRKDHPPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGL
FKLRMLFKDDYPSSPPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRAITIKQILLGIQEL
LNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS

SEQ ID NO: 4491

MCDRAVIKNADMSEEMQQDSVECATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIV
GRNFGSYVTHETKHFIYFYLGQVAILLFKSG

SEQ ID NO: 4493

MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRXDTETEGVPSTAIREISLLKELN
HPNIVKLLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHS
HRVLHRDLKPQNLLINTEGAIKLADFLARAFGVVVRTYTHEVVTLWYRAPEILLGCKY
YSTAVDIWSLGCIFAEMVTRRALFPGDSEIDQLFRIFRTLGTPEVVWPGVTSMPDYKPS
FPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPPFQDVTKPVPHRLR

Figure 2.

SEQ ID NO: 4472

AAGATATAAAAGCTCCAGAAACGTTGACTGGGACCACTGGAGACACTGAAGAAGGC
AGGGGCCCTTAGAGTCTTGGTTGCCAAACAGATTTGCA'GATCAAGGAGAACCCAGG
AGTTTCAAAGAAGCGCTAGTAAGGTCTCTGAGATCCTTGCACTAGCTACATCCTCAG
GGTAGGAGGAAGATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCT
GGCCAAAACAGGAGTCTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGAT
GGTTTACCACAAGTCCAATTGCTATGGTTACTTCAGGAAGCTGAGGAAGTGGTCTG
ATGCCGAGCTCGAGTGTCAGTCTTACGGAAACGGAGCCACCTGGCATCTATCCTGA
GTTTAAAGGAAGCCAGCACCATAGCAGAGTACATAAGTGGCTATCAGAGAAGCCAG
CCGATATGGATTGGCTGACGACCCACAGAAGAGGCAGCAGTGGCAGTGGATTGA
TGGGGCCATGTATCTGTACAGATCCTGGTCTGGCAAGTCCATGGGTGGGAACAAGC
ACTGTGCTGAGATGAGCTCCAATAACAACCTTTTAACTTGGAGCAGCAACGAATGCA
ACAAGCGCCAACACTTCTGTGCAAGTACCGACCATAGAGCAAGAATCAAGATTCT
GCTAACTCCTGCACAGCCCCGTCCTCTTCTTTCTGCTAGCCTGGCTAAATCTGCTCA
TTAATTCAGAGGGGAAACCTAGCAAACCTAAGAGTGATAAGGGCCCTACTACACTGG
CTTTTTTAGGCTTAGAGACAGAAACTTTAGCATTGGCCAGTAGTGCTTCTAGCTC
TAAATGTTTGCCCCGCCATCCCTTTCCACAGTATCCTTCTTCCCTCCTCCCCTGTCTCT
GGCTGTCTCGAGCAGTCTAGAAGAGTGCATCTCCAGCCTATGAAACAGCTGGGTCTT
TGGCCATAAGAAGTAAAGATTTGAAGACAGAAGGAAGAAACTCAGGAGTAAGCTTC
TAGACCCCTTCAGCTTCTACACCCTTCTGCCCTCTCTCCATTGCCTGCACCCCAACCC
AGCCACTCAACTCCTGCTTGTTTTTCTTTGGCCATAGGAAGGTTTACCAGTAGAATC
CTTGCTAGGTTGATGTGGGCCATACATTCTTTAATAAACCATTTGTGTACATAAGAA
AAAAAAA

SEQ ID NO: 4474

ACCGCATCTAGCCGCCGACTCACACAAGGCAGGTGGGTGAGGAAATCCAGAGTTG
CCATGGAGAAAATTCCAGTGTCAAGCATCTTGCTCCTTGTGGCCCTCTCCTACACTCT
GGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAAGGACTCTCGA
CCCAAACCTGCCCCAGACCCTCTCCAGAGGTGGGGTGACCAACTCATCTGGACTCAG
ACATATGAAGAAGCTCTATATAAATCCAAGACAAGCAACAAACCCCTTGATGATTAT
TCATCACTTGGATGAGTGCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAA
TAAAGAAATCCAGAAATTGGCAGAGCAGTTTGTCTCCTCAATCTGGTTTATGAAAC
AACTGACAAACACCTTCTCCTGATGGCCAGTATGTCCCAGGATTATGTTTGTGTA
CCCATCTCTGACAGTTAGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTATGC
TTACGAACCTGCAGATACAGCTCTGTTGCTTGACAACATGAAGAAAGCTCTCAAGTT
GCTGAAGACTGAATTGTAAAGAAAAAAATCTCCAAGCCCTTCTGTCTGTCAGGCCT
TGAGACTTGAAACCAGAAGAAGTGTGAGAAGACTGGCTAGTGTGGAAGCATAGTGA
ACACACTGATTAGGTTATGGTTAATGTTACAACAACATATTTTTAAGAAAAACATG
TTTTAGAAATTTGGTTTCAAGTGTACATGTGTGAAACAATATTGTATACTACCATA
GTGAGCCATGATTTTCTAAAAAAAATAAATGTTTTGGGGGTGTTCTGTTTTCTCC
AACTTGGTCTTTCACAGTGGTTCGTTTACCAAATAGGATTAAACACACACAAAAATGC
TCAAGGAAGGGACAAGACAAAACCAAACTAGTTCAAATGATGAAGACCAAAGAC
CAAGTTATCATCTCACCACACCACAGGTTCTCACTAGATGACTGTAAGTAGACACGA
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A

SEQ ID NO: 4476

CGGGAGAGCGCGCTCTGCCTGCCGCTGCCTGCCACTGAGGGTTCCCAGCACCC
ATGAGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCCT
CAGCAAGAAGCCCTGCCTGATGAGACAGAGGTGGTGGAAAGAACTGTGGCAGAGG
TGACTGAGGTATCTGTGGGAGCTAATCCTGTCCAGGTGGAAGTAGGAGAATTTGAT
GATGGTGCAGAGGAAACCGAAGAGGAGGTGGTGGCGGAAAAATCCCTGCCAGAACC
ACCACTGCAAAACACGGCAAGGTGTGCGAGCTGGATGAGAACAACACCCCCATGTGC
GTGTGCCAGGACCCACCAGCTGCCAGCCCCATTGGCGAGTTTGAGAAGGTGTG
CAGCAATGACAACAAGACCTTCGACTCTTCTGCCACTTCTTGGCACAAGTGCAC
CCTGGAGGGCACCAGAAGGGGCCACAAGCTCCACCTGGACTACATCGGGCCTTGCA
AATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCCCCTGCGCATGCGGG
ACTGGCTCAAGAACGTCCTGGTCACCTGTATGAGAGGGATGAGGACAACAACCTT
CTGACTGAGAAGCAGAAGCTGCGGGTGAAGAAGATCCATGAGAATGAGAAGCGCC
TGGAGGCAGGAGACCACCCCGTGGAGCTGCTGGCCCCGGGACTTCGAGAAGAACTAT
AACATGTACATCTTCCCTGTACACTGGCAGTTCGGCCAGCTGGACCAGCACCCCAT
GACGGGTACCTCTCCACACCGAGCTGGCTCCACTGCGTGCTCCCTCATCCCCATG
GAGCATTGCACCACCCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATC
GCCCTGGATGAGTGGGCGGCTGCTTCGGCATCAAGCAGAAGGATATCGACAAGGA
TCTTGTGATCTAAATCCACTCCTTCCACAGTACCGGATTCTCTCTTTAACCCCTCCCT
TCGTGTTTTCCCCCAATGTTTAAAAATGTTTGGATGGTTTGTGTTCTGCCTGGAGACAA
GGTGCTAACATAGATTTAAGTGAATACATTAACGGTGCTAAAAATGAAAAATTCTAA
CCCAAGACATGACATTCTTAGCTGTAACCTAACTATTAAGGCCTTTTCCACACGCAT
TAATAGTCCCATTCTTCTTGGCATTGTAGCTTTGCCCATGTGCTTATTGGCACATG
GGTGGACACGGATCTGCTGGGCTCTGCCTTAAACACACATTGCAGCTTCAACTTTTCT
TCTTTAGTGTCTGTTTGAACCTAATACTTACCGAGTCAGACTTTGTGTTCAATTCAT
TTCAGGGTCTTGGCTGCCTGTGGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAAGGG
AAGTAACAGACACACGATGTTGTCAAGGATGGTTTTGGGACTAGAGGCTCAGTGGT
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TGAGAGAAAGATTCTGGGGCTGTCTTATGAAAATATAGACATTCTCACATAAGCCCCA
GTTTCATCACCATTTCCTCCTTTACCTTTCAGTGCAGTTTCTTTTCACATTAGGCTGTTG
GTTCAAACCTTTTGGGAGCACGGACTGTCAGTTCTCTGGGAAGTGGTCAGCGCATCCT
GCAGGGCTTCTCCTCCTCTGTCTTTTGGAGAACCAGGGCTCTTCTCAGGGGCTCTAG
GGACTGCCAGGCTGTTTCAGCCAGGAAGGCCAAAAATCAAGAGTGAGATGTAGAAAG
TTGTAATAATAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCCTCACATTGGAT
GATTGTCATAAGGTTTTTAGCATGTTCCCTCCTTTTCTTACCCCTCCCTTTGTTCCTCT
ATTAATCAAGAGAACTTCAAAGTTAATGGGATGGTCCGATCTCACAGGCTGAGAA
CTCGTTCACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTAATCATACAACTCT
CACCATGATGTGAAGAGTTTCACAAATCTTTCAAAAATAAAAAGTAATGACTTAGAA
ACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4478

CGGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCTTGGCCAAGCTGCAGGGGATTTG
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TCCAGCTCCAGCTTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGCAGCTTA
GGCAGCGGAGGTTCTGTGTCCAGTTGTTTCCAATTTACCCGGCTCCGTGGATGAC
CGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTCCCGTGGACAGA
GTGGAACGCTTGAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGAACTT
TCCAAAGTGAGGGAATATGTCCAATTAATTAGTTTGTATGAAAAGAACTGTTAAAC
CTAAGTGTCCGAATTGACATCATGGGAGAAGGATACATTTCTTACACTGAAGTGGAC
TTCGAGCTGATAAGGTAGAAGTGAAGGAGATGGAAAACTGGTCATACAGCTGAAG
GAGAGTTTTGGTGAAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAA

TATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCCTTGCCAT
TCGCCGAGAAATCGTGGCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAG
ATCAAAACACCCCTGTCGTCCACCCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTG
GTGTGGTGAACATCAGCAAACCGTCTGTGGTTCAGCTCAACTGGAGAGGGTTTTCTT
ATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGT
ATTGGGTGGCGCCATTGAATACAGATGGGAGACTGTTGGAGTATTATATACTGTACA
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GCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACATGTACAAC
ACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAAC
CTCCCTAATGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGCAT
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ACTGGTTAACATGGTGATTAGTAACTCAATGACACCACACTTCAGGTGCTAAACAC
TTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGT
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GGTTACCTTCTGAATTATGATCTTTCTGTCTTGCAAGCCCCAGTAAGCTGTTTAGG
AGTTAGGGTGAAAGAGAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGA
TATCTGCAGATATCTAAGTAAGTGGAGAAGACTATTTTTCAACAAACATTTCTCTT
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CAGAAAGGTAACCATCGTTATAGACATAAAGTTTCTGGTCAAAAGGGTTATAGTTAAT
GCTCTGCACTTTTCTGCATCTTATGCATTACAATGTCTAGTTTGCCTCTTCCCTG
TGTTTGTGTCTATAATAGTAAAAAATCTCTTCTGTTTGGCGTATAGGGATTCTTTGTAC
AGGAAATATTGCCCAATGACTAGTCCTCATCCATGTAGCACCCTAATTCTTCCATG
CCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCTGGAGCTCCTCGAGG
GACCAAATCTCCAACCTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGT
TATGGAGAGAGGCCTTTTATGCATTAAATTGTACATGGCAAATAAATCCCAGAAGG
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GACTTACTAACCAATTCCACCCCCACCAACCCCCCTTCTACTGCCTACTTTAAAAA
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AAAGTGCTAGCATTATTTATGTTATCTAATAAAGACCTTGGAGCATAATGTCAACTTAT
GAGTGATCAGTTGTTGCATGTAATTTTTGCCTTTGTTAAGCCTGGAACCTTGTAAGA
AAATGAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTAT
CTAGTTAATCAGTGCAGTAGTTGGAACCTTGCTGGTGTATGTGATGTGCTTCTGTG
CTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTTTCTTTGATGTTCAAGTCCTA
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ATGTGCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4480

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CTGGTACCCGCATAGCCGCCTCTTCGACCAGGCCTTCGGGCTGCCCCGGCTGCCGGA
GGAGTGGTGCAGTGGTTAGGCGGCAGCAGCTGGCCAGGCTACGTGCGCCCCCTGC
CCCCCGCCGCCATCGAGAGCCCCGAGTGGCCGCGCCCGCTACAGCCGCGCGCTC
AGCCGGCAACTCAGCAGCGGGTCTCGGAGATCCGGCACACTGCGGACCGCTGGCG
CGTGCCCTGGATGTCAACCACTTCGCCCCGACGAGCTGACGGTCAAGACCAAGG
ATGGCGTGGTGGAGATCACC GGCAAGCAGGAGCGGCAGGACGAGCATGGCTA
CATCTCCCGTGCTTCACGCGAAATACACGCTGCCCGCGGTGTGGACCCACCCA

AGTTTCCTCCTCCCTGTCCCCTGAGGGGCACACTGACCGTGGAGGGCCCCCATGCCCAA
GCTAGCCACGCAGTCCAACGAGATCACCATCCCAGTCACCTTCGAGTCGCGGGCCC
AGCTTGGGGGGCCAGAAGCTGCAAAATCCGATGAGACTGCCGCCAAGTAAAGCCTT
AGCCTGGATGCCCACCCCTGCTGCCGCCACTGGCTGTGCCTCCCCGCCACCTGTGT
GTTCTTTTGATACATTTATCTTCTGTTTTCTCAAATAAAGTTCAAAGCAACCACCTG
TAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4482

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CCGCTGGGAACTCCGCCATGTCATCCACTTCGCCCAACCTCCAGAAAGCGATAGAT
CTGGCTAGCAAAGCAGCGCAAGAAGACAAGGCTGGGAACTACGAAGAAGCCCTTC
AGCTCTATCAGCATGCTGTGCAGTATTTTCTTCATGTCGTTAAATATGAAGCACAAG
GTGATAAAGCCAAGCAAAGTATCAGGGCAAAGTGTACAGAATATCTTGATAGAGCA
GAAAAACTAAAGGAGTACCTGAAAAATAAAGAGAAAAAAGCACAGAAGCCAGTGA
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CTACTTAGCCAAAGCTGTAGCAACAGAAGCCAACAACCTCAACATTTTTTCAATATC
TTCCTCTGATCTTGTCTTAAGTGGCTAGGTGAAAGTGAAGAACTGGTTAAGAATTT
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TCTCTGTGTTCAAGAAGTGAAAAATGAAAGTGAAGCCGCACGTAGAAATTAAGACGG
AGTTCCTAGTGCAAATGCAAGGGGTTGGTGTAGACAATGATGGAATTTGGTTCTGG
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GAATTTATATTCCCTTGGCGGAACCCCATGCCCCGAGCAGCAATGTTTAAACTGCACC
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GCTGATCCTAACCATCTTGTAGATGATCTGCTAACACCTTGCTCTCCAGGTGACCTT
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CATGACTTGTGAAATTAAGAAGTTTACAGAAGATTTTGGTCAAGAAGGCTAAGC
CAAAGACAAGGAAGATGCTTACCATATGTATTCTTTCTTTTCATAGATATTTTTGTCTA
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TCACTTCAGAGTTCATTAGGTTTTATATTGTACTTTTCTCCATTACTTATTAATAC
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CGGCATAAAAAACAGAAATTACCCAGTAAAAAGGATGTCAGAAATTGACATACAAAT
ATTTACAATTTTTATGAATGGTGGTCTTTGCAAAGAGCATTTATATTTCTTTTTTTT
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SEQ ID NO: 4484

GCTCACTGAGCACCGTCCCAGCATCCGGACACCACAGCGGCCCTTCGCTCCACGCAG
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AGGTCCACCGTGATTAACATCCACAGCGAGACCTCCGTGCCCCGACCATGTCGTCTGG
TCCCTGTTCAACACCCTCTTCTGAACTGGTGCTGTCTGGGCTTCATAGCATTGCGCT
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SEQ ID NO: 4486

SEQ ID NO: 4488

703

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AGTAAGGGAGCTTGTTACAGGAGTTCTTTGGAATTTATCCTCATGTGATGCTGTAAA
AATGACAATCATTCGAGATGCTCTCTCAACCTTAACAAACACTGTGATTGTTCCACA
TTCTGGATGGAATAACTCTTCTTTTGATGATGATCATAAAATTAATTTTCAGACTTCA
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CAGCCTTGAGGAATATGGCACTAGATGTTGCAACAAGGAGCTCATAGGCAAATAC
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CTTGAATACATTATGGCAATATCGGGACCTCCGGAGCATTATATAAAAGGATGGGT
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CACATCCTTCCTTGTCTACCACCAACCAACAGATGTCACCCATCATTACAGTCAGTCG
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CAGCAAGAGAACAAAATAGACGGCTACAGCATCAACAGCTGTATTATAGTCAAGAT
GACTCCAACAGAAAGAACTTTGATGCATACAGATTGTATTTGCAGTCTCCTCATAGC
TATGAAGATCCTTATTTTGATGACCGAGTTCACTTCCAGCTTCTACTGATTACTCAA
CACAGTATGGACTGAAATCGACCACAAATTATGTAGACTTTTATTCCACTAAACGAC
CTTCTTATAGAGCAGAACAGTACCCAGGGTCCCCAGACTCATGGGTGTACGATCAA
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CATCTTGCTGATTTTATGATTGAAATGTGAAAGTGAAGTGAAGGAATGAATGAAG
TGTGTTTTTTTTCTTTTTGAGGAATTATCA

SEQ ID NO: 4490

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SEQ ID NO: 4492

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SEQ ID NO: 4494

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SEQ ID NO: 1110 GGTACTATTATACTAAAAGCTCCTACTGTGATGTGAAATGCTCATACTTTATA
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SEQ ID NO: 1111 GGTACTACAAGTTTAGTGGCTTCACGCAGAAAGTTGGCAGGAGCATGGGCTTC
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SEQ ID NO: 1112 CGAGGTACATGCTCTATCTGATGCTCGATGTGTGTTGACATGGCTGGAGAAA
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GGG

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SEQ ID NO: 1117 CGAGGTACGGGTATATCCATTCCCGAGTCTGGTGGAAGATCATCAACGACAATGG
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SEQ ID NO: 1119 ACAGCAGCAGACTCTCCACGGGCTCTGTCCAATTGCAAGAAATTTCAAGTTCAT
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SEQ ID NO: 1121 ACGCCGGGCTAGTGGCTTGTAGGATATCCGCAGGAGCGCGCGGTGGCGGGAG
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SEQ ID NO: 1122 ACCTTAACTTAAATCCAGAGCAAAAGTTAAGACTCTCTCTCTATTTTGG
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SEQ ID NO: 1123 ACATGACCTAATTTTACATCATACTAAAAACAGGCCCTATGGAGAGAGGACA
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SEQ ID NO: 1125 CAAAAAACAAGGTTATGAGGAAATGAGCGATATATGAACGGCATAAAAACA
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SEQ ID NO: 1127 ACAATTCTTACAGACACATGAAGCAGAACATTTGAAAAATCAAACTTACTT
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SEQ ID NO: 1133 ACCTAGCTCAGAACTGAGGGTTTACTTTTGGAAAGAGTCAGGAGTGGATG
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ACAAAGAACGAACTNTGTCTTCAAAAAAAGAAAGAAAGGGAAGGCCCTTGGGTTGGGCCCA
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SEQ ID NO: 1134 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGGATTTAA
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SEQ ID NO: 1135 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTCTTNGAANATGGTTATTTTAC
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SEQ ID NO: 1136 ACGCGGGTAAGATAAACTATTTAGGAAAAAGTCTGACGAATTTAATGCATG
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SEQ ID NO: 1137 ACTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTNGACT
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SEQ ID NO: 1138 GCGTGGTCGCGCCGAGGTACTAGTCTCTACTTGGGGACAAGAAAAAGAATA
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SEQ ID NO: 1139 ACTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTGAATCAAAAGCAGGGT
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SEQ ID NO: 1140 ACITTTTTTTTTTTTTTTTTTTTGANATGGAGTTTCGCTCTGTTGTCCAGGCT
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SEQ ID NO: 1141 ACCTGAGATCCTGGTGCACAACATAGTGATCTTCAATGCGAAGTTCAAGTGAAG
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SEQ ID NO: 1142 GGTACTTTTTTTTTTTTTTTTTTTTTTTTNGAAATTAATACITTTAATTA
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SEQ ID NO: 1145 ACTAAGCGGCCTTGGATACCTGGCCGCGGATGCTGGGCGGCGTCAGGTGAG
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SEQ ID NO: 1146 ACITTTTTTTTTTTTTTTTTTTTTTTTNGAGGCTTGNGTATTATCAAGGCTT
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SEQ ID NO: 1147 ACACTGTTGGTGTTATATGGGGATGGGGTTCTCGTAATTTGTTTATTATTTA
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SEQ ID NO: 1148 ACCATTGGGCCCTTTGCTTCATGCCAGGAAACTTGTCCATACTAATGAAG
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SEQ ID NO: 1149 ACAAAAACTGTGACATCAAGAAGGGCAGGAGAAACAAAAGGCATTTCTAT
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SEQ ID NO: 1150 ACATGAATTAGAAGCGTGCATCTAGGATTATGGCCAACTGTTTTAAAAATG
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SEQ ID NO: 1151 ACTACCACAGCCTTAGGTGACATTGATTATAACTTGGTCACAATTCAGTGC
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SEQ ID NO: 1152 ACCAGTGAGAAGACAGCTTTGCAGTCACACTGGAGATCAGAGTTCCAGGCTG
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SEQ ID NO: 1153 NGTACTCAGCTCTGTTCTCCTACTCAGGCTGGGACACCCCTCAACTATGTCACT
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SEQ ID NO: 1154 GGTACAAATATTTAAGAGTGTGATTGGGAGTAAGGGAATGTCAACTGCCAA
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SEQ ID NO: 1162 GGTACAGCTTTTGTCCAGTTTGTCTCTCCATTACTGGATGCATTTATGGAAG
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SEQ ID NO: 1165 CGAGGTACATGAAAAAATAAAAAATTTGATCATGAATCAAACCCCTGGAAC
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SEQ ID NO: 1166 ACGCGGGGCATCACAGTCAACTTCACAGCGACCAAGTTAAAAAGAGTGATG
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SEQ ID NO: 1196 GGTACTTTACTGAAAGAACACTAGTGTCTTTCCTTTCGGTTGTGAAAAAGT
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SEQ ID NO: 1197 GGTACTGATTTCATCGTTGCATTTACAAGTCTACAAAAATGCCAGCACTCC
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SEQ ID NO: 1198 GGTACCAAGGGATGGAAGAAGTAAATATAGCTCAGGTAGCACTTTATACTCA
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SEQ ID NO: 1199 GGGACTTTTTTTTTTTTTTTTTTTTTTCTTTTTCAGCATTGNGTTTTACTTTTT
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SEQ ID NO: 1200 ACTTTTTTTTTTTTTTTTTTTTTTGGCTAAAAATTATTTTATTTTATAATTT
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SEQ ID NO: 1201 ACGCGGGGTTTTTACTTGATATAAATGTATTTTACTGTGATAGTCCAAGTG
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SEQ ID NO: 1202 ACTTTAGTAAAGACATTCATCTCAGTCATTTCTCTCTCCAGCTTGACCTTAG
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SEQ ID NO: 1203 ACTGAACACAATATTGTGTTTTTATTTATGCCACGTCAGTGGGGCAAGA
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SEQ ID NO: 1204 GGTACTCACTTTTCCAAATGATCCTAGTAATGCTAGAAATATCTTCTCT
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AAAAAA

SEQ ID NO: 1205 ACCAAAGGATAGCTGTCTGTAAAGTAGGGACCTCTCATGCGCTACAGGCTT
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SEQ ID NO: 1206 ACGCTTTTACCCACCCCAAGTCCTGGGAGAAATGCAGGCAACACTGAGA
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SEQ ID NO: 1207 GGTACTTTTTTTTTTTTTTTTTTTTTTTTCTTNAAAAAATATTTAAAT
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SEQ ID NO: 1208 ACCCAAATACAAAAAGGTGTCCCTTTAAGGAAAAATAAGAATTAAGTTTAA
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SEQ ID NO: 1209 ACAAGTGTATACAGGCACAAACATGTTTTAACAAAAGAAGGAGGAAACACT
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SEQ ID NO: 1210 GGTACGGAGATGTCTTATGGTGAAATGAAGGTAAATCTTGGGACCTAGAG
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SEQ ID NO: 1211 GGTACGCGGGGGTGGCTACCATGCTCTCTCGCGCGGGTGTGCTGGGGCTGTC
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SEQ ID NO: 1212 ACTGATACAATGGATCAAGTCTTAAAAATTTTAAAGAAATAATGATGCTG
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SEQ ID NO: 1213 ACGCGGGGACAACTTTTACAGAGACAGCAGAGCACACAAGCTTCTAGGACAA
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SEQ ID NO: 1214 ACATTTTCATAAAATATGAAGGGATAACTACAACTGGAGTAAAAATGACGG
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SEQ ID NO: 1215 GGTACCTTCATGAAAACGGTATTATACACCGTGACTTAAAGCCAGAGAATGT
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SEQ ID NO: 1216 GGACGATCGAAGGGACTATGCTTCATTGAATTTTGTGTTGAAGACAGTAAG
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SEQ ID NO: 1217 ACGCGGGGATGTAATTTTAAATACAATGCAGACGAAGCTAGAAGTCTGAAG
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SEQ ID NO: 1218 ACGCGGGAAACACAATTCAATGCAAGCTCAGTTTCTGGTGTCAAAAACT
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SEQ ID NO: 1219 GGTACTGAAGGACAAAACTGGATGGCCTCAAAAGGTTCTTGAACACCACT
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SEQ ID NO: 1220 GGTACATGGTGGTGGTTATAAATATTGGGACTTAAGGCAGCTTGTCTATG
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SEQ ID NO: 1221 ACTTCCTGAGACATGGATCTGGGATTGGTGGTGGTAAACTCAGCAGGTGT
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SEQ ID NO: 1223 ACAAGTTCGGCTTTGAGCTTCTCAGGGGCTCTGGGAACATCCTTCAAAGG
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SEQ ID NO: 1224 GGTACTATGATCCAAACACCAAAAGCTGTGCAAGATTCTGGTATGGAGGTTG
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SEQ ID NO: 1225 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATACAANAACCTTATGTTTATTGCAA
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SEQ ID NO: 1226 ACTCTGGATCCCAAGGTGACTGGTTGTTAATCGTGTGCATAGAACGAGCCA
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SEQ ID NO: 1228 ACTGGGACAGTTGGGTGTGTTATGGATACATAACCTGAGGAGCCGGGGAAG
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SEQ ID NO: 1229 ACAGACAAAGTGGGAGGTTTATTTCTTGGTCTCTTCTCTTGGATAAAGTC
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SEQ ID NO: 1230 ACGCGGGGCTTCTCCAAGATGGCGGCGATCGGGCGGCTTGAGGCGGGATCCG
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SEQ ID NO: 1231 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAAANATGGGGTTTCCCATN
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SEQ ID NO: 1232 ACCCCTTAACCCCTTCTCCTTACCCCTTAGCAGCAAGTCCCACTTTTCTAGGG
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SEQ ID NO: 1233 ACTACTGTCCAGCCTCCTCAGGAGAACCAACATCCAGTATACCTTCAACAG
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SEQ ID NO: 1234 GGNACTTNTNTNTTTTTNTNTTTTTTTTTTAAAGGGGTCATCGTCANANCTG
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SEQ ID NO: 1235 GGACGTCGGGGACGTCCGCAGCGTCACACAGAAACATATCCAGGAGTGGGG
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SEQ ID NO: 1236 GGACGCGGGGGAGTCAGTCCAGTCAGGACACAGCATGGACATGAGGGTCC
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SEQ ID NO: 1237 GGTACCATCCCTCCATATTGCCACCAAGATGCGTGAATACACCAGGCTCAT
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SEQ ID NO: 1239 ACATGGGTAATCTGTCCCCATGACCCAAACATCTCCCATAGGCTCCACCTCCA
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SEQ ID NO: 1241 CCGGGCAGGTACATAGGTAACCAAAAGTATATAGCTTATTTGGTGAATCTTCAT
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SEQ ID NO: 1243 GGTACATGGCAATTAGAAGTTGTCTATGGCAAAAGAAAACACAGCTGGCCTG
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SEQ ID NO: 1246 AATTCGCCCTTAGCGTGGTTCGGGCCGAGGTACATCATGCCGCTGATGAAGG
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ATT

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SEQ ID NO: 1249 ACAACACTATTTTCATTATCTGGATTGTCCATGCTAGAAATAAATTCATCCTTG
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SEQ ID NO: 1250 ACTNNTNTTTTTTTTTTTTTTTTAAACANCAAGANCGGGAGCAGGATTGGGT
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SEQ ID NO: 1251 ACAACACCATCTGGCTTCTATTTTGAACTCCACACCAGGTTAATCTTGTT
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SEQ ID NO: 1252 ACATTCTACCGAAGACTTCCCGCGAAGTGTCTGCCAGTGAGATAAGTGTGA
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CCG

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SEQ ID NO: 1257 ACCTAGAAGAGAGGCGGGTCAAAGAAAGTAGTGAAGAAGCATTTCTAGTTCAT
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SEQ ID NO: 1259 ACAAAGTCCAAATCTTACTTTATGGATGTAATGTCCAGGTTGCTACAAGA
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SEQ ID NO: 1260 ACTTTTTTTTTTCAAACCATGCTATTGAATCAAGAAAAGTAGAAAAACTGAA
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SEQ ID NO: 1261 GGTACGCGGGGGGAGTGATCGAAAGCATGGCGTGGTGGTGGCGCTGA
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SEQ ID NO: 1262 GGTACAGACATTTTCAAAGTTGCCAGTGTTACTTTAATTGGACTGCCTTCGTA
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SEQ ID NO: 1263 ACTGTGTGCAGCAGCTCAAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTAC
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SEQ ID NO: 1264 ACTGGCTGGCTATGTCTGGGTGCTCAAGAGCAATAATTGTTTCAATGAC
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SEQ ID NO: 1265 GGTACGCGGGGAGAAGGGGAAGAATATGGAGGATAGGAGAGGGTGATGATG
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SEQ ID NO: 1267 GGTACACAAAGAGGGGGTGGGTGTCGGATGCAGAGTGTGTGGCCTGATGCTC
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SEQ ID NO: 1268 GGTACTAGCCGGACTTGGATTTTCTGGAAAGATTTCAAGTTGAGGAACGGGAA
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SEQ ID NO: 1275 ACCCTTGAAGATGGGAAAGGTGAGGAAATATTTGAAGCAGGGTCAGAAC
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SEQ ID NO: 1276 ACTTTTTTTTTTTTTTTTTTTTTTNGGTANAATATAAAGAAATTGAGAGCA
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CGTACCT

SEQ ID NO: 1277 ACGCGGGATTGATAATAGGGTGCAATTGTTGCTTTTACTTTATTTACCTTTTGG
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SEQ ID NO: 1279 GGTACGCATCGAAAGGATTGACGGCGTGAGTTTACTGGTGACAGAGAACCATT
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SEQ ID NO: 1280 ACAATTACCCACCACTGGATTGACTCAGAGAGGACCCCCAGAGGGTGTCTC
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SEQ ID NO: 1281 ACTTTTTTTTTTTTTTTTTTTTTTGGGCTTATTTCTTTGGAGGGAGGGTCTTGT
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SEQ ID NO: 1282 ACTTTTTTTTTTTTTTTTTTTTTTGGANATGGAGTCTTGTCTGTANC
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SEQ ID NO: 1283 GGTACTTTTTTTTTTTTTTTTTTTTTTGGCCACACCTGCCCTTTATTGGTCTC
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SEQ ID NO: 1285 ACTGGAATTTGTCATATCTGTAGAGTGTATCTAAATATTCCTGCCTAAAAACA
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SEQ ID NO: 1288 GGTACTTTTTTTTTTTTTTTTTTTTTTGGGTCCTTCCCAACAGCAGTTGGAA
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SEQ ID NO: 1289 GGTACCATAAGGAGACACAAGAAGAAAGGTGACACTAAGGCTACAGTGAC
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SEQ ID NO: 1290 ACACACCCAGGAAATTTGTCTCCACCCTGAGAGTAACAACCTTATTATCATT
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SEQ ID NO: 1291 ACAGGGGCAGTCAGTGGAGGGCGAGTGGTTTCGAAAAAAGAAAAA
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SEQ ID NO: 1292 GGTACAAGCTTTTGTCCAAAATGGCACAGTGAGCACAATGAGTTCCTGTGT
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SEQ ID NO: 1293 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGGGAAAGATATATATATATAT
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SEQ ID NO: 1294 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGTATATCCATAGTCACCTTATT
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SEQ ID NO: 1295 GGTACGCGGGGAAGTCGCTTGTGTATGAACGCAGCGGGACCTGTGAGGGG
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SEQ ID NO: 1296 ACGTCATAGAAATAGCAGCTCCACCTTGTATCAATGGTATCAAAATTTGGTA
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SEQ ID NO: 1300 ACACTCCAGATATAACTGGGACTTCTGTGTAGATCTGAACGAGTGCAACCA
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SEQ ID NO: 1301 ACGCGGGGCTCTTCCCTGCCGCCGCCGAGCCGCGGAGGCGGAGGCTGTG
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SEQ ID NO: 1302 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGGAAAATCAATGTTTTCTTTA
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SEQ ID NO: 1303 GGTACGGGAGTTCTTGTTAAATCCAGAATCAGGATACAATGTCTCTTGCTA
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SEQ ID NO: 1304 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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SEQ ID NO: 1305 GGTACTTTTTTTTTTTTTTTTTTTTTTTGGINTTAATGATGTTTTTAATTGACAAT
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TGCTGCTTGAACTATATAATATATGTTAAGGAGTTTGTGTTTTCCGTCGTCATTGTAACCGTTAAC
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SEQ ID NO: 1306 GGTACTTTTTTTTTTTTTTTTTTTTTTTGANAAGTGTCTTTTATTCTGAGTCA
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SEQ ID NO: 1307 GGTACTTGCCCACTTTTCTCTTGTGGGCTGTCTCTAGAATCCATTATGTTCT
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SEQ ID NO: 1308 ACTAGGAAAAGATACAGTTACCAAGATAATGGCATCCGTCCTTCTCACTG
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SEQ ID NO: 1309 ACTTTTTTTTTTTTTTTTTTTTTTTNGCTGGGGTATTCATTCTGCATGTATAG
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CAGNCATGGAACCAACAATAATGAATAATGAGCNCNTANAATTCAAAATNCCAGATGTTTCAAA
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SEQ ID NO: 1310 GGTACGAAAAACAGAACCAATCTAAAAATGGCTGATGTTACTTTAGGAGCCTG
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SEQ ID NO: 1311 ACTTTTTTTTTTTTTTTTTTTTTTTNGGAAAGNGTAAATTTATTTAATACCA
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SEQ ID NO: 1312 GGTACTTTTTTTTTTTTTTTTTTTTTTTNGCATTTTANACTCCACAT
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SEQ ID NO: 1313 ACAAAGTAATGACCATAATACCTTGTCTAAATCAGTAGCAGGGCTTCATGGC
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SEQ ID NO: 1314 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGNGGTCAGGGTTTATTAAGTANA
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SEQ ID NO: 1315 ACGCGGGATTTCGCCATGGATGAGGATGGGGACGAGAGCATTACAAAAGTGA
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GCAGAAATATGGGGAATTAATAACATTCATCTCAACCTCGACAGGCGAACAGGATATCTGAAGGG
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GTTCCANTTTTGTTTAATAAAAA

SEQ ID NO: 1316 GGTACTGCCAGATTGCTCTAAATGTCTGTCTATGTCAGATTACTTTGCTTCTG
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CAGGGAAGAGTAAAAAAGAAAGAGGGAATACTGGGAAGATAATGCACAAAATNGAAAGG
GACTTNTTTAAGGATTAACCTAGCCCCCTTAAGGGATTAACANTTTAAGGATTAATAGCCAA

SEQ ID NO: 1317 ACTGCACCAAGCCTGGGCCTTGGCCTTGAGCATTCAAAGCCACGGTCTC
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AGTGATCCCTCGTTATTCAGCAGCAGGCTGCTCTGGACGCTCCAGTGTGGCTTGGCTTANCACC
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SEQ ID NO: 1318 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAGCANATTGGGTAATAAATGT
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SEQ ID NO: 1319 GGTACGCGGGGAGGAGTGAGAGAGCTGCTGGATATGCGGAGGGAGCTGGGCG
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SEQ ID NO: 1320 GGTACTGACAAAGTCTGAACTACAATGAGAGGAAACACATTGCCCTACTT
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GATT

SEQ ID NO: 1321 AATTGCGCCTTAGCGNGGTGNGGCGGAGGTACNGCGGGCTCACTCTGCGC
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SEQ ID NO: 1322 ACGCGGGTCTTGTCCAGTGAAACACCTCGGCTGGGAAGTCAGTTCGTCTC
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SEQ ID NO: 1323 ACCAAAAAGAAAAAGAAAAAGGAAAGGTTTCTACTGCTGATTATCTATACT
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SEQ ID NO: 1324 GGTACACAGTATTTTTATATCTATGTTTTCTGTCTCTGGCGCAAGATATTC
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SEQ ID NO: 1325 ACGCGGGGGGCGAGCAGTGGACCTATGAGCAGAGGAAAAATCGTGAAGTTTCA
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SEQ ID NO: 1326 GGTACCCGCAAAAGCCCTGTGAGCGTCTACAGACAGCTCACCATTITTTGTCC
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SEQ ID NO: 1327 GGTACTTTTTTTTTTTTTTTTTTTTTTCTTTTCAGCAAAATAATTTATTT
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SEQ ID NO: 1328 ACCAGCACACCGGCGCGCTCTGGACTGCGCCTTCTACGATCCAAACGCATGC
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SEQ ID NO: 1329 ACTGGCCCCAAAGGGAGCTTCAGGCACCCAGGGAAGACCCCTAATTTAGTCCCC
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SEQ ID NO: 1330 GGTACCGGAAGAAGCAGCTGGCAAGCAGCTCCCTGCACATGACAGGACC
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SEQ ID NO: 1338 GGGACTTTT TTTT TTTT TTTT TTTT TTTT TTTT CATGTACTTCATTTATTTTATTA
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SEQ ID NO: 1340 ACGCGGGGCTCTCTCTAAGCCGGCGCTCGGCAAGTTCTCCAGGAGAAAGCC
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SEQ ID NO: 1341 GGTACGAGGACTGGATGGAAGGTGATTTGTGGCTCCCGAGTGAGGGTTGAA
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SEQ ID NO: 1379 AATTGCGCCCTTAGCGTGGTCGCGGCCGAGGTACCAAGAAATTCATAAAATTTGT
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SEQ ID NO: 1380 ACTGCAGCTAAACCCAGCGCTTCAATAACAAGTAAGCCTGCTACACTTACAA
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SEQ ID NO: 1382 AATTGCGCCCTTAGCGTGGTCGCGGCCGAGGTACGCGGGGTCTACATGAACCA
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SEQ ID NO: 1383 AATTGCGCCCTTTCGAGCGGCCGCCGCGGCAAGTACTTTTTTTTTTTTTTTT
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SEQ ID NO: 1384 GGTACCCAGCTCCTCCAGGAOCTGCCACTATGATGCCGGATGGAACTTTGG
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SEQ ID NO: 1385 GGTACTTTTTTTTTTTTTTTTTTTTTTAAAAAGGNCAGCTTTTATTGAAC
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SEQ ID NO: 1387 GGTACAAAGAAAAGTTTAAAGTCAAGGCCTCACCAATTCCTACAGTATTAGTA
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SEQ ID NO: 1388 ACTACCCAGGCAGGTATGGAGGGGCTCCCGAGGGTCTGCGTTTCCCGGACA
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SEQ ID NO: 1392 GGTACTTTTCAATCCAAGAAAAAAATAAACTGAGACATGGTCATGAGTTC
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SEQ ID NO: 1393 GGTACGAGGACTGGATGGAAAGGTGATTGTGGCTCCCGAGTGAGGGTTGAA
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SEQ ID NO: 1395 GGTACTTTTTTCTTTTTTTTTTTTTTTTNGGCTTTAGTAANAGGTGCCTAT
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SEQ ID NO: 1396 GGACACAAGCTTTGAGGAAGTCAAAAGGACTGACCTCTAGGCCAGAACAAAG
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SEQ ID NO: 1404 AACCGGGGAGCAGCCTCCTTGTATCTCAGTTTGTCTGGAGGCCGCAACCCAGG
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SEQ ID NO: 1406 ACAATNAAGGAATGGGGAAGGGGAAATGAAAGAATAGAGAAAATATACG
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SEQ ID NO: 1411 ACNCGGGGCGCGTCTTGTTCTTGCTGGTGTGCGGTGGTTAGTTTCTGCGACTT
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SEQ ID NO: 1412 ACTCCTCATAATCCTGATAGGTATCAGAAAACTCAGACGTATTTCCCTATGA
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GATTCTCGATATTTCTCTGGATTGGGGGTGTCACTTCCATTTGGTGGTTGTTCCAAAGAAATACGAT
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SEQ ID NO: 1413 ACGCGGGGGGAGTCAGTCCCAACCAGGACACAGCACGGACATGAGGGTCCC
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GTCTCCATCCTCCCTGTCTTCATCTGTGGGAGACAGAGTCAACCATCACTTGCCAGGCGAGTCAGGA
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NANCGTTTCATNATTANCAANGC

SEQ ID NO: 1414 ACATTGGTGATCGGAGTATAGTTGGAGCGCTTTGTCATGATTTCCAGGTTGGC
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AAGCCGCCAGACCGTCTCCTTCTTTGCCATATCCACATGGAAAATCTCATCACCATCAAAGTCAAA
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SEQ ID NO: 1415 ACAACAGTTGATGATGAAGAACACGATGATAAGGAAGAAGAGGAGGAGGAA
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SEQ ID NO: 1416 ACTTGATTTTGAACACAGCACGAAAAACATTTTGGAGCTGGTGGAAATCAGCG
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SEQ ID NO: 1417 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACCAAGTGGTCTTA
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CGATGATGATNANGANGATGANTATTGAAANATGATGATTGATGA

SEQ ID NO: 1418 ACAGCTTAAACCACAATGGTATAAACTTTCATTTTGTAAATTAATAATTTCTTG
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SEQ ID NO: 1420 ACCGTTTCAAGATAAAATAACAAAAAAGAAATACATATTTTGTATGAAA
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SEQ ID NO: 1421 ACAGCAGCAGCAGACACGCATCGCAGAGCTGGAGAAGACGTCAGCTGAACA
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SEQ ID NO: 1422 ACTTGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGACCAA
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SEQ ID NO: 1423 ACGGCCAACGCCAAGTAGGGGATTGCGTTCCTCCAGTCGCAGACCCATCA
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SEQ ID NO: 1424 TAATTNCGCCCTTACGCGCTNGTCNNNGGCCNCGCACGCGGGGGCNCCCATG
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SEQ ID NO: 1425 ACAGAAAAGCCAGATTAAATACATTAAATATGTCGTTTTAAAAATGATTTT
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CTAGAGTCATTTATGGAAGCTGGAAAGGGGGCATNAAAAAAGCAAGCCAAAAGGAATGCTGCT
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SEQ ID NO: 1427 ACCCCTTAACCCCTTCTCCTTACCCTTAGCAGCAAGTCCCACCTTTTCTAGGG
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SEQ ID NO: 1428 ACTTCTACACATCTGCCTAACTTGGAATGAATGTGGGAGAAAAATCGCTGCT
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SEQ ID NO: 1429 ATATCCGCNTNAATTCGCCCTTTNGNGCGGCCNNCCGGGCGNGTNCACCTA
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SEQ ID NO: 1430 ACACAGAGGGCTATAATCAGAGATCGAGCAGCTTTAGAGAAACAAGAAAAA
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CTTCAAANGCTACAATCTCAGATGAAGAGATTGACGGCACTCAAAGGCTTAGGAG

SEQ ID NO: 1431 ACCAGGTGGGAGAAAGTGATGACAAATCTCAGTGCCAATTTGAGGGGAAGCC
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CACAGTCTCTGGCAAGCCCCACCGGAAAGGAGGGCTCAGAAGGCGTAGCGGGTCCGGATATCCT
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SEQ ID NO: 1432 TTAATTCNCCTTANCGNGGTGCGGNCNANGTACAAANATGACTATAAACA
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SEQ ID NO: 1433 ACTATCACTTTGCCTTGCTCAGTCTCTCCTTCTCCGGGGCCACAGAAGGAG
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SEQ ID NO: 1434 ACNGCGGGATAATAATTATCTTTGAAGTANAACANTTCTGTTAACTGGAAAA
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SEQ ID NO: 1435 ACGCGGGTGAGCAAACTACTCTGGATAAATCTCTTCTAGATATAATATCAG
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SEQ ID NO: 1436 ACAAACCTTTATTGAAACGCACACGCGCACACACACAAACACCCCTGTGGATA
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SEQ ID NO: 1437 ACTCCAGAGGAGTGTGAGGAGACGAGTGAAAAACCCAAAANGAANAAAAAG
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SEQ ID NO: 1438 ACTGTGCTATGGACCACGCACATACAGCCATGCTGTTTCAGAAGACTTGAAA
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SEQ ID NO: 1439 ACGGGGGATAATAGATTAAAGAATTTACCCTTTAGCTTTACAAAGCTACAGC
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SEQ ID NO: 1440 TTATCATCCTAATGTAGACAAGTTGGGAAGAATATGTTTAGATATTTTGAAG
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SEQ ID NO: 1441 ACTAAACGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGCTGAATACAAGAA
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SEQ ID NO: 1442 ACTGAATTCAGTGCTTAGAACTGAAGTTATTGAGAGGACAGCTTTAAAGAT
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SEQ ID NO: 1443 ACAAAGCAGCAACTGCAATACTCAAGGNTAAAAACATTAGAAAAGCATTGTG
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SEQ ID NO: 1445 ACTTTTTTTTTTTTTTTTTTTTTTTTATCAAAGTTTTAGTGTTAATAATGAAT
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SEQ ID NO: 1446 ACAATAGCGTCTTCTTCCAGCAGTCAACTCAAGCACAAAAGCCAGACTGACT
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CCATCAGAGAGTAAGAAGGAAGACTCCTCTGGCGCTACCCAAGTCCCCAAGCAAGTCTCAAAGC
CAGTGATCTCTGACTTTCAATCAGTTTCCAAGCTAAACCAAGGCCAAGCCATGCACATGCATAGG
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TCCCTCCCTTGGCTCCAGAACGAAGATCCACACTTGAGGACTACTCTCAGTCGCTGCACGCCAGAA
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SEQ ID NO: 1447 ACTTTTTTTTTTTTTTTTTTTTTTTTGAACAGNGGTTTTATTGGTAAANAT
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CGAATAAANAAAAGGAATGGATGGTCCGCGAGTGAAATTTNTTCGGGCATCAACATGCAAAAAGT
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SEQ ID NO: 1448 ACTGATGGGGAAGTGCCGCGCTTCTTGGATGAACTAGATGTGGTTTCAGATG
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GGCG

SEQ ID NO: 1449 ACACCTCTTGCAATTCGCTTTATGTGCCCAATGGAAGAGGTGTCCTCTGGAGC
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SEQ ID NO: 1450 ACCATTTTACGAATTTCTGTCTTCATAATATAAGTGAAAATACTGTCATTTCA
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SEQ ID NO: 1451 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGGGGGANAGTTCTGTANATGTC
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SEQ ID NO: 1452 ACGCGGGGAGCACCTCCTTGATTCTCAGTTTTGCTGGAGGCCGCAACCAGGC
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SEQ ID NO: 1453 ACAAACAAATTATGACCGTTGGAAACATCCCTTCTTCCTTGATGATCGCAGAA
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SEQ ID NO: 1454 ACTCTAGGAACCCAGGGTCACCCAGATGTCCCTTTGATGGCCGTTGTTGAAG
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SEQ ID NO: 1455 GGACAAAGATGACTATAACAAGATGCAGCCCTCGGTTTCCATGAACAGCAC
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SEQ ID NO: 1456 ACACATAAGAAAAGGATTTAGTAACACTTGGGCAAGTAATAAACTGTAGAAC
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SEQ ID NO: 1457 ACATTTGGAGGATCATCTTCCAGGGTCTTTTAAAGACTTTCTGAAAAAGCCTT
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SEQ ID NO: 1458 ACAAGCCTCACCAAGGGCAACCCAGAAAAGTGAATGAGTTTGTCTCTCCA
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CCAACAGGAAGCCTTCATCTAAATAGGAATCTGCCAAACTTCCTCCTAGCTTCTTGATAATATGAA
TTGCCTCCAGTTGCCAGAGCCITTCAGTCTGAGAACTG

SEQ ID NO: 1459 ACAAGATGCTGTGTAAGTGTTTAATACAGCAAATAGTAACTCTCCAAATCCT
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SEQ ID NO: 1460 ACACTTGAAACCAAAATTTCTAAAACCTGTTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 1461 GGTACTTNTTTTTTTTTTTTTTTTTTTTTTTTNCCAAATTTGTTTTATTTAT
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TTCCTCATGNATGNGTGGGATTTAACTATATCTGGGGCTCATTTTCATNNACTCTGTCCATCAACAA
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SEQ ID NO: 1462 ACGCGGGGGGGCGCAGAGGCCTGCGGGAAGCCAAGATGGCGCATAGGGGTT
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SEQ ID NO: 1463 ACTGGGATGGCCCTGAGGATCACAGTAATTCCTTGTAGTCATGAAAATCACC
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AATTCAGTAAAAATTTCTGGCTTTACAATTTGGACGTCCACAAATGAGTGCACATATTGGTTAATG
GTAACCTTCACTGATACCATGACAAGGGNGAGTGCATTCTTCTG

SEQ ID NO: 1464 ACAACAATTTCAAAGGCATATATATGGGTAATTAGTGTTCACATATACCAA
ACCAGGAACTAAACAAATCTCAAGGATGAGAAACATGAAGAAAACCTTCACTAAAGCGTATCAT
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SEQ ID NO: 1465 ACTGGCTGGCCACCAAAGCACACGGAGATTCTGTCAGGCGCTGAGACACCAC
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CTAGTAATGTCAAGTTGGATGATGAGAAGACTGGAACCTAAGAAGTTAGCAAGACGTGTCNATT
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SEQ ID NO: 1466 ACGCGGGGTTCCGGGGCAGGGCCGTGCTGATTGAGAATGTGGCTTCGCTCTG
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SEQ ID NO: 1467 ACAGTAACACAACATCAAAAGCAACACAGCTGTATACAGAAACGTAGGTCAT
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SEQ ID NO: 1468 ACATTTATATTCAGTGATAATACAAGCTTCTGTGGTGTGTGGACCAGACACAG
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TAAGTTACATTACCATGGGGGTCTCAGTGCTACTAACATTATGTAATCAAGGAGATACGAGCATTAA
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CCATTTATAGGTAGTCCAAGCAATATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
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SEQ ID NO: 1469 ACGCGGGGACTTAACGGTGGTGGCTGGTTCTGCGCCGGATCCGGGAGAGGGG
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SEQ ID NO: 1470 ACTTCTGTTTCTCAGTTTATCTGGATGTTATCAGATCACAGACCATGGTCTCA
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SEQ ID NO: 1471 ACGCGGGGGTTACCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTC
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CAAGTNAAGCATTTATAGGACCCATTTACAAACCC

SEQ ID NO: 1472 ACGCGGGGGGAGAAGAAACGGCGGAGACCTGAGACCCGGAGGCTGAGGCTGT
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GCTCCTGTCCCACTCCACAACCTANTTTGTGACAATTTAACAGTGGGTTTCTGGAAACAGTGCT
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SEQ ID NO: 1473 ACGAAAAGCGGCAGAACTAGCTCTGAAAACCTCTGAGCAAGGTCTGTGTGAAA
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CAGNAAAAGTGCANGAGCCATGTTGAAACCGCATGCACCAAACTCATTCCAGCTCTGCTANAGT
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GCTGCNATGGATANGTGCTCGGCTTATTGNANCCAATATTTTCNNTGATGGNAACTTNAANTGTG
CCTGTANNCCCTATNTTTC

SEQ ID NO: 1474 ACACTGTTGGTGTATATAGGGGATGGGGTTCTCGGTAATTTTGTATTATTATA
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GAATTGATAAAATCACCTGGGATTAGTTGTATAACTCTGAACCACCAAACTCTGCTATCAANCCT
TGCTACAGTCATGGCTGTCCAGAAANATTTACAGTTATTTTCTGAGAAAGGATCCATNNGGCTNT
AANAACCTCACNAACTTTAAGAAGTTNAGAAGTCTTAANTTGCTGAANCTNAANTACNAACCTTG
AATTCNATTAATAAAAAAGAAATCCCTGNANTCAANGCTTTAANAGCCAATTNTTACCTAAANGGAN
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SEQ ID NO: 1475 ACNGATACCGGAAAGGCTGGATACCTNNGTTATTAGAGGATTTTGGAGATGG
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GATTAATAANAAAAATTCGCGNGGACNNTTCTNCTTCTGNCCTGNTTGATTCTNTNTCCGAAANAT
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SEQ ID NO: 1476 ACGCGGGGGCTAAAGTGTTGTCAATTTTGTTTAACTTTTCAAACAACCAACTT
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TATCCATTGGGGGCAGAAAATNTGCTTGNATTTATTTCAATTTTTTTTTTTTTTTTNGAACAAAAAT
CTTGCTTNCACCCANGCTAAAGNGCAGGGGCGCAATTTGGTTAN

SEQ ID NO: 1477 ACATGTTTGAAGAAGTGCCGATTGTAATTAATAAATTCACATCTGATCAATGTC
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CAGCGTCGCCAGCAGGAGAATATGCTGCGCCAGAGCCCGAGAAGAACCCCGCTCCCTGAGGAG
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GCCAGGCTCTTCATGAATACAACCACTAAGAAANNNGGAAGTTCANAAAAGANGTAACATNGACTC
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SEQ ID NO: 1478 ACATTGTTTGTTCATAGGAGTTCATGGAATTTGAAATCAGAAGAAAAATC
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CTGTTCAAATCAAAGTTCATCATTGTTTGGAACTTTGNTTGAGAATCAAATGGTCACGTA
AATGACAAAACAATAANCAATATAATGACAGAAAAGTAAGTGGCAAAATAACTACAACTTTGTT
CCACTGGCTACTGCAGTAGAATAAACAAATGACAGTTANCCANANACACCTTTATTTTCATCTGC
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SEQ ID NO: 1479 ACTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGGGANACAAC
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AATTTGTGAGCCATNTCAAGCCATCAAAAAAATTCATTNTATTGTAGGAGGGAAGCTGGAAACA
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SEQ ID NO: 1480 AACTCATTAAATAATTAATAGGCGCTTGACCCACAGGCTGTCAAAATTCG
AGCAGATATTGAAGTGGCTTGTTATGTTATGAAGGCATTGATGCTGTAAAAGAAGCCCTAATAG
CAGGTTTGAATTGTTCTACAGAAAACATGCCCATTAAGATTAATCTAATAGCTCCTCCTCGGTATG
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SEQ ID NO: 1481 ACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCA
CGCATCCATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAAATGGCCAGTTTA
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TTGTCATAAATGAANAATGAAAAACCTT

SEQ ID NO: 1482 ACATGTTTGAAGAAGTGCCGATTGTAATTAATAAATTCACATCTGATCAATGTC
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CAGCGTCGCCAGCAGGAGAATATGCAGCGCCAGAGCCGAGGAGAACCCCGCTCCCTGAGGAGG
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GCTNTTCAAGAAATACANANNCTANAAAAAGGAAGTTNCCAAAAANAATGTTNNCATGAACCTTTG
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SEQ ID NO: 1483 ACAGCCAACGGTTTCCCTTGCGGGCTTTGAAATAACACCACCAGTGGTCTTA
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AANATTGGAAAAGACTCATAACCATCNTTCNNCACCAGGATCNNATGGACATGAATCTTTTNGA
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TTAACTCANTTTTTTAGTAAAGC

SEQ ID NO: 1484 ACTTTCTTATTCAACTGTGAATCTGCTCGAGAAAAGACAGAAGGTTACAGAAA
GGACTGTTTCTTTATGGTCACTGATAAACAGTAATAAAGAAAAATTCAAAAACCCCTTCTATACTA
AAGAAATCAATCGAGTTTATATCCAGTTGCCAGTATGCGTCACTTGGAACCTCTGGGTGAATTACT

ACATTAGATGGAACCCAGGATCAAGCAACAACAGCCGAATCCAGTGGAGCAGCGTTACATGGA
GCTCTTAGCCTTACGCGACGAATACATAAAGCGGCTTGAGGAACTGCAGCTCGCAACTCTGCCAA
GCTTCTGATCCCCCAACTTCACCTTCCAGTCTTCGCAAATGATGCCCCATGTGCAAACTCACTTC
TGAGGGGGGACCCTGCACCGCATTAGAGCTCGAAATAAAGGCGATAGCTGACTTCATTGGGGCA
TTTGTA AAAAGTAGATTAAATATTTGCCTCCATGTAGAACTTGACTAACATAATCTTAACTCTT
GAATATGTGCTTCTAGAATAATATTACAAGAAAACCTCAGGGCCACCGGCAATCAAAAAAANG
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SEQ ID NO: 1485 ACTACACGCGCCTGGGCNACGACTTCCACACGAACAAGCGCGTGTGCNAGGA
GATCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATGTACGCATCTGAGGA
ANCCGAATTCACAGAGGCCAGGAAGAGGTATCTCCATCAAGCTGCAGGAGGAGAGAGAAT
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SEQ ID NO: 1486 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCACANAAATCTAANCNCACTTGTCTT
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ANAATCAGTTGAACCTGNGAGGCGGAGGTGCAGTGAGCCCAAAATTGCCATTGCCTCCAGCCTG
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TTTTGTATT

SEQ ID NO: 1487 ACATCCAAAACCATAAGGAAATATTCTGATGCCAGATGATGAAGACTGGGG
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SEQ ID NO: 1488 ACAGTTACTCCCGGACCGCGCGCTGAAAAGTCTGTATATCATCGTTGAACTA
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GACAAGGCCTAGATATTTACTGGAGGGATAATTACACTTGTCCCTGAAGAAGATATAAAGCTATG
GTGCTGAGAAAAACAGGTGGACTGTTGGATAGCAGTANGGCTNTGCAGTTGTTCTCTGATTACAAA
AANATTTAAACCGTACT

SEQ ID NO: 1489 ACCTAGAAGCCGTGACCCAGGGCCATGGCGCTTACCTGATGAGTCAGGATGC
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SEQ ID NO: 1490 ACTCTGGTTCNATANACTTTTTTTTATTTTANGGTTGANGCNGACCCATNATAN
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GGCGGCNTGGNTAA

SEQ ID NO: 1491 ACCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGA
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SEQ ID NO: 1492 ACCTGCATCAGCATTAGTGATCAACCTGTTAATCCAAGGNCCTTAGAAAAAC
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SEQ ID NO: 1493 ACAAGAATCGACCTCACTGTTACATGGAACTCTGACCAGGNCCTTCTCTGC
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SEQ ID NO: 1494 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGCGNGNTCAATCATATGAACTAGAT
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SEQ ID NO: 1495 ATGCTGATTCTGAAGAGATCAACAGACAAGTTACATATTTTATAACAGGAGG
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CTCTAGACAGGGAAAAAAGGACAATTACCTTCTTACTATCACGGCNACTGATGGCACTTCTCAT
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SEQ ID NO: 1496 ACGAAGAAAGCATTTCCTCAAGCAATGAGTCTCTTAATGAAAAAATAAAAAGA
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AAGATAAATATTTTCTAGTCCCAATAATATGTGTTTGTTTTACAAGATATGCTTGAATGATGCAAAT
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SEQ ID NO: 1497 ACAACCAGGGCGAGAAGAAGAACGCGCTGGCCCAATATCAGGAGATGGAGA
AGAAAGTCAGCCTACTCAAGGACAATAGCTCTCTGGAATTTGACTCTGAGATGGTGGAGATGGCT
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CAAATCAAAGCACCAGACCACTTCAACCAGCAAACCTGCCAGTTTCCAGCAGCCTCTGGGCTCTA
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TCCAACCTGAACATCAGAACAATAAGAGAGAAATAAGAATAGAATGAATGACCCCAAAATAGGG
TTTTCTTGGGCGAGGATGTGCTGGATTANGAAAGGTGACATGACACAGGCAGAGCAGAGTGCGCAC
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SEQ ID NO: 1498 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCCCTTANAAAAAGNAGATCTTTTACA
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AAAACGATATGAATNACNNAANTCTATNTTGCNNGANCACATTTACTNNGGTTTCTCCTCTA

SEQ ID NO: 1499 ACTGGAGATGATTTTGATAACCAAGGTTTATAGGTAAATTTTACCAGTATTAG
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GATTTCTTCATGCCCCCATNGCTAATTGCCTTGTGGATNACGGGACAACCCTNTTTGCNCAAGCTA
CAGCATCATTCGATGGTATCTTTGCANCAACACCTGCANNGATAANGACANNCATTNACTGCTN
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SEQ ID NO: 1500 ACAAATCCAGTGTGCAGACCACAACCTCAAAACAAAAAGATCTATTTCTA
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SEQ ID NO: 1501 ACCTCAAAGTGACGGGGAGAATGGAACCAAGTTGGAAAACTGCAGGATA
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SEQ ID NO: 1502 ACAGGAAAACGCTGCCGCGGTCCACAGTGTGATTCTGGATGACCACATTAG
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TTAAGGAGGAGGAGAANGNGGNTCCTTCTTCTNGATGACNTTNTG

SEQ ID NO: 1503 ACGCGGTGATCCATGGGATTTCAATTAATGACCATGTGAAGATGTTTGAGT
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TATTGTTAACTCACTCATATTGAGATCATTTTTAGAGATACCAGGTTTATGTATCANGCACTAGAT
GGTCCACCCTCATGGGATAAACTGCTTACAAGTATTTTGAAAGAAAAAACTGACCAAAATTCCTTA
AATTTGTTACTAAGGCAATCACGCACAGGTGACCGTATGTCTTATCTGATTTGTTTTAACTCCTTGGT
GCCAAACTCAGAAATGGGAATTTCACTGNCANNAATGANCATNCCCTGNNAAGAAAAAGNTA

SEQ ID NO: 1504 ACTCCCAATGGTGGATTTATTACTATTAAAGAAACCAGGGAAAAATATTAAT
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AATAAATGTTTGTAANNAGTGAATAAAAAATCCCTTTGCATTCTTCTGGACCTTNAATGGGAAG
AGGAAAAGGCTCGTGACCATTTGTTTTTNGGGGTATAGTTGCTATTTNTAAACCTNCTTCAGAN
GNTTACTNAGGAGGNTNATNTACATATANCCATAATTTCTCTNGGACCG

SEQ ID NO: 1505 ACAGTGGGCATGCAGCGCCTCGGGACGACACCCAGCGTTTATGGGGTGCTG
GAGGCCGGGGCATCCGCATCTCCAACCTCAGACACACGGTGAACATATGGGAGCGATCTCACAGGC
GGCGGGGACCTGTTTGTGGCAATGAGAAAATGGCCATGCANAACCTAAATGACCGNCTAGCGAG
CTACCTANAAAAAGGTGCGGACCTGGAGCAGTCCAACCTNCAAACTTGAAGTGCAAAATNAAGCAGT
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SEQ ID NO: 1513 ACAGTTTTTATACTGAAGCTAGTATTGAGCTGCACTTGAATTCACATTCTTAG
CAAAATAATTGCCTGAGCACACACACACATTCCACACGCATCATTAAAGGATAGCCATTATTCTT
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TCTCTTTGAGCCTTTTGGCCTGCCAGGCCCTTCTTCTGCTTCACTTTGCCCTTGGCAGCATAT
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TGGCTGACTGCTNANACCAACAATTTACCCCAATNTNTTTCNNAATCNCCAAAGGANAGGGCCNG
GNNGTNNAACTTTTGTCTNTTGGGCGATGTNCANANCNAANNAGGAATAAGNCAGAATGGNGGCC
TTTAGGACATNGGGG

SEQ ID NO: 1514 ACAATGCCTGCATCCTGGAGTATAAACAGAGTGGCGAGAGCATTGACATCAT
TACGCGAGCCCATGGCAATGTCCAGGACCGCATTGGCCGCCCTCATAGACCGGCATTATTGGCA
TCNTTGACCCTGAGTGCCGGATGATTGGCCTGCGTCTCTATGACGGCCTTTTCAAGGNTATCTTCA
CTAGATCNCGATAATAAANAACTCNAGGCCTTCANCATCCGNCCTGGAGGAGCTGCATGTCATTAG
ATGTCAAAGGNCATTTTGGGT

SEQ ID NO: 1515 ACAGACAAAGTGGGAGGTTTTATTTCTTGGTCTCTTCTCCTTGGATAAAGAC
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ACCTGCGGGCCTCANCCTGGTCAGCCAGGANCCTTTCGGGGCCTTGTCTGCCTTCAGCTTGTGGA
TGTGTTCCATGANAATCCGCTTGTTTTGAACACATTCCCTTCACCTACAGGNACTGTAT

SEQ ID NO: 1516 ACGCGGGGGTTCCTTCAGTCCGCTGGTCCCGAGCACGAGCTGTGAGGGGATT
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SEQ ID NO: 1517 ACTTCAAGTTAAAGTGAATAACCACTTAAAAAATGTCCATGATGGAATATTC
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AGACCTTCTCCAAATGAGATCTAAGCCTTTCCATAAGGAATGTAGCTGGTTTCTCATTCCTGAAA
GAAACAGTTAACTTTCAGAAAGATGGGCTTGTCTTCTTGCCAATGAGGTCTAAGGAGGCTCC
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SEQ ID NO: 1518 ACGCGGGGGCTGTGGTCTGAGCTAGAGGGTGAAGCTGGCGGAGCAGGAGGA
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AGTCCAGTTCAAGAAAATTCCAGTGATTTGAATAANAGCATCTGGGATGAATTCATTAGTGATGA
GGCATATGAAAAGACTTATAATGATTCACTTTTTCNATACA

SEQ ID NO: 1519 ACATGCTCCATCTTCCAGGAGGACCACTCTCTGTGGCACCCCTGGACTACCTGC
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GCTATGAATTTTTAGTTGGGAAGCCTCCTTTTGAGGCAACACATAACCAAGAGACCTACAAAAGA
ATATCACGGGTTGAATTCACATTCCCTGACTTTGTAACAGAGGGAGCCAGGGACCTCATTTCAAGA
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SEQ ID NO: 1520 ACGCGGGGATTATTGTAAATATTTGATCTTGAATCACTTGACAGTGTTTGT
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SEQ ID NO: 1521 ACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAACATTCTACAGCG
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SEQ ID NO: 1522 ACTTTTCTTTCCTTAGACTTTGGCTTACTGGAAGATTTAATTAAGGTAGA
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GTATGTGCTATCTCTAATACGCTACTTCGATATTTATTAAGAAGTATTTTAAATGTAGTGTCCACA
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TATATTCAGAATTAATTTTGCCTGCNCCCTAAACACTGACACATTTAACTTAAANGGTTTCCATG
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SEQ ID NO: 1523 GCCCTTNNCNGNGGCCGNNCNGNCGGGNCGCGGGGAGGGGCANGTGTNGCC
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GACTTCGGAGCACGCTTTTGATTACATCGGCAGCCACCCGTGGGAACTGTTACAACAGCTGCA
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SEQ ID NO: 1524 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCTTTGAAATTTANAAACAAATTTTA
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AAAAATTGTGTATGTGTCAAAGGGATNGGAACCACCATTCAAGCAATGTTGTCAACTNNGGC
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SEQ ID NO: 1525 ACCTACATCAGATCTAACCTTGATCCCAGCAATGTGGATTCCCTCTTCTACGC
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GGAGCATCGTGGAGGAGATTGAGGACCTTGTGCTCGCCTGGATGAACTCGGGGGCGTGTATCTC
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SEQ ID NO: 1526 ACGAAAAACCTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCAGT
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CAAGAACCTCCCTTTCCCTTCCCCCAATAAGACCATTAAAGTGTGTGTTAAACAACACTACAGAATA
CTAAATAAAAAAGTTTGGCCAAAACCAACCATGAAGCTGCAAAGGTGCTTGTCTTACTGTTTCAA
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GCAATGAAGTTATCTCAACTTCTTAAAGGCTTATGACTTCTAAAAAGTGAATCTATCAGCATTC
ACATCAGATTTAAAGCATCAAATGCCTGTGAACAGCAAAGATGGTAAGCAAAGCAAAGTGT
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SEQ ID NO: 1527 ACAGACTTGTTTTGAGTGTGAGTGGCAGGGACAAAATAAGGGAATGTTAT
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SEQ ID NO: 1528 ACACTTTGAGACGCAGGAAGCAGCTGAAAGAGCTATTGAAAAATGAATGG
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SEQ ID NO: 1529 ACGCGGGGAGTCAGCCTGGCTCCTGTTGAATAGTCTACCCCCCTTGCACTCTA
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AACCTCATGCCTAAAGCTCAAGGATGAAAAGAGTCTATTGGAAACAAGTTGCCCCGAATCTGCGC
TCACAGAAAAGACATTTTGTAGATTTTCCAAGACAGCTTGTGAAAACCA

SEQ ID NO: 1530 ACGCGGGACAGAGAGCATCTCCGTGGCCAAAATCAGTGTCTATGGGACACTC
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GCCCTCCCGGACATTGATTGGTCTGTCTTGGGCAGGTCTAGTGAGCTGTANAATTGAATCAATG
TGAATCAGGGAAGTGGGGAAGGCTGACCTCCTTTTGGTGTGCGGTAAGATAACCGACAGGGC
TGGTGAAGAAGTCCAGATGGCAGGATATTTGGTTTCAGAGTAAGGACTAGGTGCACCACCATGAT
TGACTATCGATCAAAATGGTTGGAACCTAAAAATTTTAAATGAAAGGA

SEQ ID NO: 1531 ACAGAGTATGTAGTGGGCATCTGTTGAATGAATGCTTTTCCAGTAGCAGTGT
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ACACTCACCATTCTGTTCTGTAGTCAATCATTTGATTGACTTGTCTGTGAACTTGCAGGAACTGTTTC
ATAGTTTCATTAGCACAGAGTAAACATGTTTGCATGCAAGGTTATTTTGCATCTGCATTTAAGTG
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SEQ ID NO: 1532 ACTTGTATTTTACAGATGGATTATCTGGGGTAATTTTCTTCAAAGGGAGTTT
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SEQ ID NO: 1533 ACATTTCTTTCGTGTTCAAACCACGGAGTTCACAACACAGCAGCACACACAG
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GGGTCTCATGAGAGAAGTCTCTCCAAAAATCTTGGAGTGNCCCCAAATC

SEQ ID NO: 1534 ACTTCTATTTATCTTTGATTTCAGTCTTGGCAATTGTTAAAAAAAATCTA
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CAGATGCTTCTATAGAGGTTCTTTGACCTAAATAGTTCAGCATTTGTATTTTATTCTGGTATTTAA
TCAGATTCTAATCATAGCCCCGTAAGAAGGAATGTTACTTTAATATTGGACTTTGCTCATGTGCTC
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TTTTATTGATGGGCATGCAGGTGGGTGTTACTTGGAAATGGCCAATTTTATTTAAATATTTCTGG
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SEQ ID NO: 1535 ACGCGGGGCTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAGCTTGT
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TTGAANCANAAAAATTGGATATNNTTATNCAAAAGGCTTCCCTTNGGTNCCC

SEQ ID NO: 1536 ACAGATGTCTGCGTGTTCAGCCCCAAGAAGATCTAGAGACCATGCAAGCAT
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GACTGGTGTCTTCTGGCTAATGGAACACTTAATGCATCCATTCTTAATAGCCTTTATAATGAAAA
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TTCCTGCCAATAAGCAAAGTGTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAAGAG
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SEQ ID NO: 1537 ACGGGGGCTTTTTCTCTCTTCAGCGTGGGGCGCCCAAAATTTGCGCGCTCTC
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CAAGCAGATGTGGCAGTATTTGAAGCGTGTCCAGCCCCACGCGCTGCCGACTTGTGTTCATGCCCTA
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SEQ ID NO: 1538 ACGCGGTGAGGGGATTGATTTGACGCACAATCCTGAGTTACACACCTGTGA
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SEQ ID NO: 1539 ACAAACACTGAACGCCCTGATACACCTACAAACACGCCAAATGCACCTGGAA
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ATAATAAATCCTATAACAATGCAGTGTATAAAGCACTATGTTGGCCATGGAAATGCTATCAATGA
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SEQ ID NO: 1540 ACATATTTTAAAAATAGAATAAAATGTTAAACATAAAATTTTAAAAAGTAGTAG
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TATATAAATGACATTTCAAGGACTTTAAGTATGAAGATAATGGGAATTTTATTGTTTTTGTCTTTTAA
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SEQ ID NO: 1541 ACTTTNTTTTTTTTTTTTTTTTTTTTTTANANATGAGGTCTCGCTATGTTGCC
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CAGGACATTATNTTAAAGGTATTATCCAGGAAACAGATAAGGTCATTCAATAAACACACGGCTT
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SEQ ID NO: 1542 ACTTTTTTTTTTTTTTTTTTTTTTTTCTTCNATTCTTCTCAAAGGCATTTGA
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SEQ ID NO: 1543 ACTATTTTGCAGGGTTTGCACAGGCCCGTAACTGTCTACTACTTTGATATAA
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SEQ ID NO: 1544 ACACACCTAGTTCATAATCCTCATAATTTATCAACAAACACAAAAAAGTGTCT
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GCAGTGATGTTTTAGGAACTGAAATGTACACTTAAAGTCTTCAGCCAGCTACTTCCCTATTTTTG
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CAGTCCTTCTTAGTGACCAAACCTTTAATTTTAAAGAATAATATATTGACTTACTGAACTGAAGCATT
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GTATTGACTTGAGAAGTGTGCTCTGGTATTCTGGGGTCTGAAGCT

SEQ ID NO: 1545 ACATCACTGTGTCCCTAAAATAACCCACCCCACTGAAAAACTCCAGCCCACT
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CATGGACAGGGACCACTTCACCTACATAAGCCAGGGTTCACATA

SEQ ID NO: 1546 ACACTGAGCCCAAAAAGGCCCGTAGCCAACACTATGACTTGGTTTTAAATGG
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SEQ ID NO: 1547 ACAGTTTGCTGCAAATGATAATTTAATTTGGATAATGCTTTAAATCATTGATT
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SEQ ID NO: 1548 ACAAAATACAACATATAAAAGCAAGGAACAATTAATGCCATGCAAGATTTTAA
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SEQ ID NO: 1549 GGACAAAGTTGTATGACAGGGGCATATTCTTTGCTTCCAAGATTTGGGTTGGGG
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 CAAGGATCACATCTAATGCTTGTGTTCTTATACTCTATTATATAGTGTTATTTCATGATTCAGCTGA
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 TCTTATAAATGNTTGATTCCCTTCCTTGCTATTTTTTATTCAGTAATTTGTTTGGCATCATNTTNA
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SEQ ID NO: 1550 ACCAATAAATGATGTGTTAGCTGAAGATAAGATTTTGGAAAGGAACAGAAACA
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 GAACCAAGTGGGCACACTACGCAAAGCCTCTTGGGAAGAACGGGACCGAATGATACAAGTTTATTT
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 AGTATATCAAGGTTTCATACAAGACCTATGAAGATATAGATAAACGTGGAAAATATGACCTTTTA
 CGTTCAACAAGATACTTTGGTGGAATGGTGTGGTATTTTGGAAATAATAAAAAANNATGATGGNT
 TNCTGATTTGCCAGATTTTCAGAGANATTTAATCGNTGATGCCACCAACTTTGGTCCANCTTGTATC
 ACGTGCTTCCATCCANNATGGCCANTCCGGCTCAAGGGGCCAAGGA

SEQ ID NO: 1551 ACCTTCGCAGTGTAGGAGATGGAGAGACTGTGGAGTTTGATGTTGTTGAAGG
 AGAAAAGGGTGCGGAGGCAGCAAAATGTTACAGGTCCTGGTGGTGTCCAGTTCAAGGCAGTAAAT
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 CAAAATTACCAGAATAGTGAGAGTGGGGAAAAGAACGAGGGATCGGAGAGTGCTCCCGAAGGCC
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 AGGGTGCANGAGAACAANGTAGACCAGTGAGGCAGAATATGTATCGGGGATATAAACCACGATT
 CCGCAGGGGGCCCTCCTCGCCAAAGACAGCCTANAGAAGGACGGCAATTAAGAAAAGATAAAGAAA
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SEQ ID NO: 1552 ACTCAAAGACGAATCATGAAAAAGAAAAAACTTTATTTCAAACAGGTTTCAG
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 CTGAGGTGAGGAGAGACCGGCCTAGCCAACATGCTGAAACCCCGTCTCTACTAATAATACAAAAA

TTAGCCAAGTGTGGTGGCGGCACCTGTAATCTCAGCTACTCGGGAGGCTGAGGCAGGAGAATCG
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ACTCAAAAAACAAAACAAAATAAAACAAAACAAAAAACAGAACTGCATGATGTATAATTTTGACA
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SEQ ID NO: 1553 ACTTTTTTTTTTTTTTTTTTTTTTTAGTAGTCTATACATTTATTGAGTAAAAA
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CTCAATGTTTTACAAGCAGAGGGAAAACCAAAGTAGGCAGAGAACTTTCAAGAGAGGAGAGGGC
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SEQ ID NO: 1554 ACACCTTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAGGGCCGGA
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SEQ ID NO: 1555 ACGCGGGGGCGTCTTGTCTTGCCTGGTGTGCGTGGTTAGTTTCTGCGACTTG
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SEQ ID NO: 1556 ACTTTTTAAAAGTAAAAATCAGATGATTCTTTTGGGGAGGAGGATGTGCG
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CGTCTGAATGACAACAGCCTAGAGTTTCTGGGGATACAGCCAACACTTGGACCTCCTAACAGCC
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TGGGTTAGAAAATTTAGATNGATAAAGATTCATTAATGTCCAACTA

SEQ ID NO: 1557 ACTTTGGCCTCTCTGGGATAGAAGTTATTCAGCAGGCACACAACAGAGGCAG
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SEQ ID NO: 1558 ACGCGGGAGTTGATGATTTCTTTTAAAGAAATTAGTTTATTTAAAGCAAGA
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AAGCCGAAGGATGCTGACACACAGTGTGTGGAGGGCATTCCNGAGAACTTTTGCAACAAGTGT
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ATACAACCTCAGATTTAGTATTATTGNTTATCATAAAACATATTATGTTCTAGTTTTTAAAAAGACC

CCNAGTTGATTTAATATAATTTATTGGCATTTTTTCNGAANAGGNTTAAAGTCNNATTAAINGATT
TTTAAAAAAGCCAANGAAGGCNCTNGNGTCNAAATTTAAATGTTTNATAATAAAAAAT

SEQ ID NO: 1559 ACGCGGGATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAG
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GACAAATCATTGAATACAAAAACAAATAAGCCATCACGCCTGCCCTTCCTTGATATTGCACCTTTGGA
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AATCTAAATTAATAAAGAAAGAAATTTGAAAAAATTTCTCTTTGCCATTTCTTCTTCTTTT
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TTTGAATTTTTTTTCAACACTCTTACCCTGGTATTGGAAAAATGTCAACC

SEQ ID NO: 1560 ACCCACCACCTTCTTCTCCTACATATCCCTTCCAGATGGNCATCCAGACTCAG
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GGCTTCACCATCAATCCTGATTCTCTAAGTGGGCATTGCCATGTGGAAGGCCANGCCAGGCTCA
CTCAGAGANTCAAGGCCTGCTCCCTGTANGGTCCAACCAGACCTGNAANAACAGGCCNCTCCATT
NGCTCTTNANATGCCACTTCTAANAAAAAGCCTAATCACAGTTTTTCTGGAATTGCCANCTGACAT
NTTGAATNCTTCCATTTCACACAGAATGCAACCAAGTCACACGCTTTTGAATTATGCCTTNGTAGA
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SEQ ID NO: 1561 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGGGTCCAAAAATGGNGATTATTTATGGC
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GCACAAATATCCTTGGCCAGTTTGGTCTTGAANATCACAGCTTCTGGGGACATTTGCCACTGGTG
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GTTGGGACANAAGCTGGCCAGCGAGCCCTGGGGGTGAAGGCAGCTGCTATNAGCAGCAGCC
ACAGAAGTGCTGCGGAGACCTTCATGTTGGAGGCTGAAGGTGTGAGCTTTGGCGTGAGANGTGGT
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SEQ ID NO: 1562 ACACAGATTGGCTTCATATCAATTAAGAATGAGATACTTGACTGGATTTTTG
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GATTTTCATTTAATTGTAATAAATACTGACAAAAATCAGTATGTTGTAGCTAATATGTTTATGCAT
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ACTTTTCTCTTGTAGTCTGATACAGTGAAGGAGATAAACACTTCTACAACCTTAAATTTAATTTAAT
AGCAGTAGAAAGAGAACATAAGGGAATAGAGGTTAATTTTACCCANAAGCAGGGATAGAGAAAA
TATTTACGGAGAAAATCACATATCCATGGGGCTCGA

SEQ ID NO: 1563 ACAAGCCTCACCAAGGGCAACCCAGAAAAGTGAATGAGTTGTCTTCTCCA
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ACCAGTATTTGCAATAAGAATTTAGCATTTTCAATTCGTTTTGGTTGATTTACTCCAATTTTTTAT
CCAACAGGAAGCCTTATCTAAATAGGAATCTGCCAAACTTCTCCTANCTTCTTGATAATATGAAT
TGNTNCAGGGTTGCCAGAACCTTTCAGTCTGAGAACTGCT

SEQ ID NO: 1564 ACCTATTATATAGAGGGATAGCTGAATAAAGTCTGTCTCAAAACCAGTGTTA
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TNTGCATCTTCTGGGGATTGTTCTCTCCAATTTTACTTAAATCCCANACATTCNNTCTGCGANCAG
TACCTTCGNCCGACNTTCGCGGGGACACGCTANGNGCGAATNTTNANTCNACACTTGGGCGNGG
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SEQ ID NO: 1565 ACTGCAGAGGTATGTGCAGAAACACCCACCCATTTAAGCTTTCAATAAATAC
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 CCAAGCTCTTTAGACTTCAGCACTTCTCGCTCTTCAAGCCTCAGCACCTTTTTTGCAGCAATAATGG
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 AACTCTATTTATTCCCACATCAATGACTGCTGCTCCTTCTTGATCATATCTGGCTGTGATCAAGAT
 TTGGGAATACCTGCAGCAGATATTTACAATATCTGCAAGAATTGTATGTTTCTTCCAACCTGCTCTTT
 GGGAGATATCGATGAGATATTGTAACAAGTGGGATTACCNCT

SEQ ID NO: 1566 ACTCGTCAATGGGCTCGGTTCATATATACCACCTCGAAGCCCCGTTTCCGCACT
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 TGATAGCGCAGCAGCTCAGACAGGCGCGCGGTTAGTGGAGTCTTCGTGGATTCCAAGTTGAG
 ATTTTTAGAGAATGCCTCATAGAATTTCTGTAATTCCTTGTCTTCTGCCAGTTCAGAGAAGAGC
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 GGGAGATGTTCAAGGGCAGATCCTCAGAGTCAACCACACCACGGATAAAATTGAGATACTCTGGT
 ATCAACTCATCACAGCTGTCCATGATGAACACACGNGGACATANAGTTTGATGTTGGTCTTTTTCT
 TTCTTGGTCTCAAAAAGGGCAAAGGGNANCCGACCAAGGAATAAA

SEQ ID NO: 1567 ACAATGACCAAGATGCGACCAGGATCAGAGGTTCCCTTGGGGAAAGACCCACCC
 TACGAAGTTGGAAATGAGACCATCAGATGTGATAAGAACTCTTCTAGATGTCAACATAACCAACC
 TTATAAAGACTAAAATTCATGAGTAGAACAGGAAAATCATCCTGACTCATGTGTTGTGTTCTTTAT
 TTTAATTTTCAAAGAGGCTCTGTATAGCAGTTTTTGTCTATTTTAACATTGTAGTCATTTGTACCT

SEQ ID NO: 1568 ACCGGATTCTCTCTTTAAACCTCCCCTTCGTGTTTCCCCCAATGTTTAAATGT
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 TCAAGGATGGTTTTTGGGGACTANGANGGCTCANNTGGGTGGGAGAAATCCCTGCANAAACCC
 ACCAACCNAGAACCGTNGGTTNCCT

SEQ ID NO: 1569 ACAATCATATTCTCAGGTTTCATGACAGAACTAAAACTCTAGGAACTCAT
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 TTCAACTTCCAAACACTCCACCTTCTTTGGTTTAAATGTCTCTGCAAAGGTGCATTAGTTATAACC
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 TAGAACAACTCTATTTGTTTTTTGAAGGCATGTGTCCATTCTTAATTTTGTGTAAGATTTCTTTTC
 TTCTCTACAATTATGCTCCTTTCTATCANGGATTGATATTTAGTCTTCGAGCCCTCCGGTTTGTCTT
 TAAAAGACTTCTTTTTTGGGANAAGA

SEQ ID NO: 1570 ACCGTTGTGTGTTTTCTGCAATGTGGAGTTGACTTAGCTTGGCATTTTAGATTT
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 GGGGACTCAGGAGGACCTGTGAAGCATGTAGTTATCTANATCTGGGTAATTTTCATGTTTATTAAC
 TCGAACTTTGGCTAGTTAACTCATATTGAAACTTCATCTAGTCTCTTAATTTTTTAACACTAAATT
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 NTCATTATGGNTCATTGGGNTTTTGTACCTTGCCCGGGCGGNNCGCTCTGAAAGGGCCA

SEQ ID NO: 1571 ACCTACATCAGATCTAACCTTGATCCCAGCAATGTGGATTCCCTCTTCTACGC
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SEQ ID NO: 1572 ACACCTTTTGTTACAGTTACATATATGAATAGTTAGCAGAGGAGAACTCCTCC
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TATACTTGGACAAAGGCAACATTTTAATTTTGTAAAGTCTTAACCTTAGCCCANATGGGGTGGAA
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SEQ ID NO: 1573 CGCCCTTAGCGTGGTGGGCGGAGGTAAGTGGCAACAGCTGATGCGTAAAA
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TAAATCAAGGTTCTTGCTTTCTCAAAGTGATTGAGAGCTTCTAGAAATCTGTTTTTTTCAAATATA
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TAAACTGGTTTTCGGCTTCAGATAATTCCTCANGCTGTCCTATTCCAAGGAGAGAAATGGGCAAGT
CCATANACGACCAAAACATAAGTTNATCATTTGGCCAGGTTNAAATGCTTATTTTTTTGAGGATCTA
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SEQ ID NO: 1574 ACCCAGTAAAAACCAGAATGACCCATTGCCAGGACGCATCAAAGTTGACTTT
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TTCTGGATGGGAACCGCTCCATATTGCAGATGAAGTAGAGTTTACTGNGGTTCTGATATGCTCT
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CCTTCAGATNANCGTTTNTGGGNCNCGTTNAAAAAAGNCACTTTTTTTTCCAATNCTNAAAN
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SEQ ID NO: 1575 ACTTTATTTTTTTTTTTTTTTTTTTTTTGGCAGTTTTTACATTTATTTAAACAGAA
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CTCGGCACANTAAATTTGTTGCACATCAGCANCACCTNANCNTCCTTGACGTTGTGGACCAGGAA
CTTCCGGAAGCCNCTGGGCANCATGTGCTTTGTTTTTTTGTGCTTCCATAACCAATGTTGGGCATC
AAAATCTGGCCCTGAAATNTNTACNAACCCCTGTTGTCAATGCCTCTGGGTTTCCGCCAGTTACGC
TTAATTTTGACATATCGGTCTGACTGGTGCCGGATGAACCTCTTGGTTCTCTTTTTTGACNATCTTG
GGCTTACAAGGGGTCTGAGGGGCGGCCATNATNCCNAGAAANGAAATNGNTTGCCACCTCCCG
TAAGGCANCGCCNAAGAAAAAAACCCCNCGTCTCNGGCGG

SEQ ID NO: 1576 ACATTCATAGGGTTTTTCTTAGAGTGGGTCCTTTTCATGTATACGAACATACT
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ATGTCTACGATAGCATCTGGGACTATGAAATGCTTTCCACATTGCTGACATTCATAAGGCTTTTCT
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CATTATATGTTTCTCTCCAGTGTGAATCTTTTCATGGATAAGATATAAACTGAGACAATGGAAG
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SEQ ID NO: 1577 ACATAAAGTAAGTGTATATGTGCACAAGCATATTGCATTTTTTTTTTTTTTAA
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GTTATTTGTCTCACTGTTTTAACAAAAAACAACAACATAAAAAATCCTTGATACCTTGTT
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GACTTTCTTTTTTTTTTTTTTTTTTTTGGAGGCTCACTCCGTACCCAAATGGGAGTGCNGNGGCAT
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TAGCTGGGTATTANAAGCATGCAACCCCATGTCCAGNTATATTGTATTTTAGNAAAAANAANA
NCNTTTTNCCTATNTNNGGCCAN

SEQ ID NO: 1578 ACTTGATTGGTCATTTGAAAACACTGCAACAGTGAACCTTTGCATCTCAAGAA
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TCTTATGTATGGGTTTTTTTTTAATGTGATCCCTTCATTTGAATATTAATGGCTTTTCCATTAAAGA
ATAAAATATTTTGGACAATGCCGATAAATGTATGAAGTTAGTATCCACATCATAAATTCAGAGTGA
TGTTTAGCAGTAAATCAATATTTTGAAGTGATACACAGATGTCTTCCCTCCCCACAACTTTTTTAA
ACAAAAACAAGACCTCTTTCTTTAGATGGTGCCCTATGCCACCACAACAGAGATTTTACATG
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ATTATTAAGGAATCTAACTGGTTATACAGTTNAAGGCTTCTT.

SEQ ID NO: 1579 ACATCTGTCTGTTACTTTTTGATAATTCTCAAAACATTTCAAGCATTTAAATT
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ACTGCTGACCACTCCAGTCTCTCTGCCCTCTTCTCAGGCCTTCTTATTTCTGAGACAGAACAATAT
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CATCTCTCTTTTAAATCCAAAGCTAGGAATGATTAAGCTTAGTGAGGAAGGCATGTTGAAAGCCA
AGATAGGCTCAAAGCTTTGGCCTCTTGTGCCACATGGTTAGCTAAGTCATGAATGCAAAGGAAAA
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SEQ ID NO: 1580 TTTCAAGTCTTCTAGCTCGGGGCTTTTAAATTTTGAAATCTAAACATTCTTT
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TTTTTCTTTTGAATTTCTATCTTTATCTGTCTTTTGTTCATTTTAAATGCTATATATGGGCAGGG
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GCACCAGAACCCTGTCTTCTCCAGTCTCAACATGGTGTGCTCTTCAGTCATACCGGAATCTGA
ATCAAAAAAGTATTTTAAATATCCATGATTTCTCCCTGTATTGAGGCTAGCCCTGATCATGCTTTT
TGTGCTGTCAACCAGGTCTCCCAAGTGCACTTCCAGGTCAAGTGCTCAGATGTGTTAANGAGA
CCCTATATTCAGGGAAGTTGCGTGAAACTGCAGTGGGGGAGAATTGAGAATAGTCAGGCCTATC
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SEQ ID NO: 1581 ACGCGGGGAGTGGCTTGAGGTATCCGCAGGAGCGGCCGGGTGGCGGGAGGA
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GACTTCGTGGCAGAGCCCATGGGGGAGAAGCCANTGGGGAGCCTGGCTGGGATTGGTGAANTCCT
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NTCCCGGGACTGNTTTGATGCCTTCCANAGTGGTGCNACGCCTTCTTNTGATNCTCTTTGGGAAG
CTCTNAATTCCCAANCCTCNTACAAAAGTTTNNNACCGAATAAGGACTCCNNTCCCTGTCCNTCN
CAAAANGAAAAGAAATGTNNTTGTCTCCCTNNCCNGGNCNGGTTTTTAAAGGGCTAAAT
TACATCNTCAACTGGG

SEQ ID NO: 1582 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGCCATTGCTATGTTTTATTTTGCTA
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SEQ ID NO: 1583 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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GATGATGATGAAGAGGATGATGATGAAGATGATGATGATGATTTTGTATGATGAGGAAGCTGAANA
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SEQ ID NO: 1584 ACGCGGGGGGGGTGGTGCCAGTTTGGAGCTCTGGAAGGTAAAGTCTTCTCCT
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CAGCTACTTNTTCGAACAGTGATGCTGGAACCCAGTGACAATGCAGGAAAGCCATACTGAATCA
GAAAGTGGTCTTGTGAATTAACAGCTCTAATTGAANATGCANGGACAAAGATGAGTGGTGAAA

AAATATGACTTTCCTTTTGGTAATATTTTTGTGATCTTTGATGGTCTTAACCTANGAAGTGTAAT
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AGCCTTTGTTTTTAAAAAAGGCCNTTTGCCATACACCTTTTGNNTANTGNAAAAATTGACCTA
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SEQ ID NO: 1585 ACAAGACCAGCAAAGCCAGCTTCTCGGCTGTGAGCTCTGAGAACCTGGGGA
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GCAAGTTGTTCTGAAGAAGTAAGTGATTTGCTTCATCATCAAAGCCCCACTGACAAATTGCTAGGT
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TTATAATCTTCGACAGAGGTCCATCCAGCTTATGCTTTGTTTTGGTTTGGGTGGTTCAAATGGAC
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CACAATCACCGCCCTTAATCAGTTTAGTGTNCTCCAGCCTGCCGCCCACTTTGCTTCTACTTTTGA
TAAAGCTCAAAGTCAACGTCTNTCCGCTNCATATCTGCTACAGTNAGGACGGGNATTNACAGCAA
TTCTCAACCATCTTGTCGGTGNCAACTGTTGACCAACTTTGGAA

SEQ ID NO: 1586 ACCACCAAGAATCTTCAAATAAGCCAGCTGTCAACCAAGTCACTGCAG
TGAAGCCAGCTGCAGCCCCCAAGCAACCTGTGGGCGGTGGCCAGAAGCTTCTGACGAGAAAAGGCT
GACAGCAGTCCAGTGAGGAAGAGAGCAGCTCCAGTGAGGAGGAGAAGACAAAAGATGGTGG
CCACCATAAGCCCAAGGCGACTGCCAAAGCAGCTCTATCTCTGCCTGCCAAGCAGGCTCCTCAG
GGTAGTAGGGACAGCAGCTCTGATTGACAGCTCCAGCAGTGAGGAGGAGGAAGAGAAGACAT
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CTGCAAAGAAAGGGAAGGCTGAGAGCAGCAACAGTCTTCTTCTGATGACTCCAGTGAGGAAGAA
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SEQ ID NO: 1587 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAANAAGGTCCAAATCAATAGGTCT
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ACACCTGGTCTCATCCGAACCCTGCGGATGTATTTTACCCAAGAAATTTCCGGATTTCAACAANA
GACCCATTCTCCTGGATAACAACGTTGATGGGGAAGTGAGCATNCACAGACCTCATCTGTNACG
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SEQ ID NO: 1588 ACTTTTTTTTTTTTTTTTTTTTTTTTAAAAATCTGAGGAATAAATGCAAGTTTTTAA
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CCATCGGGGGGCCAAAGGGTTGGGAGAACGGGNTACTATTCTCGCTCCGGCATTITGTTATCGNTC
TTTTCNCTGNACCAACCAA

SEQ ID NO: 1589 ACAGTTTCCCAGCCACAGTCATTGCTTCATTCTTGTCTGATCAGATGGTAG
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AAATCTCCTTGGTTTAGTAACTCTTGTTGGATTTACTGCAGTTAAGACAGAACTTCATATGATTGC
CTCCTGACTGCATGGTCACCAGGTGATGTGTCACATCAGGCACTGAAGACAGGGAACGTGGGGA
TCCTTCAGCAAGCACCTCGTCATCAACTCCAGGATAGAAATGGTATTTGGTAGGTTCAAGGACTC
TCCACCAAGGCTGGGCTTGGGAATTCATAGACACCAGGTTTTTACTGGGTCNCGGGATTTTAAGG
AGAAGTAAGAGTAATGTAGTATTTTATACAAATATTTATAAAAAATAT

SEQ ID NO: 1590 ACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCTCTGG
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TGCTCTCCCGGATGAGGATGATGACCTGTGAGAATGAAGCTGGAGCCAGCGTCAGAAGTCTAGT
TTTATAGGCAGCTGTCTGTGATGTGAGCGGTGAGCAGNGTGTGTGCCACCTCATTATATCTAGCT
AAGCGGAACATGTGCTTCATCTGTGGGATGCTGAAGGAGATGAGTGGGCTTCGGAGTGAATGTGG
CAGTTTAAAAATAAATTCATTGTTTGGACCTGCATATTTAGCTGTTTTGGAACGCAATTGATTNCT
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GTTACTGGNCATTTCCCATTTCTTTTTCGTTTAGA

SEQ ID NO: 1591 ACAGTTCACTCTGCAAAAAATACTCCTTCTCAGCATTACATTCCATTTCAGCA
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TAGTCCAATTCATCACATCCCTTCACGAAGAAGTCTGCAAGACAATCGCACCACAGAATGCTC
CAAGAGATGAGTCTAGGGGCCGTTCTCGTTTTATCCTGATGGTGGAGATCAGGAACTGCAAG
ACTGGGAAGTTCTTAAAAAGGTTACAGATGAAGAGTCTAGAGTATTCCTGCTTGATAGGGGTAA
TACCAGGGATAAAGAGGCTTCAAAAAGAGAAAGGATCAGAGAAAGGGAGGGCAGAGGGAGAATG
GGAAGATCAGGAAGCTTTAGATTACTTCAGTGATAAAGAGTCTGGAAAAACAAAAAGTTTAATGA
TTCANAAGGGGATGACACCAGAGGAGACAGANGATTATAGACAGTTCAGGAAGTCAGTCCTCGC
AGATCAGGGTAAAAAGTTTTTGTCTGNTCTCACCGGAAT

SEQ ID NO: 1592 ACGCTTGATCAGATTTCTGATGCAGATAATATCCCAGGACTTTTGTTCTCAA
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TTCTTACCCTGACCTAGCTGAAGTTCATGCCCTTGAGGCTTGATTTCATTTCACCAAAAAGGACTAT
CTACAAGCAGAAAAATGTTTTAGAGAGCTCTTGAGAAAGATACCGAAGTTGCAGAATATCATT
CCAACCTGGATTAACTACTGGTTTCATGGGTGAAGAGACAAGAAAAAGATNAAACAAAGGCTCTTA
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ATTATAGAGACGTAGTGGGAGATAAAAAACAGAGCTCGNGGATGTTATAGGAAAGCCCTTTAATTA
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TGGGAAATGGNNTTTCCTTAACAACANTTACTCNAAAAAGGC

SEQ ID NO: 1593 ACGCGGGGTCCTGCTTTTGGTTCTTACAGTAGTCGGCGTAGGCCTTAGGTGGG
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TGGGAGCGGACGAGGCGCGAAGCTGGGATTTTTACTGTCTCCTGAAGAATTTAACACAAACATG
GATATCAGACCAAATCATACAATTTATATCAACAATATGAATGACAAAATTTAAAGGAAGAATT
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CATGAANATGAGGGGGCAGGCCTTTGTCTATTTAAGGAACTGGGCTCATCCACAAATGCCTTGA
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AANNAAAAATAGGCCAAAACNTGGAANAANACTGNAACAACCNACAAAA

SEQ ID NO: 1594 ACCATCTGTGGTGGCTCTCTGCAAGTTTTAAACTGCCTCTGCTGAGCTCTCA
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GGGCAAGTTCTGAACCTAACCAATGACCTGATGGGATTGCTNGACCAAGACACAAGAGNGAA
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SEQ ID NO: 1595 ACTTGCCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGACCA
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AGATTGAAGTGTAGTGCCAAGATTGAAAGGAGAAAGTGGTTGAGGGATAGTGAGGGAAGTTGGA
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TCTGAGGACCTGAGGTCCGTAAGTGGATCTTTCTCAGGGAGCAAAGAGCANGGAGGACGGAGGAT
TTGATCTCCAAGGGGAGGTCCCCGATCCGAGTCATGGCACCAAAATTTATTGTGCCGTCCATGTG
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SEQ ID NO: 1596 ACGCGGGGAAACCGGACCCGCAACCACCATGAACAGCAAAGGTCAATATCC
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SEQ ID NO: 1597 TGTACATGTTGTGGGTGCCGCTCCGGGAGTCATAGCGCAGCCAGATCCCGAA.
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GCTGCTGAGAACTAGGTGAACTGAGAACTTAGTATAATGATTGAAGAATGTGGAGGCTTANA
CAAAATTGAAGCTCTACAAAACCATGAAAATGAGTCTTGTGTATAANGCTTCGTTAAGCTTAATTG
AGAAGTATTTCTCTGTAGAGGAAGAGGAAGATCAAAACCGTTGT

SEQ ID NO: 1598 ACACCTGGCTTGAGGCTGTCTCTCTCATCGGTATCATCGTAGCCAATGTG
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CTCTTACAGAAATTGCAGGTCTTTGTAAACAGGGCAGTGTTCAGGCTAACCGGAAACCTACCTA
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AACAAAGTACC

SEQ ID NO: 1599 ACAAGCCTTTAAAGAAGCAAGACAAAATGTTGCTGAAGTTGAGTCATCAAAG
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SEQ ID NO: 1600 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGCAGAGGCNCAATCATTTTANATTAA
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ANANAACGGTCTCTCCACCAATTTTCAGCTGGTCTGTCTCATCANCTTTGGGCTGANCTTGGGGTG
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CTCATGACNATGATGATGCCATGGNGCACANAACCCAGCGCAAATGAGCCCCGCAACCTGGAG
GCTGTGCCAGTCATAGTAGAAAGGACTGTTTTATCTTNTAGGNCATTGGCCGTCCANGACAGGAA
AGCCTGCCAANAACACAAGCAGGCCAGGGTCACTTNTGCATGTCAAACCNCTGGCCTTGTGT
GGTTTNCNCAAGCNTGAGCAAAAGTCCNGGAGAAAAATCC

SEQ ID NO: 1601 ACAATTTAAAAATAAGTCTATGTTTTCACATTGATTTTAAAAAATATAGCATG
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CTTAATTGAATACTTAGAAAAAATGGCCAGTGGCCGATTGAAAGGTATATTTAAAAATTAAGGGCA
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ATCCNAGTANTNCATCCCNTAGGGCTGANTCAGTGCCATNGCCCATGCNGAACAGCATTNNTT
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SEQ ID NO: 1602 ACAGATGGGGTCTTGCTATGTTGCCCAAGCTGGTCTTAAACTCCTGGCCTCAA
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SEQ ID NO: 1603 ACAAACCTTGCTCAGAAGCTGTATCAGCATGAAATCAACTTATTCAAAAG
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SEQ ID NO: 1604 ACTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAATATTTATTTTCTTAACGAC
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AGGGCG

SEQ ID NO: 1605 ACTGAGCAGGATTACCATGGCAACAACACATCATCAGTAGGGTAAAACTAAC
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GAATTCTGCTTCACAATGATAGGAAGAGCCGACATCGAAGGATCAAAAAGCGACGTCGCTATGAA
CGCTTGGCCGCCACAAGCCAGTTATCCCTGTGGTAACTTTCTGACACCTCCTGCTTAAACCCAA
AAGGTCANGAAGGATCGTGAGGCCCCGCTTTCACGGTCTGTATTCGT

SEQ ID NO: 1606 ACGCGGGGCTTTTTTCGAGGTAGGAGTCGACTCCTGTGAGGTATGGTGTCTGG
GTGCAAATGCAGTGTGGCTCTGGATAGCACCTTATGGACAGTTGTGTCCCCAAGGAAGGATGAGA
ATAGCTACTGAAGTCCTAAAGAGCAAGCCTAACTCAAGCCATTGGCACACAGGCATTAGACAGAA
AGCTGGAAGTTGAAATGGTGGAGTCCAACCTTGCCCTGGACCAGCTTAATGGTCTGCTCCTGGTAAC
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SEQ ID NO: 1607 ACGCGGGGACGGTTCGTTTTTCTTTAGTCAGGAAGGACGTTGGTGTGAGGT
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GACAGTNAAAAA

SEQ ID NO: 1608 ACGCGGGGCTCTTCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGA
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GCTAGATACACTGTCTAGATCCTTTGGCATCCGAGAAATGAAAAGATTGCTGTCCACTGCACAGTT
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AATATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGTGTGGGTAGGCCACGTTTT
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SEQ ID NO: 1609 ACTTTTTTTTTTTTTTTTTTTTCCACACCTGCCCTTATTGGTCTCTTCTAGCAA
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GAGGAAAAGGAAACAGGCAGAGGGGAAAAGGCAAGGCTCTGCAGTGAAGGGGACTGATATCAAG
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TCAGGCTCAATGTTGATGGTTGGGAAGGTGCGGCTGTAGCGTCNGAAGGGCTCTCCTCCGGCCCTA
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GGATCGGCATGANGGGAAGTGGGTG

SEQ ID NO: 1610 ACAACAGTGAAGTGAACAAAAGGTAATGAATTAACAGGAGGACTAGAGG
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CTCTCTGAAGACAAAGAAGTATTGTCTGAGTGAAGTGAAGTCTCTTATGAGGAAAACAATAAACT

CAGTTCAGAAAAAACAGTTGAGTAGGGATTTGGAGGTTTTTTGTCTCAAAAAGAAGATGTTA
TCCTTAAAGAACATATTACTCAATTAGAAAAGAACTTCAGTTAATGGTTGAAGAGCAAGATAAT
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CTTAAAGAAATGGGATCAGAAAGTTTCAGAAGACAGTGAAGAAGAAAGATGTTGTTAATGTCCTAC
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SEQ ID NO: 1611 ACCTGGTAGAAATTGTGTCTTGGAAATGACCCTTTCGAGTTATTGACATGGCTC
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SEQ ID NO: 1612 ACAGAGGGGTCTGTTTCTAAGTCTGGAACCTCAACACGAGGCTGGGATGCTT
CACAACGTGCTCTCTCCCACTGTCCAGCCATCTTTGGTGGTCTTCCACAGTGCTTCCCCATCCTC
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CAACAGANAACCTGGAAGCAGCAGAATCTTGGAGGAGCAGGAAGAGAGCCCAGAGGGAGTGTG
TGCTGAGTGACGGTTAACATATGAAACAGAATTTTCAATGGAGATTCTTTGTTACAAGGAGAAATTGC
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SEQ ID NO: 1613 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGGAANACTGCTTTATTGGNGGC
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GGGAAATGAAGCCACAGCCNGCTCATNTNTGGCATATGCTGNTCCCAACTGNAANAATCATGG
NGGCTNTATCAGGAGGACATCAGCTACCCACCCCTTAATACAGGGGAATTTTCATCATCCTCCTGG
AACAGTTTTTGTCTCTCCGGAACCTTATTTTTAAAAATGCCTGCGGGAAGCAGTGCTTATCGTNTCTG
CCAATNTGACGAAAACCANCAAAATTCC

SEQ ID NO: 1614 ACATAGGTAACCAAAGTATATAGCTTATTTGGTGAATCTTCATCCTCATTACT
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NTTTGTTGAGCCTGGTGTCAATGCGCACATCTGGGANNTCCANTCCNTCANGGGCAAAATTTCCGA
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SEQ ID NO: 1615 ACAGGATAATATACTCAGATATTTTAAAATAAACTACTTAATAATAAGAAA
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SEQ ID NO: 1616 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGNANATTAAGGCTTGTTTTATT
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NACCTTCAGGGACCNTGCCCGGGCGGCCGNTCNA

SEQ ID NO: 1617 ACCTCGGGGACCTGCTGGAGACCTGCCATTCCAGGCCTTCTGGCAAGCCCT
GGATGAAAACATGGACCTCTTGAAGGTATAACTGGCTTTGAAGACTCTGTCCGAAAGTTTATCTG
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SEQ ID NO: 1618 ACCAGCTGGCACAGGAGCAGGGGGCATGGCACCTCTGTTGTTTATGCCATA
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CAGCTTCATCTCCATCTCCAGCTTCTCACGAGCCTCTTGATGTTGCGGCCACTTGGCTGCTGCTGT
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SEQ ID NO: 1619 ACTTTTATTCTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTCTGTCTCTGTTGCCTG
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TTTTTTGAGANNAGTTTCTNTTCTTGTGGCCAGGCTAGAGTGCAATGGCATGACTTGGCTACTGA
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SEQ ID NO: 1620 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTNGTTTTTTTTTTTTTNATATT
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TAAGANGGNTAACACCTAAACCACACGCGAGGCNTCTGAACTCA

SEQ ID NO: 1621 ACACACTTTATTTACTTCGTTTTGGTTAAGTTGGCTTCTGTTTCTAGTTGAGGA
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SEQ ID NO: 1622 ACTTCTCCGTTGACAAAGAAATTCTAGGTGAAATTAAGAGTCATGATCTGAA
ACCTAATGGTGGCAATATCTTGTAAACAGAAGAAAATAAAGAGGAATACATCAGAAATGGTAGCTG
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SEQ ID NO: 1623 ACTTAAATATATATTTATTCATTTCTACATATATAGAACTTGTAGGTAAAGTA
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SEQ ID NO: 1624 ACTGTTAAATGTGGATGGCACCCCTCCCAAGGATTGAAAAACACACAGCTGGA
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CTGCGCCTGCATCCTTGCAATCATCTCTTGATGCGGCGGAGCTCANCTTCTTTTTCCAGCAAGATC
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TTTCATAATGAAGGTCCTGGGTACCTCCTGGAGATCCTGCATGTGGGTGATGAGCATGGTTCTCA
CTTCAGAAAGTCATTGTCTCTGGGTTCTCCCTTCACAACACCCCANGGGTA

SEQ ID NO: 1625 ACCATTATTTGTCTGCCGCTTTTAAAAAATACCCATTGGCTATGCCACTTGA
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SEQ ID NO: 1626 ACCTACAGACACTTTTACAGAGTTAATACTAAAAATTACAAATTGATGACACTT
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SEQ ID NO: 1627 ACGCGGGGGCGTCTTGTTCTTGCCGTGGTGTGGTGGTTAGTTTCTGCGACTTG
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SEQ ID NO: 1628 ACGCGGGGAGTGACGGTGGCGTTTCTTGAGGAAGAGTGAGGGTTCCAACTT
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SEQ ID NO: 1629 ACGCGGGTGGACTGTTGCAGCACCTCCCTTGGTCTCCAGTCTGAAGTCTCT
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SEQ ID NO: 1630 ACTCCATCCCACAAAAGAATTCTTGTTCTGGTCTTTTCCAGCCAGGTAAATAAGG
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CACGGGGACCCNGGGCCTGNTCCACAGAGCCATTTTCTAGCTTCTGGGCCTGTGATGGGGANG
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SEQ ID NO: 1632 TACGCGGGGACGTTGCCAGCCGAGGTTTGGACATACCTCATGTAGATGTGGT
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SEQ ID NO: 1634 ACATGGAGAGGAGTATGGTGAGCTATTTCTTTTAAAGGATGAGACCTTCAT
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SEQ ID NO: 1635 ACAGAAGTTTTCATCTATGAACATGGCCTCATCATCACCTGCGCCTTGGCCT
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SEQ ID NO: 1636 ACTTTATTAGTTTAAAAAGAAATTGAGGTTGTTCAAAGTTTAAGCAATTCATT
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SEQ ID NO: 1637 ACCCACCAAATCCATGGAGAGAAAATTTCTGGTGAAGCAATTGATCTGATAAA
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SEQ ID NO: 1638 ACATGACCTAATTTTTACATCATAGTAAACAGGCCCTATGGAGAGAGGACA
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SEQ ID NO: 1639 ACGCGGGAATGAAGGACTTGGCAGATGAACCTGCTCTTGTTGATGTCATCGA
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SEQ ID NO: 1640 CGCGGGACCGAGGCCCATGCGAAGCTTCCACTATGGCTTCCAGCACTGTC
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SEQ ID NO: 1641 ACAACTTATAGAAAAAGGTAAAGGAAACCCCAACATGCATGCACCTGCCCTTGGT
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SEQ ID NO: 1643 ACTGTAGGAGAGAATTAATAAAATAAAATAGCTGTAGATAATTAAGGCTA
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TCTAGTTAA

SEQ ID NO: 1644 ACTGGGATTACAGGCGTGAACCACCGTGCCCGGCCCTTCCCCAGATATCTTCA
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SEQ ID NO: 1645 ACTTTTGTCTTATGAAAAGAAACCAAGTGAGTCCTCTAAGGATAGCAAAAGGG
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AN

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CAAGGGCTAGTCTTGATATTATCATTTCTCATTTNGTCTTCAGCAATTGTCCAGACAAGATGCAGAN
GGTT

SEQ ID NO: 1648 ACTGCATTTGTTTTATATCTTTAATTTCTGGCAAGGGTAATGGGTTGAATGG
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SEQ ID NO: 1650 ACACTTGACTGTTTCCAAAGGGAGAGAGGTGATGTAGTCTTCATTTACGGGG
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SEQ ID NO: 1651 ACAAGGAGACCAGCCTACACAGTCCATCAAATACATCTGCCCTCATAGCCA
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TGATACTATGACATGTNGCCAACACCTTGAGAAGCATTATTTGTTTNTAATAAAAGTAATGGCTT
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SEQ ID NO: 1652 ACGCGGGGGNGTCTTGTCTTGCTGCTGGTGTGCGTGGTTAGTTTCTGCGACTT
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SEQ ID NO: 1653 ACATTTTGTACAGACAGAAGGCTGATTTTGGAAAGAAAGAAACAATNGGA
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GCGC

SEQ ID NO: 1654 ACAGCAGTTGCTCAAGAACAAAGTTATTCTCCTTTTCATCTCGAATACTCAGA
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SEQ ID NO: 1655 ACCAGTGTGGAGAAATGGGCTGGTTAACTGTGTGGGGCCAGACAGTCATTTG
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SEQ ID NO: 1656 ACATAGACAAGTTTCTTGTAAAGACAGAAAAACAGAGAAATCCACAGTAACTCT
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SEQ ID NO: 1657 ACCAGTAGTTTTTATCGGTAATAAGAAAAAGGATGGCTTAATAGTGCCAATA
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SEQ ID NO: 1658 ACAAAAAAATCATTTCAAATAACTCAGGAGGATGATAATGGCTGGACTTTT
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SEQ ID NO: 1659 ACTGGGATAAATGAAGAAGAAGGCATAAGGACAATAAACATGGAACTCCAC
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AGGAAGACAGAACCATTANCAAGTGACATTGGTGAAATATGTTTCATTGATTCTCACAGAGTAA
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TTCCTGAACAGAACGCAAGAAGAGCTTGTAATATCAANAGNCTTTCATCAGGCAGTAAACCTGG
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SEQ ID NO: 1660 ACAACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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SEQ ID NO: 1661 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATNGGAAAAANACTGCTTTATT
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NAATCCTCCNGGAACANTTTTGNTTTTCCGGANCTTTTTTTTAAATGCC

SEQ ID NO: 1662 AACTCTCCATCTTAAATGAGCAGCGCATTCGGGGCATTTTATGCGATGTCACT
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TCGTAACAGAA

SEQ ID NO: 1663 ACATCTTGCTTAGATGTGCTGACTGCAAGTAATAATACAGTTTATAATGAA
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SEQ ID NO: 1664 ACACGGCCCCCTTCACTTCCCTTTTCAGCCACAGTCTGTAGTTTTCCATCCGAAT
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SEQ ID NO: 1665 ACTACAGCAGTCAAAGAGATCTCCACTAGAGATCAGAAAGAAGCACCACTAT
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SEQ ID NO: 1666 ACAACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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SEQ ID NO: 1667 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGCNAAAGTTTCATTTATTTGNGC
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TAAATTTT

SEQ ID NO: 1668 ACAGAGCACATAGACCAAGGATGGCCAGTAGTAAGGCATGCTGTGCTCTCC
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GCCTCTCAGCACGCTGAGGTTCTGCGGAGGGAAGTCCCTTGGCTTTCTCTGCAAGGCTTCTT
GGCTGTTATGGACCCGATGGAGTTTAATTATGCTTAGCATATATTTTTGGCATACTAGGATTTCTT

CCCCTAGGATTTGCCAAAAGAGGGGANGGATCAAANTTTGGCATGCTGGGGGAACAACTCNCCCC
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SEQ ID NO: 1669 ACGCGGGGGTCTCTGGTTTCTGGCCCCCTTGTCTGCAGAGATGGCTCCCAATGC
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SEQ ID NO: 1670 ACCCTTGCCAAGTTGTCTACAAATGCTTTGTGCGATTTTCTACTGAGTTAGAC
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SEQ ID NO: 1671 ACCAAGAACCGCTTTATCCAGATTAATATAAGTGAAAGCCTTTAAATGCAGG
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SEQ ID NO: 1672 ACCCCCAAATAGAAAGAAGTGACTGGATGTTGGAAGCTTAAAAATGATAC
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SEQ ID NO: 1673 CCAGTTCTTTTACAATACAATATTTTGGTATTTAAATGACCTCTAAATGGTTA
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SEQ ID NO: 1674 ACGCGGGGCAACTGATATATCTTTAGGGTGAGTTACTGAGGCTGTTTCACTG
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SEQ ID NO: 1675 ACAAATACGAAACAGGATTATCTGATAGTAGGCCTCTGTGGATGGCATCAAT
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SEQ ID NO: 1676 ACACAATTATGAAACTATGCCAGTAGCGACCTGCATGTTTGTCTCATCTCTTT
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TGGTT

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SEQ ID NO: 1678 ACGCGGGGGGATTGCTGAATTAATGACTATTGAATTTAAACTAATTATGA
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SEQ ID NO: 1679 ACTAAACCCAGTAAAAATTGTTGAAAATGTTAAAGGTCAGCATGTTCTAATT
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SEQ ID NO: 1680 ACGGTATATATATTTTAAATATTCTCACACACATGCAATCCATAAAGCAAT
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SEQ ID NO: 1681 ACTAAAAAGATTTTGAGGATTTATACACTCCTGTGAATGGATCTATAGTGAT
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CAAGAATGTGAANTNCTGTGANCATNGGCTGAAGAGTAAATCTTACCTCTTGNGTTAANGCTTT
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SEQ ID NO: 1682 ACGCGGGGATTAAATGTCCCAAGCAAGGATAGGGAAGGGGAATGGTTGAGT
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CAACAGAGCGAGGCTGTGATAACTTAGGAGGCAGCAATCCTAATAGTCTTTCAGTTGCATTTAGT
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SEQ ID NO: 1683 ACTTTTTTTTTTTTTTTTTTTTTTTCGCANATTTGAGTAACTTTATTTGCATTT
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SEQ ID NO: 1684 ACCGCCAGCTCTCTGCTCTCCACAGGGCTCCCCGCCCCACCCGGCCTGATAAA
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SEQ ID NO: 1685 GCGGTGCGGGCCGAGGTAAGTGTGAGCCCTCGGCCAAACGGCCAGACGCGGAC
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SEQ ID NO: 1686 ACTGTCGGTTTCAGAAATGCCTTGCAAGTGGGGATGTCTCATAATGCCATCAGG
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SEQ ID NO: 1687 ACCGCGGGTCCGTCAAGCTGGTGTGCTTACTAACCACATCCACAAAGCACA
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SEQ ID NO: 1694 ACAGTGGCATGATCTCGGCTCACTACAACCTCTGCCTCCCGGGTTCGAGGGA
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SEQ ID NO: 1695 ACTCCAACCTCAAGTTTACAAGTTACACCTTTGCCACAGCCTTGGCTAAATCTT
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SEQ ID NO: 1696 ACCGTCTAAAGGGGCAAGGATGCCATCACACAAGCATTGTTTCTACGAGA
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ACTGCTTTAAACAATGGTTGGCCACCGGACTGAGGTATGGGGGTTGGTTCTGTTGTCANAAGAA
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ACTCTTGAGGCANAGGATGGTGCCTTTGAGACGGATGAACCCCTGANGATCGAATCCTTTCTGCAT
AAAAGCTGGTCTTATTGCGGGANGGAA

SEQ ID NO: 1697 ACAAAGGACGGAGCACCATCAACCCGTCCAAGGCCAGCACAAACCCAGATC
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SEQ ID NO: 1698 ACAAAGAAGCAGAAGTGTAATTTTCTTTTCCAGTATGACGAAAAATTGGA
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SEQ ID NO: 1699 ACGCGGATCCACGGGTGACACGGGCACCCTGGTGGCAGAGAAGCATGTCTCT
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SEQ ID NO: 1700 ACATGAAGTATATGCTGTGGATGTTCTCGTCAGCTCAGGAGAGGGCAAGGCC
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AGCATTTGAAGATGAGAAGAAGGCTCGGATGGGTGTGGTGGAGTGCGCCAAACATGAACTGCTGC
AACCATTAAATGTTCTCTATGAGAAGGAGGGTGAATTTGTTGCCAGTTTAAATTTACAGTTCTGC
TCATGCCCAATGGCCCCATGCGGATAACCAAGTGGTCCCTTCGAGCCTGACCTCTACAAGTCTGAGA
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SEQ ID NO: 1701 ACTTTTTTTTTTTTTTTTTTTTTGCTTTTTTTTTTTTTTTTTTTTTTCCAGCC
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GGGCCAGCTGGNGTTAATGGCATGCAGGCATNTGTNATGCCAACCATGAGGGCTGGAANAACCAA
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SEQ ID NO: 1702 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTANANTTATTTTTATTGACAAGG
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SEQ ID NO: 1703 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGAATCTGAAGTCTTGTGTTTTACTAATG
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TCTCAAAGTCTNATCCACAGCGGCCAACAGGGAGGTCATTACAGTGATCTGCCGAAGAATAC
CCTTATCATCAATGATAAAAAGGCCCTGAACGAGATGCCTTCATCAGCCTTAAGACCCATAAT
CCTGACAATGGTGCCTTCGGGTCTGATCCAAAGGAATGTCATGGGTCCAGCCTCCTTGTCTT
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SEQ ID NO: 1704 ACTGGGAGATACAGCCATCCACCTTCAGATGTGTCTACGTGCGCTCTGCCATT
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SEQ ID NO: 1705 ACTTTTATCAAAATCCATCATAAAAGGGAAAGAAGACTACAAAGTTTTGCCT
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SEQ ID NO: 1706 ACGCGGGCCAGTTGCCAGAGTGGAATACTCGCTTGATAATGCACCTTTTATTG
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ATCACTGAGGTGAGGAGTTTGAGACCAGCCTGACCAACATGGTGAAACCCCTCTCTACTAGAAA
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SEQ ID NO: 1707 ACAAATTCGATTGTTAGGAAACCAAATGTTCTGAACATTATTTTCATTAGAA
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TTCAGATGTTTGAGCACATACTCTTCACACTGCCAACTGCTCCAGAAGATTGTTATTTTATTGATCA
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SEQ ID NO: 1708 ACAAATATTTAAGAGTGTGATTGGGAGTAAGGGAATGTCAACTGCCAATAA
AGTGGAAGATGAAAGAATAGGACTTTACACAGAGCATATTTAGTTATGGGTCTCTGTCTCCTCCCC
ACACAGAAAACTCCAGACATTCATGACTTCATCCACCCTGCCTGGCAGATAGGCCATATTTCTC
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ACAACTCATACTGCAGCTAAGCATCTACCCCGAGGGACAAGGCAAGCACACACTAGGGCAGCTGG
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SEQ ID NO: 1709 ACAAATGTTTTTTTATTCAAAAATACAAAATAAATTATCTGTAGGCATGGACA
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SEQ ID NO: 1710 ACACGGGGGGAAAGACAATCATTGAATACAAAACAAATAAGCCATCACGCC
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CTCTTTGCCATTTCTTCTTCTTCTTTTAACTGAAAGCTGAATCCTTCCATTTCTTNTGCCATCTAC
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SEQ ID NO: 1711 ACTTTTTTTTTTTTTTTTTTTTTTGTCTTTTTTTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 1712 ACCAGCGAAGCACCTCAGCCCCCTCGGAAGAAAAGGGCCCGGGCAGACCCC
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CANTGCCCATGTTTATGGAGCACCAACCTACTGAATNTTTGTAAGAATTGGACATTGTGGCCTNT
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SEQ ID NO: 1713 ACGCGGGGGCTCACTCTGCGCTTACCATGGCTTTCATTGCCAAGTCCTTCTA
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SEQ ID NO: 1714 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATGGAATGATTAAAGATGTCTTTAT
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GCATCATAAAATGGCCCTTTTTTGGAGGATGGGANAGGAAGGGTTGGGCAGGATGGAATATTAAAT
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GGAAACAAAGCAATCATTTGTGACAAGCCTAAAAAGCTTGACATATTTAACATACTTAGGAAC
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CTGTTGAAGTTTGCTGTGAACATCACATTCCCCCTAANAACCAAGNGGATTGCTCGAG

SEQ ID NO: 1715 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGGGANCCAAGGAAGTTTATTT
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ACATCTGTGAGGGCCTCNAGGGCTGNTGCCTCAACTTTCTCCCTACTAAGTCCACCCGCCAGGGAC
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SEQ ID NO: 1716 ACTCTGGTAAGCTTGTGTTGTGTTGCCAAGTGAAGCTCCCTCAGATGAGGCGTGT
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SEQ ID NO: 1717 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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SEQ ID NO: 1718 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGATGCTTTTCATTATCACANAACAC
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SEQ ID NO: 1719 ACGTGAACCACAAAGTGATACCAGGCATATGACATGGATCCCCCTGGGGAA
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SEQ ID NO: 1720 ACGCGGGGGGAGGGGGAAAAACGAAAATAAACGAAGCTTGCAGCACACTCT
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SEQ ID NO: 1721 ACCTTTGTCAATCCTAACACATTATCGGGAGCAGTGTCTCCATAATGTAT
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CTATAAACTTAGTGCGGCAAGTTTAATCCAGATTGCCTTTGCTTAAAGCAG

SEQ ID NO: 1722 ACGCGGGGAGGTTCTGGGAAGATGGCGAAGGTCTCAGAGCTTTACGATGTCA
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CTNTCA

SEQ ID NO: 1723 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGNTCAAGTTTAATACAACTAC
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SEQ ID NO: 1724 ACAATACTTGGCCGAAATCTGTCAGGTCAGCCCACTTTCCTTGTCTGTCAA
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ATGTATGGTTATTCAACATCATTTTACTTTGGATATATGGCGGATTACACACCTTGGGATATGGTG
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SEQ ID NO: 1725 ACACATGATGAAATGAAGCAGAAGCTGGGAGTCGGCCTTTCCTCTAGTAACC
ACCACATGGCTCAGCATCTGTGCCAAACATAGGCGCTCCTAGTCTGGTCAGTGCCAAGAGGCTAC
CAGAACATGGGGCAGGTGGCTGGTGTGGTGTCCAGCCTAAGAGCCACCTGCTGCAGTTACCAT
GGCATGCTGAGTTGATGCACCAGGTGGCAGCAGCCATCCGTTATTATTTCGAATGGAGACCTAGCC
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SEQ ID NO: 1726 ACTTTTTAAATCATGTTCCCCCTAAACATGGCTGTAAACCCACTGCATGCAGA
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TCATTATAAGCTATGAGTTGAAATGTTCTGTCAAATGTGTCTCACATCTACACGTGGNTTGGAGGC
TTTTATGGGGCCCTGTCCAGGTAGAAAANAAATGGTATGTAGAGCTTAGATGTCCCTATTGTGACA
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SEQ ID NO: 1727 ACACTTGAAACCAAATTTCTAAAACCTTGTTTTCTTAAAAAATAGTTGTGTGA
ACATTAACCATAACTAATCAGTGTGTTCACTATGCTTCCACACTAGCCAGTCTTCTCACACTTCT
TCTGGTTTCAAGTCTCAAGGCCTGACAGACAGAAGGGCTTGGAGATTTTTTTCTTTACAATTGAG
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SEQ ID NO: 1728 ACCTATTTTTTAATTGAGACAGGCCACTTTATTAATAAGGTCCAAATGTAAC
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SEQ ID NO: 1729 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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SEQ ID NO: 1730 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
GTATCTTACAGGAGTATTCTTATCCATCCCGTGGAAAAGGTTGCTTAACAACTGCAGTCTCAGAGA
CGGGCGTTACCTTCGCNAAATTTGACCAGCTTTTACATAGGCTTTCAATCAAAGCTTCTTGCTTG
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TCTTTTCTGAAATCTCAGTTCGGTTAGATTTCAAANNANNACGAACTANCAANCTGNCTTTTATT
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CTTGGCCGGA

SEQ ID NO: 1731 ACATCATAATCGGCGACACAGGTGTTGGTAAATCATGCTTATTGCTACAGTTT
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CATCACAAGGTTCGCAATTACAGAGGTGCAGCAGGAGCTTTACTAGTTTACGATATTACACGGAGAG
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GCCTANATGTGTTCCA

SEQ ID NO: 1732 ACTATAATGCCAACAGGGCATTTCAGAAGATGGACACAAAGAAGAAGGAGG
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ACATTTTCATTTGGACTAAATCCCACGAATGACAACCTACCACCTTTTTTCTTTTAAATTAATCT
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CATTATGTTAATAAACTTGTAGCTTTTTGTAAAAAAGTACTCCNAAAN
CCTATTNCCAAACAGGCAGAAATCTTTCTATATTAAATTGCACTACTAAAAATTTTTTCACGGC
CTNGAAATTGATATAAGATCATTGCTCATCATTAGGATAAAATACTGAATTTTCTGGAAATAATN
TNTTCAGAGAAAAATTTCTTTACAANTCTAGTTCTTGCCAGAAAAAGGTCTTCCNAAAAACATCA
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SEQ ID NO: 1733 ACATCCCAAGAGATGTAGATGAAACAGGTATTACTGTAGCCAGTCTTGAAAG
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SEQ ID NO: 1734 ACGCGGGGAGTTTTCAACTGACCTCTGGACGCAGAACTTCAGCCATGAAGGT
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GTGGGACTGATGGAAATACTTATCCCAATGAATGCGTGTTATGTTTTGANAATCNGAAACGCCAG
ACTTTTTCTCATTNAAAAATTGGGCTNGCTGNGAACCAAAGTTTGAAATTCATCTAGGTAACC
GNNAGGCANAACTGNCTTATTGTGAATAAATAG

SEQ ID NO: 1735 ACCTCAAATCTGCTCTGGAGTCGATTATGCCACCTGTGTGTCAGGATGCACCT
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GACCAAGACGGGACNTTACATTTTAAGTCTACATNCTAATCTTAAANGAATAAAGCACTGAATT
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CANCAGTGAANGATTCTACACAGGGAATCTGCAGTTTGTGCAGAAATGNTTTNNCTCACGTTGCTNA
TANACTGCCAAATTCAAANTTAAGCTGATTGACACAGACCTNCCTTTNCTGACCAATGTTGACACA
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SEQ ID NO: 1736 ACGCGGGAACCCAAAACCTATAAGAACTAATAATAATCCACCCTCTTTGCT
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CCTTCTGATATCCNCGTTNAAGNGTAGACNTGCNNGNACCTGCTTGNCTTTCCTTAGNCAGNCCA
TTTTTGGGAGGCANACTGCCGGCGGC

SEQ ID NO: 1737 ACAGTTGATCCCACTTTGGAATAAATGCCAGAAGGTAATAAGCATTATCAG
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SEQ ID NO: 1738 ACGCGGGGCTCTCGAGTCACTCCGGCGCAGNGTTGGGACTGTCTGGGTATCG
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CATCATCNATACCTTCTATTCCAACAAGGAGATTTTCTTNAGGAGTTAATCTCTAATGCTTCTGAT
GCCTTGACAAGATNCGCNTTGACAGCCTGACAAACCTTCGAAAGTTGACAGTGGGNTAAGAGCTG
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SEQ ID NO: 1739 ACCTACAGACACTTTTACAGAGTTAATACTAAAAATTACAAATTGATGACACTT
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CATACTGTTNGGCTGAACACTGACATTCCATAT

SEQ ID NO: 1740 TCCCCACCACTGTGATCTATGAGGATAACCAAAGACCTCTGGGGTCCCTG
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CTCTGAGGAGCTTCAAAGCCAAACANGGCCACTGGTGTGGCTCATAAGTGACTTTTCCGGGAGC
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SEQ ID NO: 1741 ACTTGTCATCAAAGACCCAGGCAGTCTCTGGAATAGGCTTTCCAGCTGCTCA
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SEQ ID NO: 1742 ACGCGGGGGCCATATTATCAGCGGTTATTCCGGTGAGCGGTGGTGGTTATTCT
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SEQ ID NO: 1743 ACGTAACTGGAAGCAAGGACGGCTGCATCAAATTATGGGATGGTGTTCAAA
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GACTCGAGGACAGCCGAGCGGAGAACCTGCTGCGTTGGGGCACAACAATATTGTACCTCGGCCG
GACCACGCTAAGGCG

SEQ ID NO: 1744 ACTGTATCCAGCACCACAGAAACCTCAGTGTTTTCTCTGCTGGTTTGGGGC
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GNTTG

SEQ ID NO: 1745 ACTGAACTTTGTGTTGACCATAGCCTTCTTGTCTTTCATCACTTTATCTCCATG
TATGTATCCTTAAAGAATAATAAATGGATTTTAACTGAANAAAAA

SEQ ID NO: 1746 ACAAACCTAGGAACACAGAAAAGGACCAGAGAGGATGTTACACTGTAAAGT
CTTAGGACCTACTCTAAACTTCTGTCCTCATCAAGACCCTCACCTAGAGACCTGAGGGTTCCCAGG
TCCACTGGAGAAAAGTAAGTAGTCTCCGATCATCACCTTGCTTCACCGAAGATGGCCTCAGGTCAC
TCGCTGTCAAACCTTAATAGAATTGACCTGGACAGAGATTGAGCCTCCCCGGTAGCTGCCCGCTTCT
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SEQ ID NO: 1747 ACTTTTCCAGACACTTTTTTGTAGTGATGATGTTTCGTGAAGTATACTGTATT
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SEQ ID NO: 1748 ACAGTGATTGGCTATAGACTCTCGCCCCCTTCAGGGCAGACTGTCTCAGTTC
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SEQ ID NO: 1750 ACGCGGGGGGAATCAAGGATCTAATTCAGCAGCATGTAAAGTTACAAAAAC
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SEQ ID NO: 1751 ACAACATGACTTAAAACTTTTTTTTCTATTAAAACTTAAAGGGGAACAAAAAC
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SEQ ID NO: 1752 ACAAAGAATCCGTGAAGAGACTATTAATGTGACATGAATTATGGAGTAGAA
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SEQ ID NO: 1753 ACTACACGCACCTGGGCAACGACTTCCACACGAACAAGCGCGTGTGCGAGGA
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SEQ ID NO: 1754 ACAAAGATGACTATAAACAAGATGCAGCCCTCGGTTTCCATGAACAGCACAC
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NTGGGATCCGGNCTGANATTTTTNTCTCTGTTTAGAACTAAANAAG

SEQ ID NO: 1757 ACGCGGTTTCTACTTCAACAAAGAAAAATTTTGTAGTTATAGGAATAAGGACG
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TTTAGGATAAGAATGTGCCTCTCAAGCCTTGACTCCCTGGTATTCTTTTTTGTATTGCATTCAACTT
CNNTTACTTGAGCTTCAGCAACTTAAGAACTTCTGAAGTTCTTAAAGNTCTGAAGTTCTTAAACC
CANGGATCCTTTCTNAAAAAANAACGTGAAATCTTTCTGGACAGCCNTGACTGTAGCAAGGCTTT
GATAGCAGAGGNTTGGTGGNTCAGAGTTATATCAACTATCCCGGTTGNTGNNCTCATCCAGGGTTA
CCNTCTTCTGAGTTTGGTNGTATNTTTGCCCTCNCCCCNGANTATTTAAGCNGGTGANTTTNAC
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ATCACTGGNACCTTGGNTACNNTAGGNTTNTCNTNGNGNCTTANANGGGCCNCGNCCNN
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SEQ ID NO: 1758 ACTTTTTTTTTTTTTTTTTTTTTTTTAAAACTTTTAAACAATTTATTAGTCTTAT
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ATTAATTCCACATAAATATTTAAAATCTAAAAACCTCANATCAGCANACCGAGTCGAAATGTGATT
CTTCAAAGCAAGTATTGCTTTACCTTGCCTGAATGCAGTCCGTCATATGACCACTAACTTGCATG
TGACCAAATGTTTGCANAGGGTTTTTANATATGCTCTNGGGGAGCCGCATCCGCAATCCAAGAA
NAANATGTTGTTGAACTGCGTTGCACAAAGTTTCTTGACCTCTTCATTTACTTCAATCAGGTTGCAT
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SEQ ID NO: 1759 ACTAGGCCATGAACTGGGGCACTGGAAGTTGGGACATNCAGNCAAAAAATATC
ATTATTANCCAAATNAATNCTTNCCNGGGTTTTTTTNNATTGGCNGAATNAATGGGCCAAANGGAN
CTTTTNGCTGCATTNGGTTTTNATNATANCCANCCCACTCTTATNGNACTATNGATCATCTTCCAGT
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TNAAGCTGATGCNTTTGCCAAGAACTNNGGAAGGCTAAAGACTTATATTCTGCTTTAATCAAAC
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SEQ ID NO: 1760 ACCTGTGTTTCATATCTCGAACTGCACCAAGGAATAGCTCCATGCTAAACTGTC
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AAACATATTTAAAAGAGTCTATAGCATCTGTCCAAAAAGATTATATNCTATACAACCTATCAANTANT
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SEQ ID NO: 1761 ACATAGTGTGCGANCTCAAATCGGCATTTAGATAGATCCAGTGGTTTTAAAC
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CCTTTTTGCTGTAATTGCACCACTTTTAAAGCCTCTGGACAGAGCAGTATTTCTGTTTAAACTTTGT
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SEQ ID NO: 1762 ACTAAGTAGGTGAGAANCTGAAGTCTCAAGTGTTCATCTTCCAACCTTTTCCC
AGTCTGTGGTCTGTCTTTGGATCAGCAATAATGCTGAACAGCTACTATGGCTTCGTTGATTTTTG
TCTGTAGCTCTCTGAGCTCCTCTATGTGCAGCAATCGCAGAAATTTGAGCAGCTTCATTAANAACCTG
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NANGTAATNANCNTNACCCTGAATNTGAANCTGGTTACCAAANCNTCCNCCAGCCTAAAAATCAGG

SEQ ID NO: 1763 ACGCGGGCTAGGTGGCTTTGACCCCTGGGGGATTAATGGCAGTGTCAAAAG
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ACGTCTACGATGTGCAGGACATGTCCCAACAGCACAGAACTATCTGGCCCCACGTGTCAATAAG
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CCTNTTTCCGGGCTGCACTGGTTTGTGATCCATNTTANTTACTNCCGTGCAAAAAGAGANTGAG
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SEQ ID NO: 1764 ACTCTTTGGAAGCATTGGACTTGGCTTGATCGTAGGAGAATCCGGTGTCCAG
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AGGCAATCCAC

SEQ ID NO: 1765 ACGCGGGTGTGGAGAAAAGAAAGACCTCTATAAAGAAATGAAGAACCTTGC
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SEQ ID NO: 1766 ACCAAGAACCGCTTTATCCAGATTAATATAAGTGAAAGCCTTTAAATGCAGG
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TGCNCGACGGTTTTTGNATCCTGTGACCAAATGNNGAAGTANTGNATGANGAAGGGANCAAG
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SEQ ID NO: 1767 ACGCGGGGCTCTAATCTTCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCC
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TTCTGCTCCTTCTACATCTGCANATAAAGTGGAGAGTCTGGATGTGGATAGTGAAGCTAANAAAC
TATTGGGTTTAGGACANAAACATCTGGTGATGGGGGATATCCAGCANTGCAATGCATTNCAGNA
ACAGNTTATCCTTTTAATTAAGATGGAAGACAGCTAAANGAGNGTGGAGAACCTTCTTTTTCT
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SEQ ID NO: 1768 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCCATTTGCTATGTTTTATTTTGCTAGTA
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ANAAATAGCCTCCTTCTNTTTNTTAAAAANANTGTTCAAACCTCCCNAAATTAATCTNGANNATN
AACGNTAAATTTGGTCTTGAATCCCT

SEQ ID NO: 1769 ACTGCAAGACCCATTTTCCCTCCAGTTAATACACTNCCAGGATGGNCNGCAG
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ACNGNTCTGCCTTTGGGCGGONAGGAAGGAAAATTTGGATCACNACGGGATG

SEQ ID NO: 1770 ACATAGAACAGCCACAGCTGATGACAAAAAGCTTCAGAGTTCTCTAAAAAAA
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TTCATTTCAACAATCCCAAAGTCCAAGCTTCCCTTTCTGCTAATACCTTTGCAATTACTGGTCTNTGC
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SEQ ID NO: 1771 ACGCGGGGCTTTTTCTCTCTTCAGCGTGGGGCGCCACAAATTTGCGCGCTC
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TTTGGCAAATATGGTCCTGCCNANGTGGAAAACACTACAGGAAGNGAANCTCAGATATAAAAAATG
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SEQ ID NO: 1772 GGCACCTACGATGGTCACATTCATATTGGGCATTGGATCTATTTAAGCCTAGA
AGTATAACAGATAATCAGTTCCTTAAGTGTAATATGTTCTTAAATGTTTGGCCTTTTATCTGTTA
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GAGACGGGACTCTGGTCAGGTATAGTGTGTAGGCCTAGCCCATATATTAGGAACTCATAAATC
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AGGNAATGTCTTTAGCAACTTTGGAATCAGCACCTTTAANTTTGATTGNCTTACCCTATCAANAG
AACCAATNAACNNTTCTTTTTTNTGTCANGGAAAAAGAAANNGGAAACATTCTNTTTNTTTNCC
AAA

SEQ ID NO: 1773 ACTACCAGCTTTCACATCAAATTTGGAACGTGGAGGTGTGGAAAAGCTATTG
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ACTGCCCGCGCTCACAGTCTCGTCTGTCTTTTGGCTCATATCGTCAGGTAGCTAGTTTCGGTT
CAGCTGCTCCTCCAGACAGTTTGATGCATCTCAATTCAGCCAAGGCCCTGTGCCTGGCACTTGTG
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GAGGCTTTACTACCAGCCCTTNTGGTGGCACCTTTCCCTGAGCTTGGATTCTCCCCCANCTTTAAT
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SEQ ID NO: 1774 ACCCCTTTATTCAGTGTGGAACTCATCTCAAAGTAGAAGATGTGAGTG
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TCTGATCCCCAAGGAGTTCATATCCAGAAGCAAAAAATTAGCCGCTTTGTAGTTCCANAAATGTT
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SEQ ID NO: 1775 ACCCATCCAATGAGTCCCCNGAGCCTCCANAAGCTGTTGTCTCCTCTCTGGGG
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CTGATGTTTCTGAAAGTTCCAGGAANTNACACACCCGTTCCCCATTCTNACTTGCCACCCAGTTG
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TTNTATAAANTGNANGGCCTAANAATACCNTTTTCTGGTTGNAAAAACNTCAGCTNAANTTNTCTG
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SEQ ID NO: 1776 CANGTTTCCCAGCCCAGTCATTGCTTCATTCTTGTCTGATCAGATGGTAG
TTAGAAAAGAAGCTCTCTACATCCATCTTCTATACCAGGAAAGAGGAAGAGTGCCAAAAGCAGA
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AAATCTCCTTGGTTTAGTAACTCTTGTGGATTACTGCAGTTAANACAGAACTTCATATGATTGC
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ACCCTTTAGCAANACCTCGTCATCAACTCCCAAGATAGAAATNGGTATNTNGGTAGGGTTCAAN
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SEQ ID NO: 1777 ACGCGGGGACGGCAGGCGTCCGCGTCTAGCTAGTCGTTCTGAAGCGGGG
CCAGAGAAGAGTCAAGGGCACGAGCATCGGGTAGCCATGCCTTTCTTGGACATCCAGAAAAGGTT
CGGCCTTAACATAGATCGATGGTTGACAATCCAGAGTGGTGAACAGCCCTACAAGATGGCTGGTC
GATGCCATGCTTTTGAAGAAGATGGATAGAATGTGCACATGGAATCGGTTATACTCGGGCAGAG
AAAGAGTGCAAGATAGAATATGATGATTCGTAGAGTGTTCCTTCGGCAGAAAACGATGAGACG
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SEQ ID NO: 1778 ACCACTGAAACCTGACCCAGAAAAGTGGCTTGCTTGGACACCCAGCTGCCT
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CAAGAAAGAAATCAATACTGTGAAATATGCAGCAAGAAAGATTGGTCTTTACCTAGGCTGTGTTCC
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SEQ ID NO: 1779 ACTATTTTCATGGTCCAAACCTGTTGCCATAGTTGGTAAGGCTTTCCTTTAAGT
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CAGGTTTATCTGGGCTCTATCATATAAGACAGGCTTCTGATAGTTTGAACCTGTAAGCAGAAACCT
ACATATAGTTAAATCCTGGTCTTTCTGGTAAACAGATTTTAAATGTCTGATATAAACATGCCA
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SEQ ID NO: 1780 ACGCGGGGGAGGCGGCACTGGTCTCGACGTGGGGCGGCCAGCGATGAAGCC
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SEQ ID NO: 1781 ACTTTTTTCTTAATTTCACTGACTTCAGAGACGATTGCAGACTTGCAGTTTAA
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ACTGGAAGAACATTTTTATGAAGAATTTTGTCTANGAGAATATAACAGTGTATACCAAGGNTGTG
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SEQ ID NO: 1782 ACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTTTCATGTGTGATGAGAT
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TTAATGCTGCCCAGGACTCCACAGATCTGGTTGCAAAATTAAGAGCTTTTCATAATGAGGCCAGG
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SEQ ID NO: 1783 ACTCTGGATCCCAAGGTGACTGGTTGTTAATCGTGTGCATAGAACCAGCCA
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SEQ ID NO: 1784 ACCTCATAGCCCTGTGTCAATTAAGTTTTCAGCACTTTTGGGAACATCAGTTGG
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ATGCCACTGCACTCCAGCCTGGGCAACAGAGTAAGACTCTGTCTTAATAAATAAGAAAATA
AAACGGAACTGCAGTGCTAACAGTAATTTATACATTTTAAATGTTCTGAGTATGTTTGGCTGGG
CTAGTGTAACAATATACTACCCTGAAAGTGCAGTTTGGATTGNTGGTTGGTGTCTTTGGGTCANGA
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SEQ ID NO: 1785 ACTTTTTTTTTTTTTTTTTTTTTTTTGGAGTCAACAACTTCTATTTTTATTGACA
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AAGGTTTAATANCATAAGCCACCAGTNTCANAAAAACATACAGTCCCACTATCACTTTTANAGCTA
GAACCTTATCAAAAANAATTAGATCCTGCATTTGATCTGCTAANATAGAGGTTTAAAAATGGTTTAAGC
CATTTAAAGCCATTTTTATAATCTGTCTGATAACTCTGGGCAATTAANAAAAAGGAAAAATCCAAAA
CGTAGCCCTCTATATCATGTGGAATGTGAGAGAATGCCAATTATGACCAAGATANGTAAAAATA
AAAGTTTAAATCTATGAGNTGGAGCTGNTGNATCACTGCNAAATGTCAACCAACAGNGCTTATCA
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SEQ ID NO: 1786 ACTATGAACACCAGAACAGAAGAGATTTTTACTATTATGACACAAACACAG
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GTCTTCTCCACTTACTTAGATATCTGCAGGGGTGTCTAAAAGTGTGTTTCAATTTGCAGCAATGTTTA
GGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCTTGATTGTTGGTGAATCTCTGGGAA
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SEQ ID NO: 1787 ACGCGGGATAACCATGCACACTACTATAACCACCTAACCTTAACCTTCCCTA
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SEQ ID NO: 1788 ACAAAGAAGCAGCTCAGGAGGCTGTAACTGTATAATAATCATGAAATTC
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AGTGCTGTTTGACGCAACCTTGCCAATCTGTAAACAGAAAGAGATTTTANAAAAGGCATTTAGTCA
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SEQ ID NO: 1789 ACCAAAACAGACATATAGACCAATGGAACAGAACAGAGCCCTCAGAAATAA
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SEQ ID NO: 1790 ACTTGCCCTCATAGCTGGTGAAGGATTCTTCTGAACCCCAACCTACCCCTAA
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SEQ ID NO: 1791 ACTATTAAGAAAAAGAAGATTGATTCTTAACCTACTGAATTGTGCAGATACA
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SEQ ID NO: 1792 AAAAAATTGCCACAAAAACGATGTTGATGTCCAAATTGACCAGGAGTCCTA
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SEQ ID NO: 1793 ACCCACAGAGACTGAGAGTTGGTGCTGGTGGTTGTGGTGGCAGATGATATTA
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SEQ ID NO: 1794 ACTTGAGTCAAAGACGACATTTAGATTCTTCAGCTTTGAAGCATTTAGTAACA
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SEQ ID NO: 1795 ACATTTCAATAGCACGTTTCATCCTCCTCATTAAACTCGTCTTCATGATCCTCCA
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SEQ ID NO: 1797 ACGCGGGAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGACCC
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SEQ ID NO: 1798 ACAAAGGAATGTTTCCTTTATAAATCACAGAAGAAAATGACAATATCTGTT
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SEQ ID NO: 1799 ACGGATCTTACTTCCTGGCTCCACGCGTCTGCTGGTGATCCTGCCGGGGGA
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SEQ ID NO: 1800 ACTTCAACCAGGCACTCCAGGCCGGGACCGTGTGGGTAAACACCTACAACAT
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CAAGCTGTTTTAAAGCCAAGAACAACCTTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCACA
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SEQ ID NO: 1801 ACTTTTATATATACTATCTATGAAGAATTCATAAAGCATGAATCACCTTATA
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SEQ ID NO: 1802 ACCCATGGATCTCTAGCATCAAGAACTTGAACACAACATCTGATGAATCTA
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SEQ ID NO: 1803 ACGCGGATTGCAGCATTATTTCAAGTTCAAAATGAACTATATGCCTGGCACC
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SEQ ID NO: 1804 ACTCAGTCTGAAAAGCTAACAAATACTGCATCTAACCACTCAATGGACCTTA
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TCAACCAACAGGTCTGAACAGGGCTTTCTGGTTCTGAAATAGAAAATCTGCTTGAAAGACGTA
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SEQ ID NO: 1805 ACAGAGTCGCATCCATTCTTTTTGAACAACATGTAGCATGTCTGCAACAGTGG
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SEQ ID NO: 1806 ACCTGTTGTACGCGTCTGTGTTGCCCTGAGCCGCTGGCTGTAGAGAAGGGC
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SEQ ID NO: 1807 ACGCGGGGCTTCAAGCAACAGCGACGCAAGATGGCAGCCACCACGGGCTCG
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SEQ ID NO: 1808 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGGNGGCCACCACATCTTTATTGCATACT
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SEQ ID NO: 1809 ACCAAGTCCAGGTATAACATTCCTATTGGAAGCCATACTTATATTTTCTTGTA
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SEQ ID NO: 1810 AAACATGATTTTGGCCTAAAGAACAGCTGAACTGTTGAGAGAAGCAAGGGCT
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SEQ ID NO: 1811 ACTTTCCTTCATCGAATGATTATTTGCCTGGAGGAAGAAGTCTTCCGTTTCT
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SEQ ID NO: 1812 ACACAGTTTCAGAAAAACNAGGAATGAATACTATTGATGNCTGGTGGCTTT
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SEQ ID NO: 1813 ACCAACAGAAAGCAGGCCAGGCTCCCACTCTCATCTATGGTGCGTCCAC
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GGGAGGCCAAAGTNCCTTGCCGGGCGGNCNTTNAAGGGTG

SEQ ID NO: 1814 ACGCGGGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACG
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SEQ ID NO: 1815 ACAGGCCCTTTGATGGCTTGGGTTACAGACAACCTCATAGCTGGTGCACCAC
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SEQ ID NO: 1816 ACTTCAAGTTAAAGTGAATAACCACTTAAAAATGTCCATGATGGAATATTC
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SEQ ID NO: 1817 ACTTNTTTTTTTTTTTTTTTTTTTTTCTGGACAGGAAGTANAATTTATTGGTGA
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SEQ ID NO: 1818 ACTTTTTTTTTTTTTTTTTTTTTTCCGGAATTTCTTTATTTTTTACAAA
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SEQ ID NO: 1819 ACGCGGGGACTCTGCGCTTCACCATGGCTTTCATTGCCAAGTCCTTCTATGAC
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SEQ ID NO: 1820 ACTTTTTTTTTTTTTTTTTTTTTTCTATGNAACTGTCCCTCATCCTTCACCA
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SEQ ID NO: 1821 CGATCGAAGGGACTATGTCTTCATTGAATTTTGTGTTGAAGACAGTAAGGAT
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SEQ ID NO: 1822 ACCTTTGAATCTCTGTTACCTGAGGAAACAGCATTCTCAGCTTCTTGGTGCTC
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SEQ ID NO: 1823 ACAGTTATGCTCAGATGAACACTGGACCCATGTGACAGGGTCAAGCAACTAG
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SEQ ID NO: 1824 ACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATTTACAAG
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CTACTCGGAGGCTGAGCAGGAGAATCGCTTGAATCCCGGAGGCAGANGTTGCAGTGAGCCAA
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SEQ ID NO: 1825 ACTGTTTACCAAACCTGAAGGTGCAGTGCTTGAATATTTTGTCTTGGGTGTCA
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SEQ ID NO: 1827 ACCTGTCTTTTCTTTTCTTTTCTTTTAAATCATAGTTTGTCTTACCTGAAAGTTG
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SEQ ID NO: 1828 ACCCGGCTCTGCATCGCGTCGCCATGATGGGCCATCGTCCAGTGCTCGTGCTC
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SEQ ID NO: 1829 ACACTTTTGTACAGTTACATATATGAATAGTTAGCAGAGGAGAACTCCTCC
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SEQ ID NO: 1830 ACTTTATTTTTTTGTTTGTGTTTTTCTTTTGGATCTTGATTGATAACTGCCAT
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NCTANGGCG

SEQ ID NO: 1831 ACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTCAGAGGCCCGTGAGGACA
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SEQ ID NO: 1832 ACAAGCTTTTGTCCAAAAATGGCACAGCGAGCACAAATGAGTTCCTGTGTGAT
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SEQ ID NO: 1833 ACTGCCCGACTTCCTCATCTTACTGGGTCCAGCATAAAGCAGATGTCCACTGT
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SEQ ID NO: 1834 ACTATGCTATGTTGGCTAAAACCTGGTGTCCATCACTACAGTGGCAATAATATT
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SEQ ID NO: 1835 ACTCAATCTGAAAGATGTAGAAGAAGGAGATGAGAAATTTGAATGACACCC
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SEQ ID NO: 1836 ACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCTCTGG
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SEQ ID NO: 1837 ACTGTGTGGCGCCTTATTCTAGGCACTTGTGGGCAGAATGTACACCTGCCG
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SEQ ID NO: 1838 ACTTTTTTTTTTTTTTTTTTTTTTANAACCTNTGCAATTATTAGTTTATTA
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SEQ ID NO: 1839 ACAGAAGTTTTCATCTATGAACATGGCCTCATCATCACCTGCAGCCTTGGCCT
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SEQ ID NO: 1840 GCCCTTTACATCGCTGAGAGCCGCTGTCTTGTTAGATGGCTCTGGATTAGG
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SEQ ID NO: 1841 ACGTGCACCTCCTGTTTCAAAAACGCAAGCAGAAAATAGGTCTGGACAAGGG
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SEQ ID NO: 1842 ACGCGGGGCTTTTCTCTCTTTCAGCGTGGGGCGCCACAAATTTGCGCGCTCT
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SEQ ID NO: 1843 ACTACCAGGTATTGGTTCGTTTACAATTATTGATGGAAATCAGGTCAGCGGA
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SEQ ID NO: 1844 ACATCCTACCCCTCTCCCATTTCCAGAGCCACCTAAGAGAAGTAAAAAATA
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SEQ ID NO: 1847 TTCGCCCTTTTTCTTTGCCCCGGGCAGGTACTGNAATTGAGCATCCGGAATA
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NCACAGCTTGTATAATGTAACCATNTTGGGGTCCCGCATNTAACTTNGACAANTGNAACTCCNT
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SEQ ID NO: 1848 GCGNGNTTGTGTTTCGAGGNACCTCGTTTTTCAGGTTTCATCCATCTCCAGTGGA
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SEQ ID NO: 1851 ACCGCGGGGGCGTGGCGGCGGTGGCGGCTGCGGCAACAGCGGGGCCGATGT
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SEQ ID NO: 1853 ACCTGAGGAAGCGGTTTGGAGGCCAGCGGATCCAGGTCTACCTTTCCCTTCTG
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TGGCCTTAGGCCTGAATCTGTATTTAGCCATCTTTCTCTTATTGGCAATCACTGCCCTTACACAAT
TACAGGGGGCCTGGCGGCGGTGATTACACCGGACACCTTGCAGACGGTGATCATGCTGGTGGGG
TCTTTAATCTGACTGGGTTTGCTTTACGAAGTGGGAGGCTATGACNCCTTCATGGAAAAAG

SEQ ID NO: 1854 ACTCCAGCAAGAGGAAATATGACACTCCCAAAACGAAGAAGAACTGATTGG
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GACTCCAAAGGGTATCTTAAATGCAATCTCTTCTCTTAGCCCTTGGCCACTTTNTCCTGGATCCT
GCCCTGCTCTCAGCCATAGTGAAGGACCNCCCTAGGAGTCTGCGAGAGCCCTCCTTGGTTCCATCGT
GAAGCCATAAACAGGAATGCCTTTGGNNATAACCTTNNANCCTAGAGGGGCCCTCTGNTNCCCN
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SEQ ID NO: 1855 AAAAAAATTTGAAAGTGTGACAATGACAATTATGAAATCCTGTGACTGAAAG
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ACTAATGCAAAACCAAGTGCTACCCAGAAGCACCAACACGTGTGTTCTCCATTCCCAATCACAGA
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CTTCTTACTACAGATGAACACGACGAATAAACCCAGCAAAAAGAGAACTGCATACCTTAAATTTA
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SEQ ID NO: 1856 ACAGTTGGAGTCTGTGTGTTTCTTGAATGTTTGAGACAGCTTCACTTGAAC
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SEQ ID NO: 1857 ACAAGTTCGGCTTTGAGCTTCTCAGGGGCCCTCTGGGAACATCCTTCAAAGG
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SEQ ID NO: 1858 ACGCGGGACACTTGGCCAACCATATTTATTTTTATTTTTATTTTTATTTGA
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ACAACATAATGAGAAAAGAAAATACAAAAATTAAGGGGTGTGGTGACACATGCCTGTAGTCTCAA
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SEQ ID NO: 1859 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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CGGGCGTTCACCTTCGCGAAAATTTGACCAGCTTTTACATAGGCTTTCAATCAAAGCTTCTTGCTTG
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CCNCCGCGT

SEQ ID NO: 1860 ACTGTTTTTCAGTATTTGGGGAGGGTGGTTTGAGCAGCATTTATTGACAATTT
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N

SEQ ID NO: 1861 ACGCGGGGAGGAAAGCCGTGCGTTGCGTTCCAAGGCATCTGTGAGCCCGGG
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CGGCGGGCGNTCGAAAAGGGCG

SEQ ID NO: 1862 ACATATTTAATTATGTAAAAATATTAACACCACCATTACAAAACTTCTAAAA
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SEQ ID NO: 1863 ACGCGGGAGAGGTGGTGGGGACCAGGGCTATGGGAGTGGCAGGTATTATGA
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SEQ ID NO: 1864 ACAAGTTCACACTCGCCCCACGGGCAAGTATATCATAGAGGGAGGAAGCCAC
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SEQ ID NO: 1865 ACCCAAATATAAAATACTTGTTTAAATGTAGAGTTTCATATCCTTTAAACCTC
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SEQ ID NO: 1866 ACACCTTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAGGGCCGGA
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SEQ ID NO: 1867 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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SEQ ID NO: 1868 ACGCGGGTATTGAAGGTGGAGTAGCAACCGGGCATTATATTATCTCTTGAA
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SEQ ID NO: 1869 ACCGGGGGAGGCAAGATGGCGGCAACCAAGAGGAAACGGCGTGGAGGCTTT
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SEQ ID NO: 1870 ACGCGGGGCTAAGTGTTCGGGTGGATTCCCAGGGACTGTGCGAGGTGTGGA
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GGGCG

SEQ ID NO: 1871 AACAGTTGGAGTCTGTGTGTTTTCTTGAATGTTTGAGACAGCTTCACCTTGAA
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SEQ ID NO: 1872 ACTTTTTTTTTTTTTTTTTTTGGTAGTTCTCACAGTTTAATAGAAAGAATGCA
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SEQ ID NO: 1873 ACGCGGGATCCAACCCTGAAGATATTTAGAGATGGTGAAGAAGCAGGTGCTT
ATGATGGACCTAGGACTGCTGATGGAATTGTCGGCCACTTGAAGAAGCAGGCAGGACCACTTCA
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GAGCANAAAATGACCACTGGCAAAATTAAGAAAGTTTATNCAGGAAAACATTTTGGTTCTGCCCT
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SEQ ID NO: 1874 ACGCGGGGACCGCGGGGCGGACGGGAGCGAGTATGTCCGCTCTGACTCGGCT
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TGGAGTCCGTCATGCCGGTGGTGGTGTACTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

SEQ ID NO: 1875 ACGCGGGAGGAACTGCTCAGTTAGGACCCAGACGGAACCATGGAAGCCCCA
GCGCAGCTTCTCTCCTCCTGCTACTCTGGCTCCCAAGGTTCCACTGGAGAAGTAGTGATGACGCAG
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ATTAGCACCAACTTAGCCTGGTATCAGCACAAACCTGGCCAGGCTCCCANGCTCCTCTGTTTGGA
ATAGACACTAGGGCCACCGGCATCCAGCCAGGTTCACTGGCAGTGGGTCTGGGACAGAGTTTAC
TCTCACCATCAGCAGTGTNCANTCTGAAGACTTTGCAAGTTTATTATTGTCAACAAGTATAATAAGT
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GTNTTATCTTCCGCCATCTGATGAGCCAATTGAAAATNTGGAACCTTGNCTCTGTTGTGGCCTGC
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SEQ ID NO: 1876 ACGGATGTGGCAGCGAGAGGACTAGACATTCCTGAAGTCGACTGGATTGTTT
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CCAAAATCTTTAAACACATTTAGCAAGAAATTATTCTGACAGCNGGC

SEQ ID NO: 1877 ACGTTGAAGGACTTTGCTGGGTTCTGAGTGTTTGTCCCTCACATAGGATTCCA
GAACAGTGCTGCTGGGTTATGAGCGTTTGTCCCTCACATAGGATTCCAGAACACTGATACTAAGGT
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TGCTACAAAATTTCTGAACGTTTGTGCTCACAGAGGATTCCAAGAACACTGTGGCTGGGTTGTGTT
TGCCCCCAGATAGGATTCCANAATACTGCTGCTGGGTTCTGANTGTTTGNCTCACGTANGATTTC
CAAAACACTGCTATGANGGTCTGAATATTTTGCCTCTTAAAGGATTCCANAACACTGCTGCTCA
GTTGTGTGNTTGTCCCTACAAGGGACTCCAANGNACTGNTGCAGGNTTTTGAANNNTTTTCCC
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SEQ ID NO: 1878 ACAGATGGTGATTACAGAAGCCAGAAAGGTTGATACCAGAGCCAAGAACGC
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ACAGCCAACTGCGGCCCATGATGTCAGAGCTGGAAGAGAGGGCACGTGAGCAGAGGGGCCACCT
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SEQ ID NO: 1879 ACGCGGGGTTGCAGTGAGCCGAGATCATGCCACTGCACTCCAGCCTGGCGAG
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SEQ ID NO: 1880 ACATCCATAAGCCAATTCTTCACTAATTAACAAGCATCAAAAGTTCCAAGT
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AATTTACGAGCAGTAGCTTGAATTTCTTCTGCTGTTGCGNGAACTCAAACTAAATCCCAATCCT
GGTTACGTTGTGCTGATGGCTTTTGTATGCTGTGATCTCCAATGAAAAACGAGAAATACTTCTCAGG
ACCCTGCAGCATCGCCGAACCCGCTGCCATGTTGGCTCCCGTTCGGGCCACTCGGACAATAATA
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SEQ ID NO: 1881 ACTTTGTAGAGATTGACTTCTAAGCTACTTAAGACAATTGCACCACTAAGA
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TGTTTAGGTAATAAGAAATATTAAAGTAATTGGCTTTAGATTTTGTAAATTTTTCCTGTGATCTCTG
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SEQ ID NO: 1882 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAAAAAGTAGTTAGCATTTAATGAAA
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SEQ ID NO: 1883 ACTTTTTTTTTTTTTTTTTTTTTTTTGCATTCTTTTGAATGTTTGGTCATTAAC
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SEQ ID NO: 1884 ACACAAAGAGGGGGTGGGTGTGCGATGAGAGTGTGTGGCCTGATGCTCCAC
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ACCGAATTCCTCTGGCTTACAGATGACCAANTCGGCCCACTGCACCACCACGATCTGACNAAGA
AGGCTGTGTGGCAGGTGAACCTCCACGATTTTCTCTGNTCATAGGGTCCACTGGCTGCCCTAGC
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SEQ ID NO: 1885 ACACTGTTGGTGTATATGGGGATGGGGTTCTCGGTAATTTTGTATTATTTA
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GAATTGATAAAATCACCTGGGATTAGTTGTATAACTCTGAACCACCAAACCTCTGCTATCAAGCCT
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SEQ ID NO: 1887 ACAGTTGAAGGTTGTGACCGGACATTTGTATGGCCAGCTCACTTTAAATACCA
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SEQ ID NO: 1942 ACGCGGGGCCCTACTGCCGATGCCAAATATTTGAGAGAAGGGAACCTTTTGCT
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SEQ ID NO: 1943 ACAAACCAAAATGTTNGTTACTATAACTTCTGCATCACAATTAATAATCCAAA
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SEQ ID NO: 1944 ACTAAATGCACAATTTAAACATCAGTTATACACTGTCATTAGTTTTCCTCTTA
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SEQ ID NO: 1945 ACTTGGCAGGGTCTTGCCACAGACACATTTGGCTCCAGGCTGCAGTTCACAG
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SEQ ID NO: 1946 GGGGCAAGACTGTGGATTTACGCAGGATAGTAATTATTTGTTAACCGGGG
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SEQ ID NO: 1947 ACTTGTGTGAACCAACCAAGTGTACTTTGCAGAAATTGCACATTAGAATA
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SEQ ID NO: 1948 ACTCAGTATAAATGCAGATGCTTATGACAGCGACATAGAAGGCCCATGCAAC
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SEQ ID NO: 1949 ACACACCTTTGTCCCTGGGTAAATTATATTCAATTATGCCCACTGATGCAGCAC
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SEQ ID NO: 1950 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNNAGGANNGAANNNGGTGACAACT
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SEQ ID NO: 1951 ACTTTNTTTTTTTTTTTTTTTTTTTTNGAGAAATGTAAACTCAGTTTAATTCA
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SEQ ID NO: 1952 ACCATCGCACACACTATTGACGTCATTGGAAAGAAGGAAGACGACTTTGTCT
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SEQ ID NO: 1956 ACAGTATTCATTTATGCTTGAAATTCAGTCTAGACCAAGCTTGTGGCCACC
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SEQ ID NO: 1957 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGGCTTNTGCTGAGGGGGCA
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SEQ ID NO: 1958 ACACATACACCTAAAGAGTCATGGCCTTCTTAAACAGCTTTCTTAATCCTT
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SEQ ID NO: 1960 ACATAGTGTGCGGAACCTCAAATCGGCATTTAGATAGATCCAGTGGTTTAAAC
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SEQ ID NO: 1971 ACTTCTGATAGCTCATCACTTTCTGTGTCAGAACTTTGAAAAGCAAAGACAGG
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SEQ ID NO: 2005 ACACCTGAAATCCAGGCCAATGAAGTTCGGAAAAGTGAAGAAATATGAACAG
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SEQ ID NO: 2006 ACGCGGGGAGGTAACAGCTCTTGACACCTGTTTCTTGCACCTGACGTGCAGC
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SEQ ID NO: 2007 ACGCGGGGTCTCTTCTCGGCGCTGCCTACGGAGGTGGCAGCCATCTCCTCT
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SEQ ID NO: 2008 ACAAAAATTTAAAGCATTCTTTCTTAATTTTGTAAATCTTTACTGTGGAATA
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SEQ ID NO: 2015 ACTTTTCAATCCAAGAAAAAATAAACCGAGACATGGTCATGAGTTCAG
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SEQ ID NO: 2016 ACCAGAAGTATAAGTTTATGGAACCTCAACCTTGCTCAAAAGAAAAGAAGGCT
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SEQ ID NO: 2021 ACGAGAAAAACGATTTGGAAATTGGCTGAAAGATGCACGTGACTGGACAATT
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SEQ ID NO: 2023 ACGCGGGAGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCCGC
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SEQ ID NO: 2024 ACATGCAAAATCACTGGCAAAGGCTGTAAAGAGATTGTAGGCTGGGGATTTC
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SEQ ID NO: 2025 ACAAGACATTTCAATTTCTTAATGTTTACAACAAGCTTGTGCCAGGGCTGA
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SEQ ID NO: 2034 CCCTTAGCGTGGCGCGGCCGAGGTACAGATCCGAAGTTTCAAGGGCAAACGT
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SEQ ID NO: 2036 ACGCGGGGCTCTTCCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGA
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NAAAAACNCAGANAGGTGTGTTGGGGCCAACCAATANNAANAGAGCATGCCTGTTCNCANAA
TTTATGGATNTTCTCTG

SEQ ID NO: 2037 ACCAAAGAACAGATAAAAGGAGGAACAGGAGACGAAAAGAAAGCGAAAGA
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SEQ ID NO: 2038 ACCTGGAGTGATGGATGGCGTTCCCTCGGCTAATAACTATCAGGGTGGATTT
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ANCTTTTAAANGTTGNNCCAGCTCTCACTAANATGAATATTNAAATCNGNTTNTCTGTTNNTTTAA
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SEQ ID NO: 2039 ACCAAAGAACAGATAAAAGGAGGAACAGGAGACGAAAAGAAAGCGAAAGA
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SEQ ID NO: 2040 CCCTTAGCCGTGGCGCGGCCGAGGTGGACCTTCAGGGGATCAAAGCAAAGTT
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SEQ ID NO: 2041 ACGCGGGCGCTGTGGAAATTTGGGTCTTGGGCTGGGTGGCATCTGGCAGTCAT
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SEQ ID NO: 2042 ACGCGGGACTACTGGAANTGCACAACTGGCCACTGACAAAAATGACCCCC
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GTACC

SEQ ID NO: 2043 ACGCGGGGAGTCCGCTGGTCCCGAGCAGAGCTGTGAGGGGATTCACTTGTG
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SEQ ID NO: 2044 GCGTGCGCGGCCGAGGTACCCCTTTCCATAGAAGGGGGAAGCCCTCTTTC
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SEQ ID NO: 2045 ACAGAGTGACATCGGCAGTTGCAGCAGCAGCAGTAGCGGCAGGAGGAGGGC
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SEQ ID NO: 2046 ACGCGGGGCGAGTGAGTTCGACACACCATGCCGACTGTCAGCGTGAAGCGTG
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CCATTTGNT

SEQ ID NO: 2047 ACGCGGGGGTAGCCGGAGCCGGCGACGTGAGGCGGGCGTTGCTCGCGCGAC
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SEQ ID NO: 2048 GCCGTGCGCGGCGGAGGTACTTTGGCCTCTCTGGGATAGAAGTTATTCAGC
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SEQ ID NO: 2049 ACAAGTTTGAAGTGGATACCTCTGAAAGAAAGATTGAATTTGACTCTGCCTGT
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ACTCCAAACAGGAAATTCAGCACCTGTTCCGCGAGCCTGAGAAGAGGCCCCCACCGTGGGTGT
CCAATACCTTCACTGCCCTGATCCTCTCGCCGTTGCTTCTGCTCTNCGCTCTGNGGATCCGGATGG
TGCCAATGTCTCAAACCTTAACTTTTGCTCCTAAGCACGATTNTATTTACCTGGGGACATTGTCTG
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SEQ ID NO: 2050 ACTGAAAACATGAAAAACAGCAAAATCCAAGGGTGAACTTTGACCTANATTG
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SEQ ID NO: 2051 ACTGCAAGACCCATCTTCCCTCCAGTTAATACACTCCCAGGATGGGCTGCAG
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GGAAAAGGCATTGTATTAATAGATACTGCTGCTATAAAATGACATNAAATTATAGCCCTTGATCTG
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TTTNTNAAGTCAAGTGCTTNTTTTTCCAAAAATAATCCTNTGAAATC

SEQ ID NO: 2052 ACCTTCTTTTCAGAAGTAAAGCCTGCAGGCCCTACTGTTGAGCAGCAGGGAG
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TTTCCANN

SEQ ID NO: 2053 ACACATTAAGCATCCCCAGTTCCCTCGCACACCCCTTTTCCAGCCACTAGT
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SEQ ID NO: 2054 ACTCCAGATGGCGCCAAAGAATAAATAGGCAGGTCTCTATGATAAAAGAACA
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NTTA

SEQ ID NO: 2055 ACTAAAGATGATGATTNNTTNGTGGNATGCCTGAAGGGGCGNGCNCATTCA
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SEQ ID NO: 2056 ACTTNNTTTTTTTTTTTTTTTTTTTTTTTTTGGGTAAGGGCCGCAAACTGCTGCAA
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AAN

SEQ ID NO: 2057 ACTGTAATCCAACACTTCTTTGTTAGCACAGCCACCCAGTCCCACACCCGGG
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SEQ ID NO: 2058 ACAAACATGGGTGAGCAAAGTTCAACTCAGGTAATAAGTGATTAAAAACA
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SEQ ID NO: 2059 ACCATTTTATTAGTGTGTAGGAAATGTTGGGTTACTTCTTAAAAACGAAAC
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GANAT

SEQ ID NO: 2060 ACCCATCATTACTCCCACTNAGAAAGAAAGAAAGTAAATGAATGTGGTGAAAGT
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NAAA

SEQ ID NO: 2061 ACAAGATCTACCCCGGANTTTGGAGGCGCTACGCCAGGACCGACGGGAAGG
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SEQ ID NO: 2062 ACCTGTCTTTTCTTTTCTTTTCTTTTAAATCATAGTTTGTTTTACCTGAAAGTTG
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SEQ ID NO: 2064 ACATATAGGTGGAATGAATTCTATCCTTGACATACTGAGGCCAAATTACAGC
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SEQ ID NO: 2065 ACTAAGTAAATGTTCCTGCTATTATTTTAAATTATTTTAAACATCTCATT
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SEQ ID NO: 2066 ACGAAGAAAGCATTTCCCAAGCAATGAGTCTCTTAATGGAAAAATAAAAGA
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SEQ ID NO: 2067 ACCAGCTACTGAATACACCGGATCTAGATATGCCAGTTCTACAAATCAGAC
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CAGATAGACAAGCAGAGATGTCCAGAAATTTAACCCACCTCCATCCTATGCTGCTACAATTGCTT
CTAAACTGGCAATTCACAATCCAAATTTACCACCACTGCCAGTTAACTCACAAAACATCCAAC
CTGTGAGATACAATAGAAGGAGTAACCCGATTGGAGAAAACGACGCATCCACTACTGCGATTAC
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SEQ ID NO: 2068 ACTGCACGGCAATTGAAGCATAGCTACTACAGAATAACTCACCTTCCAACAA
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ACGAGAATAACCATGATGGGTCTAAGACTTGGGAAAACTGGCCTAAATTATGNTGGAAGGGAATT
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AGCTTCAATCACTGGCATTATTCTAATCCTCTCCTCTTAAATTTAAGTTATGANGGTTATGGCAAA
AGCAACATTTGCAAAATGTCCCTCGGNCGCGACCCCGTTAANGGC

SEQ ID NO: 2069 ACTTNTTTTTTTTTTTTTTTTTTACCATGCAACGAAACCTTTATTAACATT
TTGAACAGGTTGAGCTATTACTGAAACTTGTAATTTCTAACTTAAGTTGGGGCAATGGCTATAG
TGCAGAATAATGCCATCACTGGGCACTGCGAATGCCATGACTGAAAAATTAACAGCCACCCNTNA
GGCGCAGGACCAGGTGCAGGTCCACTCTTCTGGATGTTGTATCAAAAAAGANTGCGGNCATTN
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ATCTTGGCCTTTACATTTTCGATGGGTGCTGCGCTCCACTCCAAANTGATGGTCTTGGCGGCA
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GGGAAGGGATGCCTTTTTTTTNTCCTGGANNTTNGCCTTTAAATTTTCNATGGGGNNTAACTGGGCT
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SEQ ID NO: 2070 ACAAATCCCAATTGCACCATTAATTATGGGGTCACATCCAGTTGACAATAA
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AAATTTCCCGAGCCAATCCCAGTATCTAGAGCATTGTGCAAACTGCANAACTGCACAGGAATTC
CATTGTTGAAACTCAACCACTTATGCCCCGTGATGAACTGATCACTCANTTTGAGCTATCAAAG
GACCTGACCCCATACCTTTGAATCACAACATGAGATTTTATGCTGNTCTTCTGGCAAGAACACT
GCTATTTCTCAACAAGGATGCTCCTCTTCCAGATGGCCGAAGTCTACAGGGAACCTTGTAGCA
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CCAAATTTGAANTGNCCCTTTTCAAAGTCTCGTTAACNTATTTTNTNANNACCCCTGNTGAATG
ACTCC

SEQ ID NO: 2071 ACTTGTGGGCCAGCTTAAGCAGCTGAGTAGCTGTTGGCGGTCCAGGGCCTG
GGTGAACCTGGTTAATCGCAGGAAGCACTTTCACCCGCTTATAGAGGATGGGCTCTGCCCCGTGC
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CTGNTTTTTTAACNAAAAGCTTGGGCCCGGAACCCACCTTTTTTCTTTGGGCTTTTTTCTTTNC
GCATTCTTGGGCCGCGGGAAGAAAAAAACCCCNNTCCNTNGGCCGNAACACCTTAAGGG
CNAATTTCAANACACTTGGGGCCGTACTTANTGGANTCCNAACCTTNGGNANCA

SEQ ID NO: 2072 CACTACAGAGCAGTTGGGGTATGATGGGCATGTTAGCCAGCCAGCAGAACCA
GTCANGCCCATCGGGTAATAACCAAAAACCAANGGCAACATGCAGAGGGAGCCAAACAGGCTT
CGGTTCTGAAATAACTCTTATAGTGGCTCAATTCTGGTGCAGCAATTGGTTGGGGGATCAGCAT
CCAATGCAAGGTCGGNCAGTNGGTTTTAATGGAGGCTTGGCTTCAAGCATGGTTTTTAATCTTTN

TGCTGGGGAAATGTAAACAGGGGGGGTTGTGGNT

SEQ ID NO: 2073 ACCCTTCNCNTTACCTATGCCCATGTGCCTGCCCTTCCGGCGGGGCCAAGGTGT
TTTCCGGCNCCTGAGCCCGGGGAATGGACCGTCACAGGCTTGGCGATGATCAGCCCATCTTTTGAT
GANCTTNCGGATCTGCTGACGGTAAGTTGGCATTGGGCGATTANATTGGTNTCATTGGTNGTCTA
NCCACACCTTTNTTTTTTGNAC

SEQ ID NO: 2074 ACTTTTTTTTTTTTTTTTTTTTTTCTGGCCATTCTTGGCACTGTTTCTAAAG
AAAACTCCATTATCCCAAGCAAAAAGCACAGAAGGTGGAGTTTGGCTTCAAGAGATGTTAACTC
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CCTCAGNGAAAGGTGAACCCATTGGGGGTGGCATGTACCTCAAGAATTAACCCCACTTAAAAA
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GCNCTGGTTNTGAATNNGGANACCCAAAATNTTNCNCTGGTATGAACTTTATGGCTCNATCC
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ACNTTNTNTTGGCANCCCAAANGAAAGGACCTNNTATTCCCATTTAGACTTNCCC

SEQ ID NO: 2075 ACCCTTCNCNTTACCTATGCCCATGTGCCTGCCCTTCCGGCGGGGCCAAGGTGT
TTTCCGGCNCCTGAGCCCGGGGAATGGACCGTCACAGGCTTGGCGATGATCAGCCCATCTTTTGAT
GANCTTNCGGATCTGCTGACGGTAAGTNGGCATTGGGCGATTNNATTGGTNTCATTGGGNGTCTA
NCCAAACCTTTGTTTTTGNCA

SEQ ID NO: 2076 ACCCTCTCTTGTCTCTTCAGGAATCAAGGGTCTGATGCGGCAAGGATGA
AGTTTTAGGAAGCTCTGGGTCAACGCTCTGCCCCCTGGCATTANAGATANTTGGCCAGTGGGC
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ATCCTCCAAATGNACCANGATTAATGGTCAAATNTATGGCTCNTATA

SEQ ID NO: 2077 ACTTTTTTTTTTTTTTTTTTTTTTNNCTGGGAAAAATGTTTTATTCCTCTTTG
CACAGANCAGTTNATGAAGNGGTTTTCTCCTGACTCCATGCATCTTACACAAAAGATGCCCCCT
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SEQ ID NO: 2078 ACACAATGATATAACCAGCTATAAGTTTAAAAGCTTAAAGCACTGTGTGAGT
GCTGGAGAACCAATTACCCCTGACGTGACTGAAAAATGGAGAAACAAGACGGGCTGGATATCTA
CGAAGGATATGGACAGACTGAAACGGTGCTAATCTGTGGAAATTTTAAAGGAATGAAAAATTAAC
CTGGCTCAATGGGAAAACCTTCTCCTGCTTTCGATGTTAAGATTGTAGATGTAAATGGCAATGTTT
TCCTCCTGGACAAGAAGGGAGATATTGGCATTCAAGTCTACCCACCGCCATTTTGGCCCTTTACTC
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SEQ ID NO: 2079 ACAAACACGGATCTGTGTCAGAAACACATGTTGAGACTCCTCCATTCTTC
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AAGCAGAAGATTGTTGAGCAGATTTAAAACCGCTGGNAAC

SEQ ID NO: 2080 ACAAGCACTTAATTAAGCAGAAAGAGCCCAAGAAGAAGGAAAAAGTGG
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SEQ ID NO: 2081 ACGCGGGGGTCTCTGGTTTCTGGCCCTTGTCTGCAGAGATGGCTCCCAATGC
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TGGGNANTNTGGT

SEQ ID NO: 2082 ACGCGGGGAGAGCGCCGAGGAGCCGGTCTAGGACGCAGCAGATTGGTTATC
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ATGCTCATTATTGGGGATGTGCATTGCCATCTTTGCTGTGTGGNCTCCACGCTTGCTGGGACAGA
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SEQ ID NO: 2083 ACGCGGGGAGAGCGCCGAGGAGCCGGTCTAGGACGCAGCAGATTGGTTATC
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NAAANGNTTNGGTTNGTNTGGGTATGGTTTGCTACGNGGGCTTACAAACCCAAATCATAAAGGC
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SEQ ID NO: 2084 ACGCGGGGACGCTCGACCCAGGATCCCCCGGCTCGCCTGCCCGCCATGGC
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CCTGCNNAATTTCTCTGATNTTCCNTTCCANTGGGGGAAATAA

SEQ ID NO: 2085 ACAAACAATGTTTATTTGTTTGTAAAGTGCCAGGTTTATATTTAAGTAAACAT
TAAATCTGCGTTGAAGCAGTGAGGCCGATCTTTAACTGGCTGTGCTGGTTAAAGGACTGTTTA
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ACGGACTGGTTGTGAGGNANCTCACAAGTTTAAAGATGCTTGTNANGAACATTACGGACAATTN
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SEQ ID NO: 2086 ACCGGGGACAGGTGCAGTCCCTCACCTGTGAAGTGGAATGCCCTTAAAGGAAC
CAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCTAACT
ACCAAGACACTATTGGCCGCTGCAGGATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCAC
CTTCGTGAATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGG
AAGCTGNTGGAAGGCGAGGAGAGCAGGATTCTTTGCTCTTCCAACTTTTCTCCCTGAACCTGA
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SEQ ID NO: 2087 ACTCCACAGAGAGATGCAGACAAAGTAAACAATGAAGGTTGTTTTATAAAGG
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CGTGCTCCAGNGGGCTGATCAACAAATTTNATGTTGNTATGTTCTAANCCACCTNCTTCCATTN
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SEQ ID NO: 2088 ACCATTGAGGACATAGGCACGGGCAAGGACTTCATGTCTAAAATACCAAAAG
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AANGAAACTACCATCAGAGTGAACAGACAACCTACAAAATGGGAGAAAATTTTGAATCTACTN
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NGNCTTTTNAACNANTGGGCAATNGGTTGNACATATTCTNTTGAAANGAANACNTTTTCTCNCN
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SEQ ID NO: 2089 ACTTTTTTTTTTTTTTTTTTTTTTATCCTCCAAACAGATTIATTGAATACAG
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SEQ ID NO: 2090 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCCACCATGGGACGTATC
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ACTCTTATCCCAGCTGCAAGGACNGGCNNAAGGATATNCCACCTCGGTTTTTANGANANGACAG
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SEQ ID NO: 2091 ACCCCTTAACCCCTCTCCTTACCCCTTAGCAGCAAGTCCCACTTTTCTAGGG
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CTCTTCAACTCACACCTGACCTAAAACCTAAATGCCTCATTTTCTTCTGCAACACCGNTTGGCCCA
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CCTAATCCAACCCAGCGTGCTGAGTGGTATATTNTTTTCNANAACCCATTGACTNTCCTTCTTTC
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SEQ ID NO: 2092 ACTTTTTTTTTTTTTTTTTNTTTTGGCCAGAAAAATAATCCGTTTAATTGA
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NTTACACAGNCTCCTTATGGGATTGCCTTCTCGTANAAT

SEQ ID NO: 2093 ACGAGGACTGGATGGAAAGGTGATTTGTGGCTCCCGAGTGAGGGTTGAAC
TCNACAGGCATGCCCGAGATCAGTTTTGATANACCACTGCCCGACGTNCCCTNGATCCAAAT
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SEQ ID NO: 2094 ACATTGACAGACTTTTTCAGTATTGTAAGACCAAGAAGACTTCTCTACATGGCA
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AGANGGAATGGAAGCAGCANTCGANAAGCANCAAGTCAGGGAAGAAATATTTGGCAAAAGGTGG
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SEQ ID NO: 2095 ACTGGCCTGCTGCTGGCCGAGGCTTCTCAATAGGTTTGGCATGGACAAGA
TCTATGAAGGCCAAGTGGAGGTGACTGGTGATGAATACAATGTGGAAAGCATTGATGGTCAGCCA
GGTGCCCTTCACTGCTATTTGGATGCAGGCCCTTGCCAGAACTACCACTGGCAATAAAGTTTTGGT
GCCCTGAAGGGAGCTGTGGATGGAGGCTTGTCTATCCCTCACAGTACTGCGATTAATAAAAAAAGC
ACTTCTGCAAAAGGAACCATGTTCCAACACCGCAAAACAAGGTGTTCTGCTTAAACAGAGTAAGATC
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SEQ ID NO: 2096 ACTCCCTACGGCACTAGTCTACAGGGGGAAGGACGCTCTGTGCTGGCAGCGG
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ACTTAAAGAATAAAATGCATTTCTACCCGATCTCGCCCCAGGA

SEQ ID NO: 2097 ACAGGGAAGTGTGAGGAGAGCAGCACCCAGGAACACCGCAGCCAGCATG
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TCTGTGATCTGAGGTATAAAGACATGTCCACCANGTCTGAGCCCTCAAAATGTCCCTGATTACAAAT
GCTGGCTGTCCAAGTGCCTGTTCAATAAAAGTAACTCAGCAGAACACCCATNTTTNTTCTTAT

GNTTTATGTTTTNTTNAANAANTGTTCTNTTGNCCGNACCCCTAAGGGCG

SEQ ID NO: 2098 ACGCGGGGACGTCGCTTTTGTATCCTTCGATGTCGGCTCTTCTATCATTGTG
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SEQ ID NO: 2099 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCA
GGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTCTCTTTGAAAGATAGAGATTAATAACAACCTAC
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SEQ ID NO: 2100 ACTCTCTGTCCACGATCATGGNAACCATCCAGTCCTTGAAGCGGCCAGTGAA
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NTTACCTTGTCCCAT

SEQ ID NO: 2101 ACATTCCACATTTTAAATAAATTAACCACAAGAAAATAATCCACATATACAA
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CNAT

SEQ ID NO: 2102 ACTTCAAGGAGAATCCCACTGGAGCTGGGCTGTGCAGTGGCTACAGAA
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SEQ ID NO: 2103 ACGCGGGGCTTTTCCCCGTTGCTGCTTGTGAGTGTCTCTAGGGTGATA
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AAAAAAATAAGGACANCGTNGAATTTTAAAGTTCCAATNCANCANAATACCTTTACACCTGT
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SEQ ID NO: 2104 ACTTACATATCTACATTTGACTACATTATTTCCAAACCAAGTATTCATCCA
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SEQ ID NO: 2105 ACAAGTCTTGTAGATCTCTGCAGGAGCGGGTGAAGACTCATGTCTGTCTCC
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SEQ ID NO: 2106 ACGCGGGTAAAGATGTCTTTTTTATTTTACTTTTTTTAAGCACCAAATTTTG
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GTATTAATGTTTTGCATACTTTGCATCTTTATTNAAAAGNGTAAACTTTCTTTGTCAATCTATGGA
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SEQ ID NO: 2107 ACCATCTCAAAGCTAGATGCTCGAATCCAGCAAAAGAGAGAGGAGCAGCGT
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SEQ ID NO: 2108 ACGCGGGGAGCTGGAGTGCCTTCTGCCGAAGCTTGTGGTTGCACGCCCATCG
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SEQ ID NO: 2109 ACCTAACCCAGCTAGTGTGTTTTCCCAATTTCAAAGCTACTCATTACTGTTC
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SEQ ID NO: 2110 ACCCAAGGATGCTCCTGGAGTATGTTGTATTGAAAAAGCAGTTGACAAACCCC
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ANGGGACTGTGAGAAACACCCAGCAGCNTTCTNTTTGGAATCAACAGGCGAGGGATCAANANT
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TCANGC

SEQ ID NO: 2111 CCGGCCGAGGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGT
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SEQ ID NO: 2112 ACGCAGGGGTATTTGAAACTCAAGGTTATCCAGATGTTCCAGGTCCTCTGA
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GGCTGANA

SEQ ID NO: 2113 ACCGCCAGCTCTCTGCTCTCCACAGGGCTCCCCGCCCCACCCGGCCTGATAAA
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CA

SEQ ID NO: 2114 ACAGTTCCTTCCAATCTGTGCTTGAACCTCTGACAGTATTGTCTCGAAAATCA
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GCAAAANTTCAA

SEQ ID NO: 2115 ACTCAGTAGTGCCTGCTTCTAGGGCTCTGAATACGGGCTTAAAGTCATCTTG
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SEQ ID NO: 2116 ACATTGACAAACACATAACTGAGGCATTAATACCTCTTTATAATAATGCAAG
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SEQ ID NO: 2117 ACTAGAAGTATACACCACCCAGCCCGGGTCCAGTTTACACGGGCAACTTC
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TTGAGCTTAAAAATAAAATAAGATTTAAACAAATGAATNTAACTACTAGGTTTTCNAAAAGGCG
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TGCTGAAAAAANNATCCCGTCTCACAANCACTCCTTTGGAGAAAAAGAGGGGTTNGTTNCCCC
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SEQ ID NO: 2119 ACAAATTTACATTCATGAGGAATGTTAAAAAAATTCAACTAAAAAACCAC
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SEQ ID NO: 2120 ACCTAGAAGAGAGGGCGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTTCAT
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SEQ ID NO: 2121 ACTTTTTTTTTTTTTTTTTTTTNGGAATGGAGTTTCACTCCTGTTGCCAGG
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SEQ ID NO: 2122 ACCAAGGGATGGAAGAAGTAAATATAGCTCAGGTAGCACTTTATACTCAGGC
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SEQ ID NO: 2123 GTACAATTCATCTAACTTCCGAAAGCACTTTTCAGTCCAAATGCANAAACCG
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SEQ ID NO: 2124 ACGCGGTGGCTCAGAGCACCCGTATCATTTATGGAGGCTCTGTGACTGGGG
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SEQ ID NO: 2125 ACAGACAGTCCATCTCTGTTCTGGCCGGGTCCACCGTGAAGATGTCCTGAA
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SEQ ID NO: 2126 ACGCGGGGAGCGACAATATTGACTCAGCCTACTCCAGAGTGGTCTGAGAG
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SEQ ID NO: 2127 ACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAGGGAC
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TGNCCAANATANAATNNTANTTNAACITTTAAATTTGCCNCANAANCTTNTAAATTCCTTGGT
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SEQ ID NO: 2128 ACTTGCCCTTCCCGAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGACCA
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SEQ ID NO: 2129 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNCGGGAGGCAANAGGACCAACCC
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SEQ ID NO: 2130 ACGCGGAAGAAGTGTTCCGAGAGATGGAAGACCATGCCTGCAAAGGAGAA
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SEQ ID NO: 2131 ACCTGGATGAAGCATACCCAGGGAAGAAGCTGTTGCCGGATGACCCCTATGA
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NCAAA

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SEQ ID NO: 2133 AGCCGGCCGCCGGGCAGGACATATTAGGCCTTTTATGAACACTAAAAACAATG
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SEQ ID NO: 2134 ACAAATAAAATCAAAAAGAGCAGTGTCTGTGTATTCAATTTCTGCATGTATA
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SEQ ID NO: 2135 ACTTAATTCTTCTGCTAGGATAATTCTTTTCACTTGTAGTTCACAGATTTCTT
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SEQ ID NO: 2136 GTGGGTGCGGCGAGGTACCGGGGAGCACTTCTTCTGAGTGGGCTTCTCT
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SEQ ID NO: 2137 ACGCGGGGGGCAGAAGAGGAAGATTTCTGAAGAGTGCAGCTGCCTGAACCG
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SEQ ID NO: 2139 ACAGGTGGAACAATCCAAAGTTTAAATCAAAGAAGGTGGTGTTCAGTTGCTG
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 ATTGGATATTGAGTTTATGAAGCGTTTGCATGAAAAAGTGAATATCATCCCACTTATTGCCAAAGC
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 GGTCAAGAGGAAGGCAGTNTCTTGGGNGTTGCTTGAANTTGAATGGTNAACATTGNGATTTC
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SEQ ID NO: 2140 ACACTGAAACATAAATCCGCAAGTCACCCACACATACAACACCCGGCAGGAA
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SEQ ID NO: 2142 ACAAGACTCTTGACAGTTGTGCTTCTTAGGAGGTTGGGTTTTTTAAAAAA
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SEQ ID NO: 2143 CGGCCGCGGGCAGGACGCGGGGGAGATGATCAGAAATCCTTCACTGTCA
 AATTCAAGAGAAGAAACATGCTGAGAAGAGGCACCTTCCATGCCAGGCCTACCTGTGCTTGAAGGA
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 GGGCCAGCCTACTCTTGNAGCCTNACCTNCNNTGCTCCCTTATGCCAATTTCTCAGCAGGTTTCTCC
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SEQ ID NO: 2144 ACCTAGAAGAGAGGGCGGTCAAAGAAGTAGTGAAGAAGCATTTCTCAGTTCAT
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SEQ ID NO: 2145 GTCGCGGCGAGGTACCGCTTCTTAGAACTTCTACAGAAGCCAAGCTCCCTG
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SEQ ID NO: 2146 ACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCTCTGG
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SEQ ID NO: 2147 ACATTTTCATAAAATATGAAGGGATAACTACAACTGGAGTAAAAATGATGG
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CAAAGAAAATATTTTATAATTAATAATTTAATGTTTTCTTCTTTTCTTACCTACTCTTGGCA
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GGNGTGCTACAAAAGCCTTGNAATTTATCAGNAGTAGTTTTTTTTTTTTTTTTTNAANAATGA
NCCG

SEQ ID NO: 2148 GTCGCGGCGAGGTACTGGCTTTTCAAAAAACAGAACAAAAAAACCCAAA
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SEQ ID NO: 2149 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNCNCAGGGGAAAAATAACTTTAT
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SEQ ID NO: 2150 ACCAAAAACATTTATGACCTTATAATTTTATAGTGCAAGAAAAAGGACAAAAGA
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SEQ ID NO: 2151 ACAATCAATAAGTCTTAAATCTCTCTTCCATGGATTTCCCCATCTCCCCACTT
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SEQ ID NO: 2152 ACGCGGGGACTGTGAGGTGACGCTTCCGGCGCAGAAAAATGGCAGCCGCGG
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SEQ ID NO: 2153 ACGCGGGGGGGCTCTGCGTTCTGTAGTGGCGCTGCTTGGGCCGCTGGCGGA
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SEQ ID NO: 2154 ACAAAGGAGGTTATAATGGACTTAACCAAGTGTGTTGACAACTACTGACAGCAA
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SEQ ID NO: 2155 GTCGCGGCGAGGTACATTTTCATTTTCTACCCATCAATTTAAAAAATAAATGT
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- SEQ ID NO: 2156 ACGCGGGGGCTGCCGTCGCCGCCGCCATTTTGATGGCAGGAAGAGTCCGGTT
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- SEQ ID NO: 2157 ACCTTGAAAAGACACTGAAAGCATTTTGGGGTGTGAAGTAAGGGTGGGCAGA
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- SEQ ID NO: 2158 ACCTGAACTCAGCAGTGACATAGACAGCAGCAATTTGATGACATTGAAGAT
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- SEQ ID NO: 2159 ACTTTTTTTTTTTTTTTTTTTTTTGGTACCTGAATAATCAGGNCCTTTATTCAAAA
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- SEQ ID NO: 2160 GGAAGCCGGCGCCGGGCAGGTAAGTCTTGTATGAAAGACCGTGAAACCAACAA
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- SEQ ID NO: 2161 ACTTTTTTTTTTTTTTTTTTTTTTGGACACACCTGCCCTTTATTGGTCTNTTCT
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- SEQ ID NO: 2162 ACATAAGCTATTCAAGATTTCTCCAGCACTGACTGATACAAAGCACAAATTGA
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- SEQ ID NO: 2163 ACAGAGAGGTGGGCCTTGAAGCCAATAAATACAAAGCTTCTCTGCCTTGTGA
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SEQ ID NO: 2164 ACATTTTGTACAGACAGAAGGCTGATTTTGAAAGAAAGAAACAATAGGA
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SEQ ID NO: 2165 ACGCGGGGACGGCGGCAGTGCAGAGAAAGCCGAAGATGGCGGTCCCGCGG
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TACAACCTCGAGTGAACAATGAANATTTNAAAGACCTGGANAAANTCTNGTGGTATTNAATTCNC
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SEQ ID NO: 2167 ACCAGCTGTGGGATTCGTCTTCGGATTCATTTGTTGCTTAACTTGGGCTTTT
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SEQ ID NO: 2171 ACTGTCTCTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCA
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ACAAGAAAGGGATTGTCGATCAGTCACAACAAGCATACCAAGAAAGCTTTTGAAATCAGCAAAAA
GGAAATACAACCAACNCATCTATCAGACTGGGTCTGGCCCTTAACCTTCTGTGTCTATTATGA
GATTCTGACTCCCCAGAGAAAAGCCTGCTCTCTTTGCAAAGACAGCTTTTGATGAAGCCATTGCTGA
ACTTTGATACATTAAAGTGAAAGAGTCATACAAAAGACAGCACGCTNTTAATGCANTTACTGAGAG
ACAACTTGACATTTGGGACATCGGATACCAAGGAGACNAANCTGAAGCCTGGANAAGGAGGGG
GAANTTTAAACCGCCTTCCACITTTGNTGCTCATTTCTTAAATTTACACAGTNACCTTTGTCTATCC
NTGCTGCCCCANAAATAGNTTTTGTTCATTATGANNNGGTTNTGTACCTTTNTTTNAAATTCNT
ATTTCCNATNTGGTTTTTANGTTAATATTNAGGGGAGTAGA

SEQ ID NO: 2172 ACTTTTTTTTTTTTTTTTTTTTTTTTNAACAAAAGCAACAATTTTTATTATCTTG
CTTTATATTTAATGGATTAGAACTATAAAGATTCTTAACCTTTGAAAGCANAAATATAAGTTGGATA
GTAGTTGCAGATCTTTAATAACATTTTCAATTTTCAATTTATGAGCTGCTCATTATAAATGANATGCTC
TAAATAATAAATCGCTTTTGTGTTGTTGTTATAAAACAATGAAAAATCCTGTTCGGAAACACAAGT
TGCTNTTTATATTTGCTTGCTCTTAAATANTATTGANAAGGTAANGNGGANCTTGTTGGNGAA
AGCCCCCTTC

SEQ ID NO: 2173 ACGAGTCTGAGGCGGAGGGAGTAATGGCAGGACAAGCGTTTAGAAAAGTTTCT
TCCACTCTTTGACCGAGTATTGTTGAAAGGAGTGCTGCTGAAACTGTAAACCAAAGGAGGCATTAT
GCTTCANAAAAATCTCAATNGAAAAGTATTGCANGCAACANTAGTCTCTGTTNGGATCGNGG
TNNTAAAGGAAAGGGGTNGANAGATT

SEQ ID NO: 2174 ACAGCTTTTAGCAAACTGCTTTCCAGAAAAGCAAAATTAATAATGCAAT
CAGCAGATCAAGGAGACTACAGCTAGACATCAGAGCTACAACCTTCTCATATCTGTGTGAGAAAAT
CCTATTTACCCAGAATAGACTAAAATTTAGGACAAAACAGGGACTTTTTAACATTTCTTACTTTA
CCCATTTTAAGTTCTTTTATCTCCCCACCCCCAAGCCACTAATTCAGCAAGATCCAGGAGAAA
GAGGGCTACTTTTGAATTTGGCTACTTTATTTTCTTTCTATGGCAAGACTGCATGGAGCCTGGATA
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ATCNACAGCCCGTACGGGCCCTTTCTGNCCG

SEQ ID NO: 2175 ACGCGGGTGAAGATAAGAAGTTTCTTGACAAATACATGCCCCAGTTCATGAA
ACATCTTCATTATAGAATAATTGATGTGAGCACTGTTAAAGAACTGTGCNGACGCTGGTATCCAGA
AGAATATGAATTTGCACCAAAAGAAGGCTTGCTTCTCATAGGGGCACTTGATGACATTNATTGAA
AGCATCAAANGAGCTTTCANTTTTACCGAAATAACATCTTCAAGAAAAAATGNTGATAAGAN
GNAAGGAAAATTTATNGAAAAATGGGGNAANATGAAAAACCGGTGAGTTNNTGCCANNTTTTATG
GCTGCCNCTTCNATTTGTATTNTGGAGGCACTTNTGGGTGGTTTTTTTTTTCTNNCNCCTGATG
GCTTTGGCAAAGCACCTTCGGGTATCCTTGATCTNAA

SEQ ID NO: 2176 ACTGAGAAATGCCGTTTCGGGGGCTTTATGGCGACGTAAGAACGGGCTTGGAC
TTGGTCTGTGAATCCAGAATCCAGAGGTGCAGGTAGCACTATGGATCAGGGTTAGCCTCGGGGG
CCAAAAACAGGCTTCAGTTTCTCCCCACTCTCACTTAGTGTTAAAGAGTGGCAGAGGTGGGGTGT
GGGAGCTTCCCNAAAGACCTGCT

SEQ ID NO: 2177 ACTTTTTTTTTTTTTTTTTTTTTTAAAAAGTTAACGCATATTTGTTTTATTTA
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GCATACTACGGCTAAGGAGAAACAATGTTCTACATATTATGGGTAGTGAGAACATTATCTGTATA
ACAGGGAACCTGTGATTATTTAAAAATATGCAGAACTTATTTTCATCTGTGCTTTANAATAACTGTT
TCAGTGTATAAGTTGAAAAGAACTCAAAATACTAATACCAAAATNTACACCTTGNTTANAATTCA
AAAAAGCTGCTTTCTGTGAAGTCAATCAGCTTTATTAATAAATGACACAAATCCAAAAACAAGATG
CATGTTNTATATAAAGGGGACATTGTAAGTTCCTTGCTGCANTTAAACCCATGGTTAAATCCATGA
AATTCCTTTTAAATATCATTTAAACAGAANTGCAATAGTCTCAGGATCTCTTAAAAACCTTTCC
CAATCCCACTNNTTCACTCCCCCTTTTNAAGAACTAAACAGGTATTTCGGGTANCTGNTTCTCTTTN
CATAANTTNGNTTGTNTAATTTTNCNAAAGGTTNGGGCAAACCGNGCCCATCTTATTGNGGGG

SEQ ID NO: 2178 GTACAAACAGCACTTTTACCTTTGCCATAACCTCAGGATCAGGATCTTCTATA
GGATCAGCCCATTCACAGTTTCAACATTCCCCANACCTTGACTTTACCACTCATTAACTACGC

CTTGCTGGGCAGCTGTTTTGTGATCTTCATATTCAAGAAAGCAAAGCCTNTGTTTTTTCTTGT
CATCCGGTGGTGGGTATAAAAAAGACGTCTGGAAAGAACCTCTGTTACTTTGCTAAANTCTTTAA
GANTCTGTNCCTTGGTTTNCCTNTTAGGAANTAGAAGCCCAAAAAAG

SEQ ID NO: 2179 ACTTTTTTTTTTTTTTTTTTTTGGGTTTGGNATGCNCTATTTTGCCTTAAAAAT
TATTTACTAGTCTCAGTAATACATTAGTAAAAATCATGTCACTTAATTAATTGTGTTANAATCAAA
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TNATTTCTCANNTAATTTTGGGAAAAANNTCCANAAAGATGTGTTCTNTNANTAAAAANNTTAAANA
AAATAAGCTTTTTGANCCCTNCCAANCCCCATCCCCA

SEQ ID NO: 2180 ACGCGGGTGCATGCCTGTAATCCCAGCTACTCAGGACACTGAGGCANGAGAA
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CAACAGCATGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAATGGAGTTTCAGGATCGTGGAG
AAATGATGAACCATATCATGTCCGCTGGGTCAAAAGCATTGACATGAAATGACACCCACTGTGTT
ATTTCAATTTCTAAATGCCTTAGAAAAAGACCAGAAAGAAATCTGCCAGGATNTCCACAAGGG
TTGCCTTTAATGGTGAGATTATNGGAAATACTGTTGGTINTANACTTTGCCAAATTCANGAAANCT
NTGCAATCCCTTTTNGCACNATTNCANCTCCAGNAAAAAAAAANAATNAANCCNGAAAGGAAA
AAGNACCGCTCTT

SEQ ID NO: 2181 ACCCCCTTTCCATAGAAGGGGGAAGCCCTCTTTCTGTCTGCCAACCEGATCG
CGACCACTTGAGTAGAGATCACTTCGGCTGCTTGAGTAACTGTCTCGACTTCCACCATATCCGTC
CGTGAGCTGCTGTAATCATCATAGCGACTGCTTCCACCATAAGATGGCGGGGGCCCTCGTGTAGGT
GGAGCACTACGTNAGTACCATAACTCTTATATGAATCTCTGTAGGAACCTCCACTTGGATGAATCT
GAATAGTCNCGATCACGACCATATCCATCTTATCCGCTATATNCTCTTGAATGGATAGNCATNAC
CGTGAACTGGGAANTGACCATTAAATNACGGTAAAGTATNAATCTCGNNGGNGGTGGNGCATAATC
CTCTANTTTTACGAAGAACCTTNGGNAATCTTTNGATTGAATNGCTGTNTTTATAANAATAACC
CATNATNTCTTTGGGGACAAANTAAANATTCTAACANAAGGCAANTNGGTTCCNTTC

SEQ ID NO: 2182 ACTTCAGTTGGTGCACAAAATACTGTCAATTTGCTCAAAGCTGGTTGCCAAATG
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GTGCACGGCCCTTCATTGTGCTGGTGTGTGAACACTGCTGGGGTCAAGAAACATACAAGGNCCC
TGGANNTAACCTGCTCTGAGCGAGTGAAAACCTCTGGATCATCATTGAACATAAACACAANAN
GAGAAAAACCTTTGATAGTNAAGATTGCGNAGTGNACTTCANAAGGAGTCNCAACCCNTNTT
AACTGGATCCAAAAATTTATCCNGAGTTTTTGTTTAAAAATATGTTTTCACTNTTGACTGGNTNAAA
TCNTCCAAAAACTNAAATNATGTGGACATTNCTGATGTGGGCTTATNTTTTAAAAANATNTTAA
AGGGGAATCCTTGTTNNTTCTAAAAAAATGNNCCTGACATTNNTTGGGNGACACCTGGNTCCTGG
ATCCTGNCAAACTTTTAATTTATTTNTT

SEQ ID NO: 2183 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCCACCATGGGACGTCATC
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AGATGGGAGGCAAGTTTATGAAAAAGCCAGGGGCTAAGCCANCTCTACCATAACCAAGAGTCAA
GGGACTCTTATCCCACTGCAANGACAGTCCAAGGATATGCCACCTCGGGTTTCTAAAAAAGGAC
AGCTTAATGCANATGAAATTAGCCTGNGCCTGCTCAATCCGTCCTAATGAATAAAAAATCAAGTGC
CAAGGCTTCAGCCCCAGATAACTATGATTCTTCTAGTGACACACCCACGCACTTAAACACCA
CCTTTTGGGACAGACACTCAACTTGGTCTNAACTTATCCACCATTANTCNAGGAAAACTGGC
AAGACCCAGAAAAAGCCCCACCGNCNAANGGAAAACTCCTTAACTAACTGAACCTTNTNGA
CTNNATTTCTAANTANNGGAAATNCNAAATGAAGCTTGTAAATGGNTGTAAAGAAANTONAGGCTCT
AAAACTTTCTTCTGATATNNTAACCAAGGTATNATNCNGNCCNNGATANAANCCATAANATAAA
NAAAAAGCANNTTNTT

SEQ ID NO: 2184 ACAGACATGAGATGCTTCCAGCCAGCCTNATCCAGGCTCATCGGGATTACTT
CNGGGCTCACACCTATGAACTCTTGGCCAAACAGGGGAGTTTATCCACACCAACTGGACAGGGC
CATGGTGGCACCGNGTTATCCTCATACATAAAATGCCTGATCATGCTGCTCCTGTCAACCTCCACG
ATTTCCANAAACCAGGACATTCCATGTGCCTCATGGCCTGCCANCTGGCCCTTTGNCCTNTTT
TNTGTTCAAGTTNTTTAAANCGGTTGGTAAGANACTTCTTGNAGAAAAACACACAATTTNTT

SEQ ID NO: 2185 ACGCGGGCACTTGATTAGAAGAATGACACCAACACATCGCTGAAAAAAT
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TTATTTCTATGCTGATTCTGGAGGGAGTTAACTCCTGCAAAAAAGGCATCTTGTCCCTACATCTT
CTTTCTGACTTTTGGCTTCATCTTAATAGTAAGTTCAAGAAGTAGTTTCATGAATAAAATTTGAAAT
ATNATGGNCATTTGGAAAAAATGATTNATGTTGAACCTGNNACCCCAAGTAAGAAAGTGGAT

CTGCCTTTCCANCTTTTGGNTTTCATTTNGGGCTGGGCTTTACCAAAAACCACAACTTATATTA
AAATACNNTTCATTTTGACANAGTTTTAATGAGNGATTNATNCCCTNNGTATTTGGTATGNTTA
AGAA

SEQ ID NO: 2186 ACGCGGGATGGCAATGTGGAGAAGGTGAAATTCATGAAAAGCAAGCCGGGG
GCCGCCATGGTGGAGATGGCTGATGGCTACGCTGTAGACCGGGCCATTACCCACCTCAACAACAA
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TACGGGTTGGAAGACGGNTCTTGCAAGTTCAAAAACCTTCANTGAATCCCGGAACAATNCGGTTCTN
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GCCCTNTGGAAAGTGACCCGANGAAAACCTTNTTNAATCTGCNATGAGCTGGGAATTAACCCGC
CNTNTTCINTGAAAATATTCTNANGCCAAAATTGAGCGCAANTCCTTTTGANTNCTTNAATGGGNA
TCNAAANCCAATGCCCT

SEQ ID NO: 2187 ACGCGGGGATTTTCTCCCGAACCTCTGCTCAGCCTGGTGAACCAACACAGGC
CAGCCGCTCTGACATGCAGAAGGTGACCCCTGGGCCTGCTTGTGTCTGGCAGGCTTTTCTGTCC
TGGACGCCAATGACCTANAAGATAAAAAACAGTCCITTTTACTATGACNGGCACANCCNTCAGTTT
GGCAGGCTNATNTGCGCTGGGTTCTGTGCGCCATNGGCATCATNTTTCNTNATGATTGCTAAAAAT
GCAAAATGCANTTTTNGCCANAANCTTCGNTAACCATNNAGGGNNAATNGTAAATTTNAT

SEQ ID NO: 2188 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAATACATTTTGC
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TCTATATATTTAAATTACAAATTTGGCCAAATACATATTTTCCATATTTAGATCTTTAATTATAAA
TATTAATTTGAAAAATCAAANGTGAAAGCANAACTGNTNTTCAAGTTTGGANAAATATTT
ATTTTATNATTAAGTTTGGTTGAATATNCCCTCAATAGGNTTCTAANAAACACCNATTATCTG
NNTCTTATGNAATTGGGGANNTTNTGNAAGNATGGTGAANCGGGTTTAACTTTAACTCTGGG
NT

SEQ ID NO: 2189 ACGCGGGGCTCTTCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAGGA
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ACAGACTGACGCCNAGCAGCCAAANGTGTGGAGCACTCACANGGCNTACCCCTGTNTTTTCAA
ANCTAGATACACTTGTCAAANTCTTTTGGCCTTCCGNANAAATGAAAANAATTGCTNGCCANTGCC
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SEQ ID NO: 2190 ACTTTTTTTTTTTTTTTTTTTTTGNGCTTCTATGTTTCTCTGTGCTGATTCT
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GGAAAAATTTNNNCTNANCCCATTTNGGCCGTCANTNGNTTTTTACCCCAAGGCCCNTTGGNNA
NAANCCCATNCCCTAATTTATTTTAAANA

SEQ ID NO: 2191 ACCTGCATCAGCATTAGTAATCAACCTGTTAATCCAAGGTCTTTAGAAAACT
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GAAGGTTATGTTTCANCATCCTAGCTATTNAGTAATAACTCTACCTGCCCTNTTAATTNAANCTC
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SEQ ID NO: 2192 ACCCATGATTTGGACACTTTGTGGGCCCATTTACTTATACTGCAAAGCGTCC
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GACCAAGGATGTATTTAAATCAGAAAGTCATAGGTGATGGGAATCAGATTGAGATTGAAATCCCTC
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ACAACATT

SEQ ID NO: 2193 ACTGGATGGCCCCACAAGATGCTGCCACTTTAATAAGGCTGCAATACACTGT
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TCCTTCANACACATCACAGGCTTCAATAATTGAGCTAAATCAACATGAAGTCCACCTTCCGAG
TTCTCTTCTGAAATCTCAGCTCCTTTAGATTTTCAGATAAGCACGAAGCTCAGCAGCTGATCTTCTT
CACTGATGTCGATGAAGGCCGGGACGCTCATGGTGCAGGCCNGGCACAGCGGACACTCCACTCG
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SEQ ID NO: 2194 ACAGTTTAAACAACAGCTGAAAGAACTAAAGAAGCAATGTGGTCTTCAAGCT
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ACCTATGAAGAGGACGCCATTGGTCCAGGCAAAAGCGGAAGAAAAAGGCCTATTGCCCTCAAATT
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TGAGAACCATAACAAGAAAGGACATCGTCATTCCGAGTAGGAAAAGCCCTGCCTGCAGGGAAC
ACCAAGCAGCTACCTCTACCCCACTGTCTGTTGAGAGCAGTGTGACCCAGCAGTTAGGGACTG
GCTGCATAGCATCTGTTGGGGGTAAAACCTGTGTCTTTATGTGTCTTGAAAAATTTTTCAAA
GTTTCACAAACAGAAAAATGCCATTCATATTGTTTATTTTAAAGTGTCTATAATGTAAAAATAAACCT
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SEQ ID NO: 2195 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAACAAGTNTCACAATGTTT
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CTT

SEQ ID NO: 2196 ACGCGGGTATTTATATACTTGGTTTTAAATAGGTTCATATGTTACATGGTT
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GAGTTGTAATATATNCATGCATACACNCACACACACNCACACTCNCNCACACTCACACACACC
AANTAAAAACCCNTTAAANAAAGACATNTTATCCTATCACTANAAGAAAAATNTCCTACATGAAA
NGAAGACANGGNAATTAAGNGAAGGAAAGANNATTATAAACCTAAANNTNACCATTTTCAATT
TNGCNGGAGTAAGTNTTTAATTATCATTTNGNTAGCNTTCGANTATAANTGGACTAAACTTTCNATC
AAAAGAAACAGACTGNCTGAATA

SEQ ID NO: 2197 ACGAAGAAAGCAATTTCCCAAGCAATGAGTCTCTTAATGGAAAAATAAAAGA
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AGCCAGAAGCTCATCACCTAGTGCATCCAACTCTGCTTCTAAATCATCTTCATCCAGTTCTGGGGT
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SEQ ID NO: 2198 ACTTTAGATACTTGGCATATTTCTGGGTCTTTCCAGTAAAGCAAGTATTTAAGA
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GCTAAACATTGCACAAATTCAACTCCAAGTGAACCGAAGTCGATTNCCAGCATCATCTGACTCC
ATAGCAACAGCATCNGGCCATAACAAACNAAGACNCCAAATCGCCGCCANCTGACAGAGCAAA

ACCCANAAACGCCNGCCCNAGTTTCAANATAAACCTGACTNACTTANAATGAAACATANTAATT
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SEQ ID NO: 2199 ACAAACCTGGTGGGTCANATCGTCTCCTCTAACATGACGCTACACTGTCGCTGA
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CATAGGTGGGTTTCATANCTCTTAACCTATNCAGGAACAAATTTGATNCTTACNTATTAACNACNT
TAATNCNTTCAATGTTGNAAT

SEQ ID NO: 2200 ACGCGGGATCAGACACTGGATCAGACACTAAACGAACTTAACTGTATATAAG
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GAAGTTCCTTTTGTATTGCCATCTTCGCTTGTCTGGAATGTCAAGCAAATTATGAATACATGACC
AAATATTTGTNTNGAGAAGCTTGACCACCAATAAATTTNATNCTTNCCTTTTTTTTTTNGAATG
GCACCAGNTTTT

SEQ ID NO: 2201 ACCCCTTAACCCCTTCTCCTTACCCCTAGCAGCAAGTCCCACTTTTCTAGGG
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CTCTTCAACTNACCTGACCTAAACCTAAATGCCTCATNTCTCTGCAACACCGNTTGGCCC
CAATACAAACTTGACAATGGCTCTAAATGGCCANAAATGGCACTNTCNATTTCTCCATCCTACAA
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SEQ ID NO: 2202 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTCANAACCTTCCCTCAGCATCAGAT
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SEQ ID NO: 2203 ACTCCACAGAGAGATGCAGACAAAGTAAACAATGAAGTTGTTTTATAAAGG
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NGTAACCAATGTATCTGTGNGCCTATTCTCTNTACCTT

SEQ ID NO: 2204 ACCTTCATCTTTACTTCCAAGTAAACCCGTGGATGATTTGATGAGGGATAAAT
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CAAAGGATAGTTGTACCAACTCATNTTATGGTCCATAATGAAATAAAAAATTTGTATACTGT
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SEQ ID NO: 2205 ACATAGTGTGCGGAACCTAAATCGGCATTTAGATAGATCCAGTGGTTTAAAC
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NCTAGGGG

SEQ ID NO: 2206 ACATTCTGGGAGAATATCACTGACGCTCAAACCATTTTTATTTCCAATATGTA
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SEQ ID NO: 2207 ACGCGGGGGTAACGGAGTGGTGACCAACGTGAGAGGAAACCCGTGCGCGG
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SEQ ID NO: 2208 ACTGTCTCTTTTGGAAAAGTTCTTGATCCCAATGCTTCACAAGCAGAGAGCA
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GGAAATGCAACCAACATCTATCAGACTGGGTCTGGCCCTTAACCTCTCTGTGTTCTATTATGA
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ACAACTTGACATTGTGGACATCGNATCCNAGGGANACTANACTGAAGCNGGTTAAGGAGGNGG
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SEQ ID NO: 2209 ACAAAGGCATGGGGCTGTCCATGGGCACCATGATCTGTGGCTGGGATAAGAG
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SEQ ID NO: 2210 ACTACAAGAAAGAACTTTTTATATGAAGGATTCTTTATGTAGAGTATCTTTTT
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ACTCCCAGGCTCAAGCGATTTCTGGCTAATTTTTGTATTTTAGTANAGATGGGGTTTCGCCATGTT
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ACGCCCGGCCCTGACACATATATTTAGTGCCATCTTTCTGCATAAANTGTATAATTATTAGGGT
AACCGTGTNCANTTCNCTGTCTTATTTCCAGTGCTTAACAGNNGGNGGCAAAATAGTTTANTGATC
ANT

SEQ ID NO: 2211 ACGCGGGGGACTTTACCCAGTGTGCACCACAGAGCTTGGCAGAGCTGCAAA
GCTGGCACCAGAAATTTGCCAAGAGGAATGTTAAGTTGATTGCCCTTTCAATAGACAGTGTGAGG
ACCATCTTGCCTGGAGCAAGGATATCAATGCTTACAATTGTGAAGAGCCACAGAAAAGTTACCT
TTTCCCATCATCGATGATAGGAATCGGGAGCTTGCCATCCTGTTGGGCATGCTGGATCCAGCAGAG
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TCCATTTTGGCAANAAATTCCTCCGTTACACCCCAANCTTAAATTTCTTTTGGAAAANCTTGGN
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SEQ ID NO: 2212 ACACCGGGTGGCATTAAAGGGTAAAGATGTCCCCCTTACGGAGCAGACCGTG
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CCTCAACCTCCCTACACCTTCTCTTTTCACTTCTTGTGAGTCTGGGAGTAAAGCTCCC
AGCATATTTAGATAATAGGGCAGGGGAAGCACCCCTCTTTCTTAGACTGGATTATGCTCACATG
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CCCN

SEQ ID NO: 2213 ACTCTATGCATTCTATCTATACAGAAACACCTATTTATTATTACAGTTGATTATG
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GGG

SEQ ID NO: 2214 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCACTGCTGCCACCACCATGAAANAN
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SEQ ID NO: 2215 ACCCTGGGATAGGGAGCGATCTCCGAGCGAGGCGGCAAGATGGACGCGGGA
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SEQ ID NO: 2216 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCCAAANAATTGAAAAATTTATG
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SEQ ID NO: 2217 ACGCGGGGAGGGAAGAATGACAGCCACAGGGAGATGGTGGTGGGCAAGAA
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CAGAAAAAGGTTGCAGCTGCACACCATAGCCACCTNTCTGANCAACTTTGGTTTTGTGTGGTGA
CGTGGCACATGTTTGT

SEQ ID NO: 2218 ACAACCTGAATTGAGGCTTCTCTTCACTGGAAGTGCACCTGCCTCTACCTCAT
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ATCCCTCGCTGCTGATTCACTTCTTACCATGCACCTTCTTGTGCTGAGGAGAAATGGAAGTGG
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SEQ ID NO: 2219 ACTGTGAACATGACTTTCAGATGCTCTTTGCCCTTGTGTCATCACTGTGGT
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TCATCGATGAGCAGCCTCTGATATTAAGAACGACCCCTACCATCCAGACCATTTCAACTGCGCCA
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SEQ ID NO: 2220 ACGCGGGCGGGTAAC TCCAGGAGAGTGT CACAGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT
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TGTTAGAGGGAGAGTGTGCGCCCACTGCTCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCC
TCTGACCTTTTTCACAGGGGAACTAGCCCAATTTGGGCTCTCCAGCTCATCTTTCACCTCACCCC
CCTCTCTCTCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAGTGAACTTTG
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SEQ ID NO: 2222 ACAGTTTTCTCAGAAGACTCAAGATTTGCCCCAGATCCCTTTGAGCTCCCGCT
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SEQ ID NO: 2223 ACTGCCCTTGGGCCTCTCTCTCTCTGTTTTCCTCTCGAATCTTGTTCTT
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TTGTTCTGACAAAGGATGGTGCAGCTTTTCTCTGCTGCTTCTCTAATGCTCTCTCTTCGCTAAATAGA
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TCTCGTACAGATTTCTTGTAACCTTGCTGTATTTCAAGTTTCTTNGAAAAGCAAAGCCTTGCTC
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SEQ ID NO: 2224 ACCATAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTGGGCTGTAAAA
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AAGTGGTTT

SEQ ID NO: 2225 ACTTTTTTTTTTTTTTTTTTTTNGNATTGAGTTTTATTGATGATTCTATGTG
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NAATCCTATTAGCAGCGCTTCTCTCTGAGGNGGTTCACTAGCAAGCTTTGCTTTNAGTTTTT

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SEQ ID NO: 2226 ACATCACAAGTGATAACTTCAGCTTTACCACCANAAGCAGCTTCAATAGAAA
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SEQ ID NO: 2227 ACGCGGGGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTACGTT
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SEQ ID NO: 2228 ACTTTGTTTGTGATACAAGGTGAGCCAAAGGGGTGGTGAAGAACACACA
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SEQ ID NO: 2229 ACTCATTAAATATTAATAGGCGCTTGACCCACAGGCTGTCAAAATTCGA
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SEQ ID NO: 2230 ACAGAGATAACAGAGGTAACATAAATACAATCCTTGTCTTGAGGGGCAAT
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GANC

SEQ ID NO: 2232 ACGCGGGGGTTTTTAAAAAGGAGAGCCTTTCTGATGCCACTTTTCTGCTTGACA
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SEQ ID NO: 2233 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAG
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SEQ ID NO: 2234 ACGAGTCCCCTATGCGCTGCCCTGGGCCGCAAGAAGGGAGCCAAGCTGAC
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SEQ ID NO: 2235 ACCTGCACGTCTCATCGTTTTCTGCCGAAGCAAACACTCTACGAAATCATCAT
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SEQ ID NO: 2236 ACTTATACCCCTAAATATATAAAACATTTTAAAAAGAAAAAGGAAGAAA
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SEQ ID NO: 2237 ACTAGGACAGTCAGTAATTAATGCATCATTAGAGGATTATGGCTGTTCTTA
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SEQ ID NO: 2238 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATCCACACCTGCCCTTATTG
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SEQ ID NO: 2240 ACTTTGACCTGGAAAGGTATGGGTCTGCTTAAAGAAAGAAAGAAACATACA
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SEQ ID NO: 2241 ACCTCACCCATATGCTGAAGATCTTTGGGGCCGTAGAAGAGGACAGCTCCCT
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SEQ ID NO: 2242 ACGCGGGGGAGTGGTGTGCTGTTGTTGTGAGCCTGTGGCGGGCTTCTG
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SEQ ID NO: 2243 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGTTTCGTTGTTTTCANAGGCTTTTGAAC
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SEQ ID NO: 2244 ACACAAAGAGGGGGTGGGTGTCGGATGCAGAGTGTGTGGCCTGATGCTCCAC
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CAGGTAGGTTTGAGGGGATACATCCTAANACAACACCCATTCCANGGCAGTANGAAAGGAAAGC

SEQ ID NO: 2245 ACGCGGGGAAACAATGAATCAGAAAATTTCAAGTTCTAGTTCACCATGACTT
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SEQ ID NO: 2246 ACTGGGTCCTTCCCAAAGGGAGAGAGTCTCTGCTGGCTCTGAAGAAGTGAA
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SEQ ID NO: 2247 AACTGTATACATCTTGTCTATGATGGTCTTTACCAATGGCCCAATGTTCTGT
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SEQ ID NO: 2248 ACITGATGATAACGGTTTTAAAAATCCTTCACTCGTCTTTCTCAAACTTCTCCCA
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SEQ ID NO: 2249 ACTTTTTTTTTTTTTTTTTTTTTTTTGGANANACACTTCTTTATTAGGAAG
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NCA

SEQ ID NO: 2250 ACTTTTTTTTTTTTTTTTTTTTTTTTINACANAAGGGAGGGANATTTAATGTT
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SEQ ID NO: 2251 ACAAGATGTGTTACTATCGCTTTGGACAGGTTTACACAGAAGCCAAGCGTCC
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SEQ ID NO: 2252 ACGCGGGTGTGGATCTAAGGGGAATGCTTTATTATGGCTGCTGTGTCCAACA
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GGAACAAA

SEQ ID NO: 2253 ACTGGTCCAGGAGTTATCCAGGATAGATTTTACCCACCATGGGACGTCATC
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SEQ ID NO: 2254 ACGCGGGTATTATTCATCCAGCATATGGGGACCAACATGTGATGGCCTCGAT
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SEQ ID NO: 2255 ACGCGGGGCTTTTCTTTTCCGGCGTTCAAGATGTGGAAGCGAGGACGT
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TCAGAAAAAAGGT

SEQ ID NO: 2256 ACCAAGAGGCCAGTGTGCTCTGTGGACCTCAAAGTTCACCTGACTTGCTTCAG
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SEQ ID NO: 2257 ACGCGGGGACCTAGTGTCTGAGCGGCACAGACGAGATCTCGATCGAAGGCG
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SEQ ID NO: 2258 ACATGTTGAAAGCTTTAAATAAGGATCCTTGGATACAAAATATGGTCCACAT
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SEQ ID NO: 2259 ACGCGGGCTGAACGTGAGAAATTGACCCAGCAGATGATCAAGTATCAGAAA
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SEQ ID NO: 2260 ACTTTTTTTTCTTTTTTTTTTTTTTTTTTAAAAATTTATCGGTTCCGACTTAA
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SEQ ID NO: 2261 ACAGAAATTAAAAATCAGGAAAAAATAAGAAAAAAGCATTACAGTAAGAT
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SEQ ID NO: 2262 ACGCGGGGGGTGTGTTACCTGCCACAGCATAATGCGAGGCAATGTCCAGCC
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SEQ ID NO: 2263 ACATCCTCCCAAGTCTGGAATACAGAATTGATGGAGGACACTTAACTTGCTT
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ANAGCACTGGAACCAAGAACCACTTAAAAATTTAGAATAAATTAGGAAATTTCAATCTATAAGTG

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AGC

SEQ ID NO: 2264 ACAAGATCTACCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAGG
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NCAANTNCTGC

SEQ ID NO: 2270 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGTAAAAAAGCTGA
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SEQ ID NO: 2271 ACTGTTAAATTATTGCTAGCCATATCTTTAAAAATGGTTTTTCAGGAATATTTCT
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SEQ ID NO: 2272 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCTGTCTAAATGTTTATTAAGTATGA
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AACCTTGCTTGGCCTTGTACCCATTCGGCNCNTTTATAGGCCGGGTGGGGCGGNAACCTNTGG
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SEQ ID NO: 2273 ACCTTGATACACATAATCAGCCTTTTCAAAAAATGCCTGACAAGAAATTAGTCTT
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GNTAATCATTTTTTGTATCAAAAAATCAAAATNAAGGAACCCCAANTTCTTGCCCGGCGGC

SEQ ID NO: 2274 ACACAGCAGCCAGTTTTCATCGGTGATCATGCACAGCAATGCCATTGCTGCC
ATGACCAGCAGCAACCACAGAGCCTTTTCAGACCCAGCTGTCACTGCTCCCTGAAAGATGACAG
TAAGCCCGAGCCAGATAAAGTGGGTAGGTTTGCAAGCAGACCCAAAAGCATTAAAGGAGAAAAAG
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CAGGATTCCCTGACAAACCGTGGCGCCCTTACTACAACTACAACCCC

SEQ ID NO: 2275 ACTTTTTTTTTTTTTTTTTTTTGGGATTTTAGTAAANACATGGTTTCGCCAT
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CAGTCCCTTTTATTGGCTCTGGATGGAAAAATCCCTACCCATGTGATGGCCCTGGTCTCTCTATAGTT
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GGTCTGTNTCTTCAAAGTGTGGGGCTGCCTATTCTCCANGAACCAAAATGGCCCCCGCTTAAAN
AAAAGTNTGCTTACTANGAAATACCCCTGCCTNCCTTANGAAATAAATGCTACTTAAGGAAAAAAT
TANAAACCTN

SEQ ID NO: 2276 ACAAGATCTACCCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAGG
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SEQ ID NO: 2277 ACTTTTTTTTTTTTNTTTTTTTTTTTTNGGCTTNGAAATTACTTTAATTTANAAA
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SEQ ID NO: 2278 ACGCGGGGGCTCGGCGATGTGCTGGGTTCAAGCAGCCTCCTTGATCCAGGG
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SEQ ID NO: 2279 ACCAGCTGGCACAGGAGCAGGGGCATGGCACCTCTGTTGTTTATGCCCAT
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AATCCTTCTGCTGTGCGCGCATATTCTCTTGTCTGCCGCGCATCTCTTTCACGGCGCTGCG
GCTCTTCTCCTGCTGAGCTCCAGTTGCTTTCGTTTTTGACCTCTTGGTTGTGAGCTCTTCCATC
CTCCGANGTCTTTTTTNGCGCCTAATCAAATCCTGTCTCATTAGCATTGACCTGTAGCTCATGGCG
TGATCTTCTATCTNTCT

SEQ ID NO: 2280 ACTGTTAAATTATTGCTAGCCATATCTTTAAAAATGGTTTTTCAGGAATATTC
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CAAAATTGCAAAATATATGGAGCCAGGAGTTTGTCTATAGAGAATTCTACCGAATCTTACAGCTTGT
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CTNAAATCCATTTCT

SEQ ID NO: 2281 ACTTGTTTTCTGTATGAATTGAACTTTTGAGCAATAAAAGTGCTCTGCATA
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GGAACCAAGGCTGATCTCTTTCCAGAGGGCACTATCCGACCAAGTGCATGATGATATCCTCATCGCTC
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AAGTCCAAGGAAAAAGGTGGCCAGAGTTTGCCAACCTCGGCTGGATACCTTNAGCAGAGAA
NTCTCCGGAATNGAGAAGCTAAAGAAGGTGTGAANGCTTG

SEQ ID NO: 2282 ACTGTTAAATTATTGCTAGCCATATCTTTAAAAATGGTTTTTCAGGAATATTTTC
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CAAAATTTGCAATATATGGAGCCAGGAGTTGTCTATAGAGAATTCTACCGAATCTTACAGCTTGT
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CATACTAAAGGAAAGGCCAATTTTTTTTCTCTTTGNANACAAANNTATGAAATNATNGNNAAG
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SEQ ID NO: 2283 ACGCGGGATACAAAGATATCCTAGAGACCCATCTGAGAGAGAAAAATAACAG
CACAGAGCATTGAGGAGCTTTGTGCGGTCAACTTGATGGCCCTGACGCGCAAGTGGACAGGAGC
AGGCTGGCTGCTGTTGTGTCTGCTGTAAACAGCTTCACAGAGCTGGGCTTCTGCATAATATATTA
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SEQ ID NO: 2284 ACTGCTAAGAGGTATTATTAGAAACAAGATTTAAAAATATGTAACAAAAATCT
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GGGCAACCGTANTATAGGAAATATACCTATTTTGAATGTGGCATCTTTGTTTGAAGAGCTGGC
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SEQ ID NO: 2285 ACACCANATCACGAGACATCGTTTCATCTCCCAATAGTTTTATATTTTATG
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GTCTCTTACACCTTTCTGGGCCTATTCACTTGCAGAGAGGAGTCGAACTGTAACCAAGGCTCTTCA
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SEQ ID NO: 2286 ACCACACAATACTAACCTTCCCCTCTCTGATGTCTTACATCACCTCCCAGG
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TTTNTAGGCTGGGCTGACATGANACNATNAATTTGTCNGACAGCTGGANTTCAGTGAGCCANAC
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SEQ ID NO: 2287 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAG
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SEQ ID NO: 2288 ACNCGGGGGCAGTGAGTTCGACACACCNTGCCGACTGTCANCGTGAAGCGTG
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SEQ ID NO: 2289 ACGATGTCTAGTGATGAGTTTGCTAATACAATGCCAGTCAGGCCACCTACGG
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SEQ ID NO: 2290 ACTTTTTTTTAAAAAGNGGCCACCACATCTTTATTGCATACTCAGGTGA
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SEQ ID NO: 2291 ACTGTGTAGAATTAAGCAAAACAGNGTGATGTTTCAGAAAGTAACCCATTACTG
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SEQ ID NO: 2292 ACAAANATGGCTATAAACAAGATGCAGCCCTCGGTTTCCATGAACAGCACAC
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SEQ ID NO: 2293 ACGCGGGGGATAATCACCCAGAGAAACAGTTCTCTACTGATGTTTTGAAGCA
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SEQ ID NO: 2294 ACGCGGGGAGCGCGCTCCAGCCACAGCCTCCCGCGCTCGCTCAGCTCCA
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SEQ ID NO: 2295 ACGCGGGGGCTGCCACCACCTCCGCTGCTGAGGTTGCAGATGGCTCTTCCCC
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SEQ ID NO: 2296 ACTTTTTTTTTTTTTTTTTTTTTTTTGGGAATGGTAGTGANAAACCAACATTTAT
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AGAGCCAANATTTGCTNTTTGNTTTGAATNAAANTCCAACAATTCNAAATTTTAACTTGNTTTAT
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SEQ ID NO: 2297 ACTTTTTTTTTTTTTTTTTTTTTTTTAAACANAGCCTGCTCTGTTGCCAGGCT
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SEQ ID NO: 2298 ACTTTGCCTACGGCAGCAACCTGCTGACAGAGAGGATCCACCTCCGAAACCC
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SEQ ID NO: 2299 ACGCGGGTTATCAGAAAAAATTTCCAGCTCAACCAAGATAAAATGAATTT
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SEQ ID NO: 2300 ACTTTTTTTTTTTTTTTTTTTTTTGGGTTTTTAAANCCAAAATGTGTTTATGANA
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SEQ ID NO: 2301 ACACAGTATGTCCCTCATTTAAACCAAAAGTGATCCCAAGTTTTGTTGGTCACT
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SEQ ID NO: 2302 ACCTTCAAAAGTGAGATTCTGAAAGCATGAGTAAATTTGGGGGTGGTAATA
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SEQ ID NO: 2303 GGGGTACATTAGGATCCCTCGGCCAAGGACTGGACCAGAAGAACAACCTGGG
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SEQ ID NO: 2304 ACTGCGATTAAAAAAAAGCACTTCTGCCAAAGGAACCATGTTCCAACACCG
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SEQ ID NO: 2305 ACGATGACATCTCAAGGAGTCACTGGCCCTAGGTTTCTGCAAGTAGGATCTTA
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SEQ ID NO: 2306 ACGCGGGGCTTTTTCGAGGTAGGAGTGCAGTCTCTGTGAGGTATGGTGTGGG
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TTTNNANCTCAAACCTTTTGGGGTTAAGNTGATCCTTNAANCNCCAATGNGNCTTTNGANANTGC
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SEQ ID NO: 2307 ACAGTCTTTCATTAATAAGAATACTTACACATACATTTTCANATATTTCTAC
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SEQ ID NO: 2308 ACTATTTTCATGGTCCAAACCTGTTGCCATAGTTGGTAAGGCTTTCCTTTAAGT
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AAA

SEQ ID NO: 2309 ACCCTTGGACAAATTTGTTCCAGCAAGAAGCTAACTCGACCACTGGTGATGA
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SEQ ID NO: 2310 ACATTGAGAATATGTGTAAGTCATTTTTTAAAAGGCTTCTTGTGATTAAGA
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SEQ ID NO: 2311 ACGCGGGCAAACCCCTGTTGAGATAAAGCTGGCTGTTATCTCAACATCTTCATC
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TCTATAGCATGATTCTTCAAGTAAAGGCAAAAGATATAAAATTTTATAATTGACTTGAGTACGGC
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SEQ ID NO: 2312 ACAGAAAGAGCAGGGCCAGCTCAGCCTGCCCTGGCCATCTAGACTCAGCCT
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TCAGCTTGTCTGCTNTANCCNTNATTTNCANAAGCTTNTTCTTTGGCATCTATTGTCAGTCCCTN
ATNACACCAGTTTACGGCCTNNGAAAGTGTTCAGACCANATGGCATAAAGGCACNTCTTTATTGT
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SEQ ID NO: 2313 CGNCGAGGTACTAGAAGTATACACCACCCAGCCCGGGTCCAGTTTACACG
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SEQ ID NO: 2314 ACACCAACCTGAACAGATTTTGTGCCACAATTTCAATCAAAGGGTTTGTCAAT
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SEQ ID NO: 2315 ACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACCTTCTGAT
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GCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCAATCTCAAAAAA
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GGGGA

SEQ ID NO: 2316 ACTATTAAGCCATGGTCAACCCACCGTGTCTTCGACATTGCCGTGACGGN
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TTTTT

SEQ ID NO: 2317 ACTTGATTTTGAACACAGCAGGAAAAACATTTTGAGCTGGTGAAATCAGCG
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SEQ ID NO: 2318 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGTGCTGCCNCCACCATGAAAGAGTGG
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TTTTT

SEQ ID NO: 2319 ACACAAAGAGGGGGTGGGTGTGGATGCAGAGTGTGTGGCCTGATGCTCCAC
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CAGGTAGGTTTGAGGGGATACATCCTAAGAGCAACACCCATTCCAGGGCAGTAGGAAAGGAAAG
CAGCCAGGGCTGTCTCTTCAAAGAGGGCCAAATATCAAGATCTTGTCTTCATCCCTGTGGGAAGA
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SEQ ID NO: 2320 ACTGTGGAGGCTGAGGCAATTTTCTTCAGGCTAACCCAGATTTTCTAAAGCCC
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TTTTCGGCCTGCANATGTCAGCCACG

SEQ ID NO: 2321 ACACCTAGGACCTCTAGTAAACCTCATAAACATCTGCCTCCTGCAGCCCTACA
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CGGAAAGAAATTTTGAAGAAAGAACGGGAGGAGCTGAAAAAGAAAGTTGAAGGAAAAAGCCAAA
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ANTTCCTTAACTG

SEQ ID NO: 2322 ACCTTGTAGCATTCTGAGGACAGGCCTGATTTCTGAGAAGGAAAGTGTAA
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ATGTGTACGGAAGGNA

SEQ ID NO: 2323 ACTGTCTCTTTTGGAAAAGTTCTTGATCCCCAATGCTTCACAAGCAGAGAGCA
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SEQ ID NO: 2324 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGATTATAAATGCATTTTAATACC
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SEQ ID NO: 2325 ACAACTAAAGGCAACTGGCATGGACTCAAATATTTTGGGGAAGAAAAAGACT
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SEQ ID NO: 2326 ACGCGGGGGCGGGAGAGAGGCGGAGATGGCAGATGAGATTGCCAAGGCTCA
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SEQ ID NO: 2327 GTTGGTGAAGGAGTGCCAGTCCCAGGTGACACTGGACAAGAAAGAGGC
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SEQ ID NO: 2328 ACTCGTCAATGGGCTCGGTTCATATATACCACCTCGAAGCCCCGTTTCCGCACT
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SEQ ID NO: 2329 ACTACGCAGGCCTTGGCATCCCTGGGGTTACCTGGCTGACTGGGATGTTGA
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SEQ ID NO: 2330 ACATTACGCACCATTAACATGCGTCTTTAAAGCCTTCCCAAAATATTAGTAATCT
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AAC

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SEQ ID NO: 2333 ACACATACACACCTAAAGAGTCATGGCCTTCTTAAACAGCTTTCTTAATCCTT
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SEQ ID NO: 2334 ACTATGCCAAACACTTATAACTTGTATAAAAAATCCACATCCCATATTGGCC
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SEQ ID NO: 2336 ACGCGGGGGGAAGGGAGAGAGCTGTGCGAGCGTGGGGGAGAGTTTTCGTT
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TCACTAGTGCCTAAATGTAGTAAAGGCTGCTTAAGTTTGTATGTAGTTGGATTTTGGAGTCCG
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TTTT

SEQ ID NO: 2337 ACGCGGGGAGGAAGAACTAAATCCAAAGATACTAGCTTTGAGAATGCTCAG
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SEQ ID NO: 2338 ACCACTACGATGCTGGTGACCCAGCTGCTGTTGCCAAACCTTGACCAGCG
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SEQ ID NO: 2339 CGCCGGGCAGGACTTACTTGGAGAGACATATGTCTGAATTTATGGAGTGTA
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SEQ ID NO: 2340 ACGCGGGATTCACTAAAACCATGTGTCTGAACTGAAGAAGCTTGGGCTCACT
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SEQ ID NO: 2341 ACTACCTGATGGATGCTGCCTCCTTGTGCTGCTGTTCTGGCCCTCGGCCTGCA
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SEQ ID NO: 2342 ACATTAGCACCATAACATGCGTCTTTAAAGCCTTCCCAATATTAAGTAATCT
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SEQ ID NO: 2343 ACGCGGGCTATTTGAAGATATGACTGATTCTGACTGTAGAGATAATGCACCC
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GGNTACTCANGAGCTGANGCAGGAAAAATCACTTGCNCTCCCGG

SEQ ID NO: 2344 ACNCGGGTGATCGACCANAGCTAACAGGTGCCAAAGTGGTGGTATCTGGTGG
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ANTTGGTGTCTCCCGTGCTGCTTGTGATGCTGGCTNTG

SEQ ID NO: 2345 ACTAACCTCATTGTAATGAGGTTTAAAGAGAAGGCCAGCACTAAGCCAGGCT
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AGATGGCAAAACACATGGGCTTTGTACTCCACTACTGACTTCCAGGCTAAGGAAGGACTGACTT
AGTGAGCTGTTCCAAAGCACTGAGTCATGGTTCCTGTGGCTGGGACCTCCATCATGACCGGGG
CTTGAAGAGGGT

SEQ ID NO: 2346 ACTGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAACTGGAAGAG
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CGTGTGAAGGAAAATGATCAGAAAAAGAAAGCAAGCAAGAGAAAGGTAATACCATGCCGGGCC
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TCAAGTGATCCTCCTGCCTCAGCCTCCCGAAGTGCTGGGATAAAAGGTGTGAACCACTACCCA
GCCAGTATTATCTTTTCATTTTCCAGTTGAGTTTATATTGGCTACATTTGCATACCCGACAA
TTGTTTCATTTTTTAAACCATATTTTGTGTTGTTCTGTTGCTACAAATTAAGGAGAAATTCNATGATA
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SEQ ID NO: 2347 AOCTGCATCAGCATTAGTAATCAACCTGTAAATCCAAGGTCTTTAGAAAACT
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SEQ ID NO: 2349 ACGCGGGATTGCAGCTTCAACTTTTCTCTTTAGTGTCTGTGTTGAACTAATA
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SEQ ID NO: 2350 ACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAGGACCAAGAAAGAGGA
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GANGAAGGGGAAAGAAAGAAAGGGGAAAGAGATCANAAACCCACCTTGCCCCANGCTTANCANGGA
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SEQ ID NO: 2351 ACGAAGAAAGCATTTCCNAAGCAATGAGTCTCTTAATGGAAAAATAAAAG
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SEQ ID NO: 2352 ACAAAAATACAGTTGATGACTTGACAAAATGGCTACACCTAGGGCTTGAAGG
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TTNTTGTANGATAACTCTTCCAAA

SEQ ID NO: 2353 ACATAGACAAGTTTCTGTNAGACAGAAAAACAGAGAAATCCACAGTAACCTCT
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SEQ ID NO: 2354 ACGCGGGGGCGGGAGAATCGCTTGAGCCGGGAGGTGGAGGTTGCAGTAAG
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SEQ ID NO: 2355 ACCCGACCTCCATCTTCACCAAGAAATGTTATCTCTAATATAACAGAGACCTC
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SEQ ID NO: 2356 ACGCGGGGAGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAG
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SEQ ID NO: 2357 ACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTGCTTTTGTGTC
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SEQ ID NO: 2358 ACGCGGGGCTCTTCTGCTCTCCATCATGGCGCAGGATCAAGGTGAAAAAGGA
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SEQ ID NO: 2359 ACTGGCCCTCAGTGCTGGCAAAGGTGTAGTTCCACTGGCCGAGGGAATCAAG
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SEQ ID NO: 2360 ACATCAAGTCAGAATGATGTTGACATGAGTTGGATTCTCAGGAAACATTGA
ATCAAAATCAATAAAGCTTCACCAAGAAAGTTGCCAGGAAACGGGCACAGAAGAGATCAGTGGG
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CGGCTGATGGGATTGAGTGCTAGAGAANCCATGT

SEQ ID NO: 2361 ACCGGAAAGGAAGCTCCATTCAAAGGAAATTTATCTTAAGATACTGTAAAT
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SEQ ID NO: 2362 ACTTTTTTTTTTTTTTTTTTTTTTAAATNAAATCAGTAGTTTTATTACAAT
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CGGGGA

SEQ ID NO: 2363 ACTTGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGACCAA
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SEQ ID NO: 2364 ACACCTTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAGGGCCGGA
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AGACGGCCTTTTGACCTTTAAGGGTCTANAGGCTGTAAAGTGTCTCAGGGTTANTANCNAACAAA
CCATGANCTGGNNTGGGATTTTNTNACTNGANAAAAANNAGGCTTGNTT

SEQ ID NO: 2365 ACGCGGGGGAGGAGACTATACAACCTACAATAGAAGCATTTATATCTGCTAGT
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SEQ ID NO: 2366 AACTAGAGGCTTTGGTAAAACATCTTCTCTCCAGAGGGTGAAGATAAATAA
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SEQ ID NO: 2367 ACCCAAAGGAAGAAAGGTCTGCCCTGCCTTCTATAAACACATGCATGTGGCTC
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SEQ ID NO: 2368 ACGCGGGGGTGTGCTGTAAGGGGTCTCCCTGCGCCACACGGGCGTGGCCATG
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SEQ ID NO: 2369 A C A C T A A C T T T T A A G T G T G G C A C A A A T G G A A T A G A G A C A T G A A G T T T A A T
G A G A T C C A A G C T T C C A A C T A A A T G A T T T C A C A T T T G A A A A G C T A T G G A A A G A T A C A A T N A T T T A C T
G T T T T A C A A A T C A A A T G C T T A A A C C A A G T T T A A A A G T T G A G A C C G A A A A A A A T T G A T G A A N A A A A
A A T G G C C A A A A A A T T A A A C A A A A T C N T I G G T T T C C T T T A C A G G T T A C T T T T N T T G C G T T T N A T T N
T T T T T C A A A T T T G C A T T T T A C A N T T A N A A N T G C A N A N C A C T T T G G A T T A G C T A T T G G A T C N A A T A C
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SEQ ID NO: 2370 A C A C T G A A A A C T G G A C A T T N T A A C A T T A A T T T T A T T A G C T C T G G G A G T G A G
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A A G G A G T T C A T T A C T A C T T A A C A T G A T G A A G A C A A A A T A C T G C T G T C A G A C C A T A C T G T T T C A T T
G A A T T T G A A C T T C A T T C A G A G G A C C A A G C A G C G A T A T A A T A A T C C C A G G T C T T T T C A A C A A A G
A T A A A T C T T T C T G A C A T G C A N A C G G G A A T C A A G C T G A A G G C C T C C T A T C N A A T T T C C A N N G C C A A
C N N G G G N T C A C C C A T T G N A N T C N N T C A C C N T T T T T G T T G A C T G A A A A G N G C T G G T A A A A T T T C
T T C T G T C A C C A G C N A C T G G A C C A G C A A C T C T G T C A G G G A T T G T A G G A T T T A T C C T T A G T C T T T T A T G
T G G A G C T C T G A A T T T A A T T C G A G G C T T C A T G C T A T A G A A A G T C T C C T G C A N A G N G A T G G G T G A T G
A T T T T A A T T T A C A T C A T T G C T T T T T T C C T T G G A A C A C A G C C T G C C T T T N C A A G N G G T A T T A C T T
G T C T A C T A C A C C G G C T T G G N G G A A T G G C A A A T N T T T T G A C C T T T N G G C T T A A T C T G C T A T T G C A A
N A T G G

SEQ ID NO: 2371 A C T A G G C T A A C T A G A A G G A T C T C A T C C C C A T A T G T G G T C T C A T T T C A A G T C T A
T G G A T G A C T A C C T T C A T T G C T G T G C G A G A T G G T T T C A C C C C T T G A A A A T A T G G T C A C T T C A G C A
T A A A A T A G T T A A A T C T T T A T A A T G A T C A A T T C A T C C T A C C T C C T T T T A C A T G C A G C T G A A A A A T G A
C A G G C T A G G G A C A T A G A A T A T T G T G A A C T T T A C T G T T A G A A T C A C T G T C C A T T A A A T G A T C A C T
A G C T A A T G G T C A C T A A A T T T A C A A A T T A A G G A A A T T A T A T A G A A T A C T G C A A A A C A C N A G T A A
A A A G A C T G A A G T T C G C C C A T T T C T G C T C A N G G A A G T C T T C A C T C C T A A G C T T C A T A T T G T T G C
C T T C T G G C T N C A A A A A T T C T G C T A T T A T T A C T G N T T T C C T C C T T T T G A T C T T C C T T T T G G T T C C C C A
G T G C C A G A A C T T C C A N A N C C T T C T G C T C A A A T G C C A T C T T T T G T N T C C A T T T C A A A A C A G C T T C
A A G T G A T G C C T T G T G G A A N A A A A G G A T G C T T C C C T G T C T A A N A T T T N C T N C T T G N T T

SEQ ID NO: 2372 A C G C G G G C T T A C A A G T C C T T T G A T C C T G A A C T G G G T T A G G T G C C G C T G T T
G C T G C T C G T T T G A A T C T A G A A C C G T A G C C A G A C A T G G G A C T G G A G G A C G A G C A A A A G A T G C T T A
C C G A A T C C G G A G A T C C T G A G G A G G A A G A G G A A G A G G A G A A T A G T G G A T C C C C T A A C A A C
A G T G A G A G A C A A T G C G A G C A G T T G G A G A A A T G T G T A A A G G C C G G G A G C G C T A G A G C T C T G T
G A T G A G C G T G T A T C C T C T G A T C A C A T C A N A A G A G G A T T G C A C G G A G G A G C T C T T G A C T T C T T G C
A T G C A A G G G A C C A T T G C G T G G C C C A C A A A C T C T T A C A A C T T G A A A T A A A T G T G T G G A C T T A A T T C
A C C A G T C T T C A T C A T C T G G G C A T C A G A A T A T T C C T T A T G G T T T T G G A T G T

SEQ ID NO: 2373 A C A A T G C C T G C C A T C A T G G G T C A G A A A T T T G A A G G A T G A A G A A A T C T A C T G T
T T G A A A T C C T C A C C T T T C A G A C G T A T T T T C T T A T T C A C A T C C C A G G A G C A T C C A T T T T A A G G A A C T
A T T C T T T G G A A A A A C A A A A A C A A A A A A C A A C A A A A A A A G C T A A G T T A T A A G T G A A C T G T
T T G G T G C A C T G T A T G T C A C T T T T G C T T G T T G T C A T G T G A A C T T G G A A C T A A G G T T A C T C G T G T C
A T A A A A A T T C T A A A T G A A A G G G T G T G G G T T C C A T C A A T C T G A T G C T G C C C A T C G C T T G C A C T G G G
G T C T T T G T G G A T C G G G C A G A N T T N T C A G T G T C T G G G G T G T G T C C T T C C T A T G T G T C T T T T G A A
T C T G A G G C T G A C A T T T T G C T T G G A A G G C C A A C C C T T G C T C C A T C A N A G A G G G C N A G T G G C N A A A G
G C C A A T G A G G C A G C T G T G A N T T G G A C A G G G T T C A

SEQ ID NO: 2374 A C A G A A A C T G G T A T T T T T G G T G C T G A T A C A A G A G A A A T G T A T T T T T A A A T A T C
C C A C A T C C T G G A C T T T T G T G G G T A T T T A G T A T A T T G A C A T A T A T T T T A A G G T G A G G T A A C T C A
G A A C T T A A T T T A A A A G T C T T A A A T A T T C T G A T A C A A T T C A G C T G T C T C T C N A C C T T A C C A T A N G C C
A G T T G C T T T C A T T T T A A C C A A G C A A G T A A C A T A T T N A G T G A C T T G A A T C T T C A T A A G T T T A A A A
G T A A A A C A G C N A A A N A C C T A N T C T T T G T C T T T N A A C N C N G A N C A T T T T C N A G G A A

SEQ ID NO: 2375 A C C T G T T A T T G A A T C A A C A G A G A C T A T A G A G G C T A A G G C T G C C C T T A A A C A G
T T G C A G G A A A T T T T T G A G A A C T A C A A A A A G A A A A A G C A G A A A A T G A A A A A T A C A A A A T G A A C
A G C T T G A G A A C T T C A A G A C A A G T T A C A G A T T T G C G A T C A C A A A A T A C C A A A A T T T C T A C C C A G
C T A N A T T T T G C T T C T A A A C G T T A T G A A A T G C T G C A A N G A T A A T T G T T G A A G G A T A T C G T C G A T A A A
T A A C A T C C T T C T T G A N A N G A A A T T A A N A A C T C G C T G C N A C A A C T N A A A A G C A N G A A C N G A T T A
T C A A T N C G A T G A C T C A A G A T T T G A N A G G G N C A A A T G

SEQ ID NO: 2376 A C A C T C G A G A T G A A G A T C A C A T T G C A T T G A T C A T A G A A C T T C T G G G G A A G G T
G C C T C G C A A G C T A T T G T G G C A G G A A A A T A T T C C A A G G A A T T T T C A C C A A A A A A G G T G A C C T G A
A A C A T A T C A C N A A T C T G A A A C C T T G G G G C C T T T T T N A N G T T N A G T G G A N A A G N N T G A G T G G T C T

NANGAAGAAGCNATNTGGCTTCACACATTANTG

SEQ ID NO: 2377 ACATTAGCACCATAACATGCGTCTTTAAAGCCTTCCCAAATATTAGTAATCTT
GACCAGCAATGACAAGAAAAAGAGGAGCACCTTTACAAGCAGTTGATATCCAATATTTAAATAA
TTGTGGCTTTAAAAATATTTCTTTAAATTCCTGCATTACACTTTTCTTTTAAACCAATCTTCCAGG
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GAATACAATCTGTGTTCTGACCAAGTTGAGGTAGTTAAAAATAGGGGAGGGCTTTCTAATTTGTA
TTTGACTATTTAGAAAAAGAAAGGTTATCTTTACTGGTGAGCACAGTNATTGGCTCTGGAGATGG
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SEQ ID NO: 2378 ACATGGCTACACTGTGCTCTAAAATTACTTGCATTAATGAGGACATTAATTTT
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SEQ ID NO: 2379 ACGGATGTGGCAGCGAGAGGACTAGATATTCCTGAAGTCGACTGGATTGTTT
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AATGGGAGAGGGCATGCGTTGCTCATTTTGGCCCAAGAAATGGGTTTCTTCGTTACTTGAAA
CAATCCAAGGTTCCATTAAGTGAATTTGACTTTTCTGGTCTAAAATTTCTGACATTCAGTCTCAGC
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CATACGAGCCTATGATTCCCATTTCTGAAACAAGATCTTTANTGTATAAACCTAAATTTGCGCTC
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SEQ ID NO: 2380 ACACAGCTGTACAGGAAAGTCTGATGGCCACAGTGAAAAAGGTCATGGGTG
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SEQ ID NO: 2381 ACGCGGGGCGAGGCAACCTGAGGTCTCAGAATGGCGGGCACAGGTTTGGTG
GCTGGAGAGGTTGTGGTGGATGCGCTGCGTATTTTGATCAAGGTTATGAAGCCCTGGTGTGCGG
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ANAAAAAT

SEQ ID NO: 2382 ACCATGAAATATCCAGAACATACITATATGTAAAGTATTATTTATTTGAATCT
ACAAAAACAACAAATAATTTTAAATATAAGGATTITCCTAGATATTGACGGGAGAAATATACA
AATAGCAAAATTGAGGCCAAGGGCCAAAGAGAATATCCGAACTTTAAATTCAGGAATTGAATGGGT
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GATCCACAAAGTCCITGTTCCACTGGGNCITTTGGTTNCTCCCTTATTGCTANGGTGGGAAAAAAG
GNTTTGCCACCATNTTACCTTACAGTGAATG

SEQ ID NO: 2383 ACGCGGGGAGCTCTACGCTCTACGTTTACCTGTCCATGTCTTACTACTTTG
ACCGGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGGGG
AACATGCTGAGAACTGATGAAGCTGTANAACCAACGAGGTGGCCGAATCTTCTTCAGGATATC
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SEQ ID NO: 2384 ACTGTTCAAAAAGGAATGCCCCACAAGTGTACCATGGCAAACTGGAAGAG
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AANTNNGG

SEQ ID NO: 2385 ACGCGGGGCTCACTCTGCGCTTCAACCATGGCTTTTCATTGCCAAGTCCTCTAT
GACCTCAGTGCCATCAGTCTGGATGGGGAGAAAGGTAGATTTCATAACGTTCCGGGGCAGGGCCGT
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AGAACTGTCAANAATGAGGAGATCCTGAACAGTCTCAAGTATGTCCGCTCTGGGGGTGGATACCAG
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GGGAGGGAGAACCCCTTTCGACGCTACAGCCCGCACCTTCNAACCAATTAACATTGGAGGCTGAC
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TCCATCC

SEQ ID NO: 2386 ACTTCTAATTCCTCTATTACTGTGCAATCTAGAATTTCTATGTAAAAGACA
GTGCTGGCAGCATCAAAGCCCTGTAATAGTATGAAATAGTGATTAGGATTTGAAATGAAGAGATA
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SEQ ID NO: 2387 ACGCGGGCAAACTGTCAAGTGAACCCGCGGTATTAAACGATTGATTAGTGTG
TTAAACAAAAGCACGGGTGAAGTCACAAAGAAAAAGCCTAAGTTTTTGACTAAAGGCCAGAAATGC
ATTGGTAGAGCTACAGACACAAAGACCAATAGCTCTTGAGCTATATAAAGACTTCAAGAGCTGG
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TANTN

SEQ ID NO: 2388 ACCAGGGCAAGAAGCCGGATGTCTGCCCTTCTCAACCCAGCTCCCTCAGGAG
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SEQ ID NO: 2389 ACACATCCAAGCCTAAAGAAAAATTAGTCTATGCCATTTTCTTAAATGGCCC
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AGCTAACCAATTCATCAGATGCCGTGTAATGGGGCTGGGCTCTAGCCCTGACTAATGTGATCAAA
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TCCCTTTTTCCANTTAAATTTTTNTTAAAAATTACCNTTGTAAACCAATTTTAACTCTTCCA

SEQ ID NO: 2390 ACACAAAGAGGGGGTGGGTGTGGATGCAGAGTGTGTGGCTGATGTCCAC
GGCGTGCAGGACGGGGGCTAATAGTAGGTTTCTTCTCCACCCAGCCNCCAGGGCGTGCCTGA
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ANCCANAGCTGTTTTTNNAAAGATGNCTCAAAATTCATNATNTNTTTTTNTNCCCTNTNTNTAAG
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G

SEQ ID NO: 2391 ACTCATTTACAATAAAATAACCAAGTGAAGTTACAAAGGCATATATTACTG
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GAATATATATCTATTGCTTTTCATCATACTTGATAAATACAGTATGAACAAAAATTTTCATTGTATAC
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ACTCAAAACAGCTAAAAATTCACAGTTATTCTNCAACAATTACAANGTAAGCTCTGCGCAAGGC
TTNCAGA

SEQ ID NO: 2392 ACAGAGGGGTCTGTTTCTAAGTCTGGAACCTCAACACGAGGCTGGGATGCTT
CACAACGTGCTCTCTCCACTGTCCAGCCATCTTTGGTGGTCTTCCCACAGTGTCTCCCCATCCTC
TCACACTCTCTGTGGAGGACCATGGGACGGGCCAGGAGGAAACCTGGGATCACTCTGACAGGAA
ACGGACAAGCACAGCTGCCAGGAGCCAGTTGCTCTGGCCTCAGTCTCCAATTGTTAGTCTCAGGAT
CAACAGAGAACTGGAAGCAGCAGAATCTGGAGGAGCAGGAAGAGAGCCAGAGGGAGTGTGT
GCTGAGTGACGGTTAACAGATGAAACAGAAATTCATGGAGATTCTTTGTTACAAGGAGAAATGTC
TCAGTCTCAACTCCCAAAACGTGAAAGTTGCCGTGGTTAAGANACCTATGTTTTCTTTTCAGCTCT
TCAAACTCCGGGAAAGATCATCAAAAGTCAATGTCTTANATGCTGAGGTGCTGGCACCANCANA
TCAGTTGGTANTGTGTCTGGCCAAATGGCAACNTCTGGTANGGACAAAANTNGTCATANTNTNTT
GCAGGTCTTGAAGGAAACTTTGCANAAGCTTNTGGNTTGGGTNCCAGAACCAACAATNTTGTGC
ANAAAAAT

SEQ ID NO: 2393 ACAGAAAACATAAATCATCGAGGTGGATACCATGGTGGAAAGTCCCGTCTCTC
GTAGCAGTATTTTCCATGCAAGGAAAAAGCCAGGACTACATGAAAAACAACATACCTGACAATGAA
ACCGGGAGGAAAGAGACAAGAGAGAAGCAACAGTTTGAAGCTGAGGATTTCCGTCTTTAA
ATCCTGAGTATGAGAGAGAACCAATCACAATAAGTCTTTAGCTGCAAGTGTGTGGGGCTACAC
GCCANACACACATCCCAACCAAAAAATCTCCCAAGCTCCTCTCTTANAATATCTCTNCGAAT
CCTAATNTANAGCTCCAAGGATGCTNNGNCATTAANAAAAGGTAATACA

SEQ ID NO: 2394 ACAAACCATCGCCATCAAAAAACGCTGTTCTGACAACACTGAAGTAGAAG
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CGTATGCAAAAACTTGCAAGCAACGGCGCGTTGGGATAATGATGATGACAGATGACATTCC
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TTNTACAATAAACAATGTTTTTGGAAATAAANNNTTTACTTTTTAAAGTTGGCACCAGGCTGTG
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SEQ ID NO: 2395 ACACCTCTAAGTGTGCAAGTGAAGAGCTTGTTTATATTTTCATACTTTTTATACT
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AAATTCAAAAAATAGCCTCATGAGACTTGGCATAACACTCATGGGATTCAGTTATTTAGGAGTG
CTTCCATCCCTCTCCACCCCTTCCCCCAAAAGGTTTCTTTGCAAGTGCTTTTGGAAGTAAAGAGCT
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SEQ ID NO: 2396 ACGCGGGGAAGCCAGCTGCTCGGAAAGCTCTGGACAGATGCAGTGAAGGCT
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SEQ ID NO: 2397 ACGCGGGACCATGGCGGGCGGCGGACNANCGGAGTCCANAGGACGGANA
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SEQ ID NO: 2398 ACGCGGGCAGGAGAAGAGAAGGAATTGAAGAGAAAAAGGAAAAATAAAAAT
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SEQ ID NO: 2399 CGGCCGAGGACGCACTGAAGGAGACAAGAAAGCAGCAAAGGTTCAAAAGCT
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SEQ ID NO: 2400 ACGCGGGGATAGGGAGCGATCTCCGAGCGAGGGCGGCAAGATGGACGCGGGA
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SEQ ID NO: 2401 ACCCTTGGAGATACTGGAGCGCTTCTGCATTTCAGGCTGGTGTCTACCATTTGAT
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SEQ ID NO: 2402 ACGGTAAATTCAGTGGCAGATACAAAAGCTTATTTGGGAGACAGCAGATCTC
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SEQ ID NO: 2403 ACCCATAAATTCATCTTCCAAAAACAGGAGCTTTTTAAAGAAAAACCACAT
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SEQ ID NO: 2410 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCA
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SEQ ID NO: 2411 ACCTTTGTGACAACTCTAACACATTATCGGGAGCAGTGTCTTCCATAATGTAT
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SEQ ID NO: 2412 ACTGCTAAAGATAAAAATACAGGGAGAAAAATAACTTGTAGCAATAGATCCCC
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SEQ ID NO: 2414 ACTTTGCTACGGCAGCAGCTGCTGACAGAGAGGATCCACCTCCGAAACCC
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SEQ ID NO: 2417 ACGCGGGGAGGTGCCGCCATTTTCATCTGTCTCTCTGCGCCTTTTCGCA
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SEQ ID NO: 2418 ACGCGGGCATCTGTTACCCAGATCTACCATGCAGTTGCAGCTCTAAGTGGCTT
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SEQ ID NO: 2421 ACGCGGGGAAGATGAAGGTAAGTAGAAACCGTTGATGGGACTGAGAAACCA
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SEQ ID NO: 2422 ACTGGATTCCATTAAACAGGGTTAATTGGAAGAATCTTCAGGAGTGGAA
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SEQ ID NO: 2423 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGANACANAGTCTTGCTCCATCAC
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SEQ ID NO: 2424 ACAGGCTTAAATCTATGTCAATTTACACTCACTGAATCATCAACCTCATACCA
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SEQ ID NO: 2425 ACAAAAAAATCCCTTGCTTGAGAGTTTTGTACTTTTACTTAAATATTTA
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SEQ ID NO: 2426 TACGGTCTGAGACATCACCGCCAAGCTGGGCATCGGGGAGATGGCCGAGACT
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SEQ ID NO: 2428 ACAGGTGGAACAATCCAAAGTTTAAATCAAAGAAGGTGGTGTTCAGTTGCTG
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SEQ ID NO: 2429 CNCGGCCGACGTACTTCCACTCTTNCCTTAAAAANCTTGCCATTTGCTTATCA
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SEQ ID NO: 2431 ACCAATTAAAGTTGAACAAATTGAAGCAGGGACACCAGGCCGACTCAGAGT
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SEQ ID NO: 2433 ACTCTCCCTACTTCCCTTAACTCACTGTTTCTGAGAACAGTAATAAC
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CTGTCCGGTCACTACTCTATTCTCCATTCTCAACTACTTATAAATGCCCTACTCCTGTTTACACTGC
TGGTTTACACTGTTCTTCAAACCATCACAGCTGATATCTTGTGGTCTATCCCCAACTGCCACTC
TAACTCCCTCTTAGAGTGGGTAGATGATCTTGTGGCAAGGCAGCTCTCAATACTTCCACCTG
ATGAAGTTCTATTCTTACTTTTACTCACTCTATTCTCATCCCATTTCTATGCCACCTCTACCT

CTCCCCAGCTATCTCCACCACACTATCAACCTTACCCATTCTCTCTAGCCGCTTCTAATCTCTCCT
TGGCGAACAACTGCTGGCTTTGCAATGCTCTCTTCTCCAGTGCCTACACAGCTGCCCGCTTACAG
ACAGACTGGGCAACACCTNCCGCTCCCTACACCTTTTGAACCTCTTAACAGCCCTCACCTT

SEQ ID NO: 2434 ACATAGTGTGCGGAACCTCAAATCGGCATTTAGATAGATCCAGTGGTTTAAAC
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CCTTTTTGCTGTAATTGCACCACTTTTAAAGCCTCTGGACAGAGCAGTATTTTCGTTTAAAACTTTGT
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GGACACTGGTGGCAGGTTAAGGGATACTGCACTTAAAGAGCCTGTGATTGAAGTGAACATN
GGAGAAATNAGGGGTGATTTTTTAACTGTGTGAGATATT

SEQ ID NO: 2435 ACTTGGCTTGGAGACTGGCGCGGCGTTCTGTCTCGAGTTCTCTGCAGGTCACT
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AAATTCATAAATCAAGTGAAACTCTTGAAAAAGGATCCAGGAAACGAAGTGAAGCTAAAACTCT
ACCGCTATATAAGCAGGCCACTGAAGGACCTTGTAACATGCCCAAACCAAGGTGATTGACTTG
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SEQ ID NO: 2436 ACTTGTATTGATTATGTAGTTCAGTAAGATGTGCCCAAGTCATTTAGAAAA
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SEQ ID NO: 2437 ACAGGATGAATTTAAATGTGTTTTCTGTGAGAGACAAGGAAGACTTGGGTAT
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GGGC

SEQ ID NO: 2438 ACCTAGAAGAGAGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTTCA
AGGCTATCCCATCACCTTTTATTGGAGAAGGAACGAGAGAAGGAAATTAGTGATGATGAGGCAG
AGGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGATGAANAAAAGCCCAAGATCGAAG
ATGTGGGTNA

SEQ ID NO: 2439 ACATTAGCACCATATAACAGGCGTCTTTAAAGCCTTCCCAAAATATTAGTAATCTT
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SEQ ID NO: 2440 ACGCGGGGCGACAGCCAGAGCCTAAAGGCTAGAGCCGGAGCTGCCGGGCCA
GTCGCTAGCAGGTCTCTACCGGCTTATTCCTGTGCCGATCTTCATCGGCACAGGGGCCACTGA
GACGTTTCTGCCTCCCTCTTTCTTCTCGCTCTTTCTTCTCCCTCTCGTTAGTTTGCCTGGGAGCT
TGAAAGGAGAAAGCACGGGGTCCGCCAAACCCCTTCTGCTTCTGCCCATCACAAGTGCCACTAC
CGCATGGGCTCACTATCTCTCTCTTCTCCGACTATTGGCAAGAAGCAGATGCGCATTTTGAT
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TTGCA

SEQ ID NO: 2441 ACATTTAGAATTTTTGGCCGGGTGCAAGTGGCTCACACCCGTAATCCAGCACT
TTGGGAGGCCAAGGTGAGCGGATGGCTCGAGGTGAGGAGTTTGAGAGGTGAGGAGTTCAAGATCA
GCTTGACAAACATGGTGAAACCCGCTCTCCACTAAAAAATACAAAAATTAGCCAGGCATGAGGG
TGATGCTGTANCCACGCTATTCAAGAGGCTGAGGCAGGAGAATCNCCTTGAACCTGGGAGGTG

GAGGTTG

SEQ ID NO: 2442 ACACAATGTGTAGCTCATATGAAAACCTCATGACAAGTCATTGAGTTCTGTAACTGCCATACAACTTACATGTGTAATATTAATTGCACAAAGTATATCAAGACATATTGAAGAAAACACAAAAATTAAGTGCTATTTTAACGGTTTCATCTTTTCAGTATGTGAATACGTATACAAATTTAACTGCACAGTTTTGTGAAAAATAAGTTTCAACAATAAGACTTCAGTTGTTAAAAATTAACCCAAAAATATACTTTAATTAATTAACATCACTACAATATTAATCTCTTATCTTGTTTACATTTTGGTGTGTTGGGACTTTTGTAAAAAAAATCCAANTTCTAGAATTGCAAAAACCTTCATTGTTGCCACTGAGAGAGCAACATATNGTNGCGGGGGGGGAGACCANANATCTANCGACTGAANCANATTGGCCAAACCGNGTGGGGT

SEQ ID NO: 2443 GATCTACCATGCAGTTGCAGCTCTAAGTGGCTTTGGCCCTTCCCTTGGCATCCCAAGAAGCACTCATTGCCCTTACTGNTGCTCTNAGCAAGGAGGANACTGTGCTGGCAACANTCCANGCTCTGCAAAACAGCATCCCACTTGTCCCAACAGGCTGACCTGATGAGCATCTTGGAGGAAATTTAGGACCTTGTGCTCGGCTNNATGAACCTCNGGGGGCGTNTATCTCANNNTTAAAAAATGACTGGAAACAACATCCCTTTTTTGTGGGCTTGCCACCCTACAAAGCTCATTGNATCATNTTGGGACTTGAACCATCCATTAAANGGNAGGATNAGGTCAATCCAACCTTGATNAACCCNATCTTTAACAAATAANTAANTTTTGAATTCNCTCTTACTAANCNTTAAACAGGGAGCCTCTTGCAACNTGGTTTCCTTTGAA

SEQ ID NO: 2444 GTACATACACACACACACANCNCAGAGAGAANACAGAGAGAAANTCCTGTGCCAAAAGATCAGATGACCTTACTAGTGTTCCTCCANTGACTGTAATTTATAAACTAAAAATTTTACAAAATCCACTGCTATCTTCTCTGCTCCTGAGTTTNGGTNGACTTTAATGGATGCTCCAGCAATAACAGANTCTAGGACATGCAAACTCACTGTGAGCGAGAGGCTAGGGATCTGCCCTAACATAGGAACCTGTTTCTATCAAGCCTGAATGAGGCGAGCTNTGNTAGANTTAATGACAAATCAATGCCAGNGAANTATTCTGCAAAACAGGGTAGCTTTTGTGCTTCTTTTATTTATTTTNTTTTGGGGAGATAAAAGTTTTTGANCCATGGGTCTACTAATTTATCACTAAAGGACTGGGACCACTTCTNAGNAANACANCATGGTNTTACTGTCCANGGAGGGAAAAATCCC

SEQ ID NO: 2445 ACCTTAAAGTGTCTCACCTAGAAGGCCCTCTACCTGTAATCACATTAATTTTTCTAAAGACAATTTGGTGTTTTGAAGATAAATGTCAATAGTCTATGATAAATAGCATATAGGACAAATAGCCATTTTAGACTTGACCATATTTTCTCITTTTAGCATATAGCCATCTTGATATTTAGGTGGGAGACTACTCCAATGGAGCAACAGTTTCATTTTACATGATTGGATTTAANAATTTACAAATTTTAAACCTCATAGAAATTCTTAATAATTTNAAAAATNGAAACATTNNACCCANAGCTCTANCANCNTAAATANTTTNTAAAAATACITTCATTG

SEQ ID NO: 2446 ACGGGTATCACTTTCCGGAGCTGGTGAAGATCATCAACGACAATGCCACATACGCGCTCTTGCCCACTTTATTGGAAACCGAAGGGAAGCTGAATGAGGACAAGCTGGAGAAAGCTGGAGGAGCTGACAAATGGATGGGGCCAAAGGCTAAGGCTATCTGGATGCCCTACGGTCCCTCCATGGCATGGACATATCTGCCATTGACTTGATAAACATCNNAAGCTTTTCAGTCTGTGGGNGTCTTTTATCTGAATACCGNCAGANCCTACACACTTACCTGCGCTNCAAGATGAGCCAAAGTAGCCCCACCCCTGGGACCTAATTGGGGAANNCGGTAGGGCACNTNTNATNGNACATGCTGGANNCTNACCAACCTGNCAAATTATCNACATCCACAGTGCAAAATCTTNGGGCTGAAAAAGCCCTGTTNA

SEQ ID NO: 2447 ACCAAAGCTCACTACTGCGGTTTGCTGTGCTGGACAATGAGGCGGAGCCA CTGTTGGGGCACCCCTTCCCTCCCGGGTTTGCAAAATAGAGGCTACCGGGTGCTGTATTACAGCAACACCTGTTTACTATTGTTTATTAACATATCATCTCCACCTTCCCTTTGATTAGCAATTTGTACACTGTGAAACAGCTAAGTCGAGCTAATTAATGCACTGCCACACATACCTGTCACTTTTGGGGTGAGACACTTAAATCTACTCTCTAAGTGGTTTATTATTATTTTGTGAGACGGAGTCTGTCTGCCGCCA GCTGGATGCAATCGTGAATCTCGGTTACTGCAACCTCCACCTCCAGGT

SEQ ID NO: 2448 ACTTTTACITTTTAAAAATTTCAAACITTTTATAGTATTCTGCTAACATATCTCC TGTGAGGAACACTTAATACTGAATTTTCCCTCAATAGCCAAGTCAGAAATATCTTATTTTCATTTTT CACCCAAGTCTTTGTTTCTAAACGCATTATGTAGAATAGATTGATCCGTACAGCATCTTGAGTACGCTAATGAGGTAGGAGTATTCTTAAGTCTTAGGCTTANTGAAGCAAAAGCAAAAGCAATCAAAAT TACAAAGATTTTCTTTTGNAGTGGGTGNNCTTTNAANNAAAAANNNGCTAAAAANCACTGGNAANT TGANCAAAATGCTACTAACATTAAAAAN

SEQ ID NO: 2449 ACAGCATCGTAGGGTCCCTAAACCTTGCCCTGTTTTGTTTTTTAGTTTGTATCCCTTACTGAGCGGCCCTCTACTAGGTGGCTGTGATTAAATGTCCCAAGCAAGGATAGGGAAG GGGAAATGGGTTGACCTCTGGAGATCATTGTAAACCAATCCTGCCAGACCTGTTTGGGCAAGTGGGG AGCAAAACCTAGATAAGGACCTGTTGGGGCACAGGGAGCAAAATCTCTTTAAACCAACCAANCAAGTT CCTATTACATCAACAGANCGAGGCTGTGATAACTTAAGGAGGCAACATCTTAATAGTCCTTCAGT

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SEQ ID NO: 2450 AAATTTACAAAANAGGTTTATTGGACTTACAGTTCACGTGGCTGGGAAGGC
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NAAAA

SEQ ID NO: 2451 TACGGNCTGAGACATCACCGCCAAGCTGGGCATCGGGGAGATGGCCNAGAC
TGACCCCAANACCGTGACAGGACCTCACCTCGGTGGTGCANACACTCTGCAGCAGATGCAAGATA
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TAAAAAT

SEQ ID NO: 2452 CCGGGCCATCATTTANTNATGGAATATATCTGCGTTTATAAACTANTTTTT
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SEQ ID NO: 2453 ACTTTTTTTTTTTTTTTTTTTTTTNNNGGAATGCGTTTATTTAACAACCAAAA
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SEQ ID NO: 2454 ACAGGATGAATTTAAATGNGTTTTCTGAGAGACAAGGAAGACTTGGGTAT
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SEQ ID NO: 2455 ACTGAGGACATGGCTGTGAGCTGGTTTCTTATCTGCTCTGAAGGCATGCTTTG
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SEQ ID NO: 2456 ACTCATTTGTATTCACTGTCACTTTTCTCATGTTCTAATTATAAATGACCAAA
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SEQ ID NO: 2457 ACGCTGGATAGCGTCCAGGCCAGAAAGAGAGAGTAGCGCGAGCACAGCTAA
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GAGATCAAGAGAACTGTGGCTGCACCATCTGTCTTCACTTCCGCCATCTGATGAGCAGTTGAAA
TCTGGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCCANAGAGGCCAAAGT

SEQ ID NO: 2458 ACAGCTAAGCGAACTTTAAGTAAAAAGGAACAGGAAGAAATTAAGAAAAAG
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ANGGTC

SEQ ID NO: 2459 ACGCGGGGAAGCTTGGACCGCATCTAGCCGCCGACTCACACAAGGCAGGT
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SEQ ID NO: 2460 ACCITTATGGATTTGACCCACCTCATTCTGGACAAAGCCTCAGGAGGATCTCTT
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SEQ ID NO: 2461 ACCATCTCTGTGGCTCCTTAAGGAGGCTTCTCTTTAATTCCTCATGAGGCAT
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SEQ ID NO: 2462 ACAACCCATAATTTCTGTGTCATCAAAAGAAAAGGGATCAGAATCATCTGGT
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SEQ ID NO: 2463 ACGTTCAATCCGGGGAATGATGACATGTTCAATGGCATTACACGCCTGTTGG
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SEQ ID NO: 2464 ACTACTGCTGTTTTCTGAAGACGCGAGGGCAAGTGCAGCCAGCGGTTCTTTT
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NCT

SEQ ID NO: 2465 ACGCGGGGGAACACCACCCAGTGTGGAGCATCCCACTGCTCACTGAGGCA
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SEQ ID NO: 2466 ACTTTTTTTTTTTTTTTTTTTTTTTGGCTTNCATTGAACATTTAATAAAAAAT
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SEQ ID NO: 2467 ACTTGTAGGGAAAAAAAAGTTTGACACCCCAAAAGTCTGTATCTTATG
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NGTTCAACAT

SEQ ID NO: 2468 ACTACAGACCTCCACATGTTGGACAGTAGGATTACAGCAGAGAAATGAGTCCCA
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TTTACTGCTCAATCTGGATTTTGGGGAACCTCTCCCAAAAGGCATTAGAAGGAAATGCCAAGC
ACCGAAATTTTGTCAAGAAGCGGAGGCTCTTGAACGGAGAGGCTTCTGAGTAAAAAGAACCAA
CCCTTAGCAAGGCGCTAAGTTGCACTCTGAACCTTCAAGAAAGGGGAACTCTACGGTGA
TGGCACTTGGAAAGACCCCTTCTTCCCAAAAGAGACAGCTGCTTCCAGCAATGGGTGAGGAC
AGCCCTGGACAAGAAAGCTGCAGTGTCTTGGTTGACCCCTGCCCTTCAAAAAAGGCTGATTCTG

TTGCTGCTAAAGTAGATTGCTGGGGGAGTTCAGAGTGCCCTTCCAAAGATCAATAGCCACCCAA
CCCGTTCTCAAAANAAGAGCTCCCAAAANAATCCTCTAAAAAAGAACCATCCTTANAAGAATGCC
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ACNGGAANAAGGN

SEQ ID NO: 2469 ACTTTTTTTTTTTTTTTTTTTTTTTGGAAAAAATTTTAACAATTTATTAGTC
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SEQ ID NO: 2470 ACTTTTTTTTTTTTTTTTTTTCCNAAAGTGGTTTATTGCAATTTACATGGATT
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SEQ ID NO: 2471 ACTTTTTTTTTTTTTTTTTTTTTTTTAGGATAAATACTATGCTTTAATGAN
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NAATGCNATTTCTAGGCCATCTTGTGGGACTGATGAACAGCATCTNTGATCTCATGATTTAAACAT
CTGGTTATCCAAAGGGATGGGATTGGCTAAAAAACCAGATCAATTCNCGATTGGTTTGTGTTTC
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SEQ ID NO: 2472 ACTTTTTTTTTTTTTTTTTTTCTGGGACTCTGGAGATGCCGAAGCACACGCCTT
CAAGAGTCCAGCAAAAGAAAAATAAAAGAAAGACAAAGATNTGCTTGAAGATAAGTTTAAAAAGC
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GGGACTTCTCCATCCTGTGGATCCCATTTGTAGGAGAGCCAGGCTACTGCCCTGTGAGACTGGGAAT
GACAACTGGAAGACTTCAGTCTGGAGTGAATACTTTGCAGGGGTTCAAAGAGGATAAAAGGAACA
AAGTCACTCCAGTGTATATTGAATTATGGGCCCTACAGTTCTTATGCACCCGATTATGACTCCAC
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TGTCTNTCTGAA

SEQ ID NO: 2473 ACTGAAGAACATTCCTATGGATATCGGTTAACTTGCCCTCCACAGCATGTAA
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CATAGCAGCAACACAGTCAAGTAACCAACTTGTGCTATGGGATCGAGTAGTTGTGATAATGTGTTT
CCCAGCAGGACTTCTTTCAGCTGAAACCCAAAGCGGCTAAACCTAAAACTCCCAGATTGTCTT
CCCCAACACAGCATCTGGTCTGCTCATAGTTGTAATATGGCTGGTTAATAACTCCTGCTATGGC
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SEQ ID NO: 2474 ACGCGGGCAACATGACTGTCCTTTAACTCCAGTGGCTGGCCAGGCACGGTA
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CAAGACCAACCTGGCCAAACATGGGGAACCTGTCTTTACTAAAAATATAAAATTAGCTGGGTG
TGGTGCNG

SEQ ID NO: 2475 ACTTTTTTTTTTTTTTTTTTTTNGGTTTTTTTTTTCCACACCTGCCCTTTATT
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ACCANAGGGTTGGGANAGGAAAAGGAAACAGGCAGAGGGGAAAGGCAAGGCTCTGCAGTGAAG
GGGACTGATATCAAGGGAATGCTGAGGTCCAGCAGTGTCTCTGAAGGCATGCTGCATCCTAAGG
CTCCTCAGGACTGGATGGAGTAGGAGATCTGGGTGTTGACCANTTCACATNTATATGGCAACTTTA
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SEQ ID NO: 2476 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGNTTCAAAAGGGTGTTTACTATTTGG
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CATTGTTGGGCTTTGTCAATCATTTCTCACCATCAAAATCACCCCTAAGTGACTGGGAGTGTGAAT
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TTAATCTGCCTTGATGT

SEQ ID NO: 2477 ACCGGACCCCTGCAGCCGAGAGATGTTGATGCCTAAGAAGAACCGGATTGCC
ATTTATGAATCCTTTTTAAGGAGGGAGTCATGGTGGCCAAAGAGGATGTCCACATGCCTAAGCA
CCCGGAGCTGGCAGACAAGAAATGTGCCAACCTTCATGTCATGAAGGCCATGCAGTCTCTCAAGT
CCCAAGGCTACGTGAAGGAACAGTTGCCTGNAGACATTNTACTGGTACTATTTTTTTTTNTTTA

SEQ ID NO: 2478 ACGGGTATCACTTTCCGGAGCTGGTGAAGATCATCAACGACAATGCCACATA
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SEQ ID NO: 2479 ACAGGAGATCTCATTGGGACAACCTAAGGATAAAATGCTGGTCAATCGAGCAG
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SEQ ID NO: 2480 ACCATAGGATTTTGAAGATGGTATCATCAATTTCTTAGTTAGTGATGGTGT
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AATTCTAATNTCCACGCTNTTGGCAANCTGCTTCNATTGATATCATC

SEQ ID NO: 2481 ACGCGGGTCTTTCTCGGGACGGGAGAGGCGGTGAGCGTGGCCGTTACTC
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TGAAAAAACCCCTTTT

SEQ ID NO: 2482 ACGCGGGTCTCCCGAGATGACAAATCTCTCGACACCGAATCACCATCAA
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SEQ ID NO: 2483 ACTTTTTTTTTTTTTTTTTTTTNGGAATCCTAACTCTATTAAATAGTGTGATACA
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TACCTCGG

SEQ ID NO: 2484 ACTTTTTTTTTTTTTTTTTTTTNGCCAAAGACAACTANAGCAATGCCTATGTAA
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NTAAAA

SEQ ID NO: 2485 ACCAACCTGGCTACTGGAATCCCGAGTAGTAAAGTGAAATATTCAAGGCTCT
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SEQ ID NO: 2486 GGTACTTATATAAAATCTAGTCCAGTTCTCTCATTTAANAAAAATGAAGACAT
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SEQ ID NO: 2487 ACTTTTTTTTTTTTTTTTTTTTGGAGCTGAGACCAGGAGAAATAACTTTAT
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SEQ ID NO: 2488 GGTACTTTTTTTTTTTTTTTTTTTTGGTCCANNGATCCTTTACTGAGA
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CCCAGAGGGTCTTATCTGTGTTGAAGACAANAAGCTGGATCCCGAATCTCTGCTGTGAG

SEQ ID NO: 2494 GGTACACTTGAAAACCAATTCTTAAAACTGTGTTTCTTAAAAAATGAGTTGTT
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SEQ ID NO: 2495 ACTTTTTTTTTTTTTTTTTTTTTTTGAGTGTGGGTTAGTAATGGGGTTGT
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SEQ ID NO: 2496 ACATTCTAGCTGAGAAGCAATGGGTCACTCATTAAATGAATCACATTTTTTAT
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CAA

SEQ ID NO: 2497 ACAGCCAGCAAAGGGCGCTATATCTCTCTCATTAAAGGAACCGAGAAGCTA
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SEQ ID NO: 2498 CGAGGTACTGGCTGGGATGGCTCTGATATAGCAGCCTTGGTGTAGTTTCTGCA
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CTCTTTAAATTTGGTAAGATAATGCTGNAACATAGAATTTCACAATCAGCGCCTTGTGCAGGTAATTT
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CCAATGNTTACTTTACACATCCTAATACACTGGTTATTCAATCCCGGGGNCCTGGTAAAGTANACC
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NAAANGGNGAAATTCNATGTGAACCTTTGGTGCCANAANAAACCGGGGCGNCCG

SEQ ID NO: 2499 GGTACACTGAAACCAAAATTTCTAAAACTGTTTCTTAAAAAATAGTTGTT
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GTNGGGN

SEQ ID NO: 2500 GGTACTTTTTTTTTTTTTTTTTTTGATAGATACAATGGCTTTTATTGTGATTCA
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SEQ ID NO: 2501 ACCTGAAAAATAAGAGAAAAAGCACAGANGCCAGTGAAAGAAGGACAG
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SEQ ID NO: 2502 GGTACTATAGAGACTCAGTTGCAAAAATTAACAAATATGCTGCTTGATTAA
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SEQ ID NO: 2507 ACTTTTITTAAGCAATGGGTCACGNATTAATGAATCACATTTTTTATGCTC
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SEQ ID NO: 2509 GGTACTATACTCTGTATTCTCACAATAGAGAAGACTAATATTGCAGACCTG
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SEQ ID NO: 2513 ACGCGGGGGCCAAACACCTTCTGACACCATGAGGGCCAGCAGCTTCTTGAT
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SEQ ID NO: 2514 ACGCGGGGGTATTCTTCCCCAAGTCTCTATGGTAGCGTCAGCGTCGGAGGC
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SEQ ID NO: 2515 ACCCACTGTATTTATTTATGTGCAACAAGAAGTGCAGCAACTGCACAAACTC
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SEQ ID NO: 2517 ACTGTGGTGTGTGAGTCTCAGCAGCCGCCACACGCTCCTAACTCTGCTGCAT
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SEQ ID NO: 2521 GGTACAAGATCTACCCCGACACGGGAGGGCTACGCCAGGACCGACGGGA
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SEQ ID NO: 2522 ACGCGGGCTGGACGCCAATGACCTAGAAGATAAAACAGTCTTTCTACTAT
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SEQ ID NO: 2523 GGTACCTCAATTTTCTTCATCCAGTAAGACAAGTATGCATCTTAAAGGGAAA
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SEQ ID NO: 2524 CGAGGTACGAAACCAACGCCCCGAGGGCTGGTCGCGACTACAGTGCAATATTA
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SEQ ID NO: 2525 GGACGAGTCAAGCACAACTGCTGCGCCAGGAAAAGACAAGGCTAATTGGG
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SEQ ID NO: 2527 ACAATTCAGTGTGCAGACCACAACCTCAAAACAAAAAGGTTGGTCAATGC
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SEQ ID NO: 2529 GGTACGCGGGGATTTCTCCCGAACCTCTGCTCAGCCTGGTGAACACACAG
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SEQ ID NO: 2531 CGAGGTACTGGTTTTGGATTAGGAATGTTTTCTCACTTACCTTCTTTAAAG
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SEQ ID NO: 2532 ACATATTAGAAGTCTAAGGAGTAGCAAGTCAGTGGGAGGACTTTTTACCCC
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GTGTATGTCAOGTGCAGGAACAGTGAGGCAGGGACAGGGTTCTGCTCCTTCTCACTTCAACCCG
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TTCACTGGTCCCTAACCTTGGGTTTTAAAAAGAGGCTTCTCTGTTGGGTAGCGTAAGAGCTGA
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AATGTTTAAATGGAANAATCTTTTNAATAAACCAATTTTGTNTNGTANNAANAANTTNCNTNTN
TNNNTNTTNTNANTTANNNTNCCAATNNNAATAANATAAAATNNCTTNNCTNANCNTAGGG
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SEQ ID NO: 2533 GGTACTGGTTTTCTGAGAAACAGTCCCTCGTGAAGTACAGTACGTCAGAG
AGTCTAGTCTCAATCTGCTGTATGGGCTGGTAACCACTGAGGCAACCGATTTTCCACTGTTTGTG
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CCCGGCTACTACTTCAGGTAATCATTGTTTTACTTAAAGTTCAGATTCAGCATATATTGAGATGA
ATATCCCTGGTTATACCTTGTCAATAGTTTTCTCATTGCTACAGTGTATTGGTTAATTGTACAAA
GCTTAATTTAAAGACATTGGAATACCTTTGGATCCATTGTCACTGGAAGTGTCTTCAATCCCA
CTTACAATCCTAATCTTGAGCNAATGAAAAAGCCTATATCAATAATGATTGTGTAATATTATAA
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AATTAACGAACTAAACACTTTTGGCCCTNACTGATACATTTCAGAAATGGGCTTTTNAAGGCTTG
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SEQ ID NO: 2534 CGAGGTACTTTGACTTACTAGGGTGATTCAAAGTTTCAGGAAAAAGAAAAAT
CCCAGTATCATTTTCTTAATCTTATTAACCCAAACATAAGAAATGCCAAAAAATACAGAGCTCACA
TTTTGCTGGCATACATTTCCAAATTTTAAATGCTCCCTGACAGGTGAATTTTAAAGGATAAAAAA
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CTGGATTTTGTCTCAATTTCAATTACTTTACAGTCTTCAGCAAAATCCCTTACTTTGAGCTCTA
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AAGCTGCCAGTATTATTAAGGAGCTTATTACAGAAAANCCAGCCTCATTCATTACAGGNTATGT

CTCATATCTCTTGGNCAATGGTTAATAGATGAGTATNTTGAGAAAAAGTNGGAATNANCTAG
GAGACANACCTGGGCAGTNAATGCTTCTCACGNTTTAAGGGTAAGNGTAGGCACCTCNGANA
TCCTANTGGGGTTTACCNAANGCCAGGNCNNNGTCCT

SEQ ID NO: 2535 CGAGGTACCTCCAGGTCATGGTGATTTTACGCCAGTTTCTACAACCTCGGA
TTGCTTGATACCTTTATAGGAGAAGCAAGAGTATATTTTGTGTCTAACATAGATAATCTGGGT
GCCACAGTGGATCTGTATATTTCTAATCATCTAATGAACCCACCCAAATGGAAAAACGCTGTGAATTT
GTCTATGGAAGTCAAAAATAAACACGTGCAGATGTAAAGGGCGGGACACTCACTCAATATGAAG
GCAAACTGAGACTGTTGGAAATTGCTCAAGTGCCAAAAGCAGATGTAGACGAGTTCAAAGTCTGT
TCAAAGTTCAAAATATTTAATACAAACACCTATGGATTTCTCTTGACGCAAGTTAAAAAGACTGCA
GGAGCAAAATGCCATGACATGGAAATCAATTGTGAATGCNAAGACTTTGGATGGANCTGAATGT
CATTCATTAAGAACTGCAGTANGGGCTGNCATCAAAGTTTGTAGAATTTCTTAAGNATTAATGTG
CCAAGGAGCCCGTTCTGGCTGTCAAACCACTTAGACTCTTGCTNGNATGGCCAACTCTATAG
TCNTAATGCAGGATCTNTGACATGATGNAACCGGAATTTCTANGTGCCCTTGGTAAATAGCNGT
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SEQ ID NO: 2536 ACGCGGGGGGAGACGTGCTAGCGCGTGAAGGTAGCTCTATGGTTTCTCG
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CGCTCCAAATTTAGATCACATTTCTCAAGGTCAAAGTCTAGATCAAAAGTCTAGTTCTCGATCAAG
ATCAAGATCTCATTCTAGAAAGAGCCGATACAGTTCTAGGTCTCGTTCCAGAACATATTCAAGG
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CTANTGGATCCNACCTCGGNCACANCTTGGCGTATCATGGGCATAACTGTTNCTNGGGNAAATG
TATCCCGTTACAATTTCCNCACTCNAACCCGAAGNTTNANTGTAAACCTGGGNGCCAAATAGN
GACTNACTNCATAATGNGTGGGNCANNTCCNTTCNATNGGAACNNNNCT

SEQ ID NO: 2537 ACATGCAGAGGTAAAGCTGAAGCTGGGCAGGGGATGGCTACAGTTCATGATC
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GGCACACTGTGAGCTGAAGCTGAAGTTTCCAAAGGGTGAGTACATTACACACCAAGTGAATAGTA
ACAGATTGTTAGTATGTTCAAGCTTTGTGTTGCATGATGGTAACTATAGAGTTTGGGGTCAAGTTG
TTTGACAGAGGAATCCAGTACAAGAGATAGAAAGACCAAGTCTTGTCTGAAAGCAAAAGTCTGAAT
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CAACACATAGCAATTCAGGAATTTGACTTTCCNTCTNTGCTGGATGACGTGAGTAACCTGAAT
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GCTTGGTCCAATTTGGGTANN

SEQ ID NO: 2538 ACGTCCAGCGAGTTGCAGATCTACACTTGGATGGATGCAACCTTGAAAGAA
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ACATAGCAATTAACCCCTCCAAATCGGGCACCACCTCCTCAGGGCGCATGAGACCATATTAATTC
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SEQ ID NO: 2539 ACGTGGGCACAACCTCCACCTCCTGGACTCAAGCAATCCTCCACCTCAGCCT
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GCTGGGATTACAGGTGTAAGCCACCATCTGGTAACAACTAGCAGTTTATAGCTGACAAAGAAAT
TCAGCCCTAAATGACCTGCTGAAGTTATTTTGACATGTATCTTCCCACTGTCTGCACAAAGGGG
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AAGCAAGGGCTTGTGAANTGATGGATGCTGTGTAACAAAGAAAGTNTNGCAGGATGGACAGA
AAAAAGTGGGAACCGCTTNGGANGGTGGGAAGGNTNAAAGTNCNAAATNAACNCTGAAANGAN

GGAAAAANNTGGGCCCATGANGGGGGAANCCAGGNTNGGGGACCCCTNAAGGG

SEQ ID NO: 2540 ACCATTCTTCTGAACTATTCCAATCAATAGAAAAAGAGGGAATCCTCCCT
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GAATCCAGCAGCAGCATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCATCCCTGGGATGCAA
GGCTGGTTCAACATATGCAAAATCAATAAACGTAATCCAGCATATACACAGAACCAAGACAAAAA
CCACATGATTATCTCAATAGATGCAAAAAGGCCTTTGACAAAATCAACAAACGCTTCATGCTAG
AAACTCTCAATAAATGAGGTATTGATGGGATGTATCTCAAAATAAAGAGCTTTCTATGACAAA
NCCCAGCCATTTATCCCGAATGGGGCAAAAATGGAACCTTNCCTTTGAAACAGGGCCAANA
NANGGGGGCCNTTTTACCATTCTATTAAAAATATNGTTGGAAATTTTGGCCGGCCNTTTGCCN
GGAAAGGAATAANGGGTTNCATTGGAAAAAGGACCCAANTTGC

SEQ ID NO: 2541 GGTACCCCTAACTGGCAGGACATTTTGAATCACAATTTGCACATAAAG
AATGTCACGAACGCCATGTATCCATATACAGCAATCAAAATAGGAACCTTATGACCTAAAGCAAA
GGTAAACTTTCTTGAACCTTAACATTCTATACCAACTAGGCAACCTCTGCCAGGATGAGAGTTGG
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CTAAGTTCAATTTTGGCAGTTGGTTCTGTATTTAAATTTAAAAAAAACACACTTCCCTTGGCANG
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AGGNTAACCNAACTTATTTTTT

SEQ ID NO: 2542 GGTACAGTTTCCCTTCTCCAGGGTGACAGATGAGCCTTTTCCGAAGTTCTCAG
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AAGTTTCCAGGATCCCGATGTTGTCATACACTCCGAACATGGCCCTTTTCTCGTTCCAACGATCA
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TCTGCAAGCCAGAAAGCACCAAGTCCACAGGCGCTACCTGGCCCGGATNAGANGGTCCCTGGCA
TTTTTTNTAGTNTCCCNCTTNAACAGGACACCAAAATAGCCCAAAAAAAATGACAGGAACCGNC
CCCGGCCAATTTANAACAATTCCTGCGCGGNGGCGCTTTAAAGGGGNAATTCACACACCTG
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SEQ ID NO: 2543 ACTGGAAGTGCTATATAATGCAGTGTAAAAAAGAAATAAATGCA
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TTGTTAAGTGAAAAACCAATCTGAAAAGGCTTTCTATTTGTATGATTGCAATTATATGACATTTTGG
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GATGGCAGGTAAAAAGNGAATTTTAAAGGAGTGNAAGTNCNNGNCGGACCCCTTAAGGCCGAA
TTCANCCACTGGGGCCGTATTATGGATCCGNTCCGTTNCCANCTTGGNGNATCATGGCCANACT
GGTTCTTNGNGNAATTTTCCCTTCAATTTCCCCACANCCAACCGGAGCTTAAAGGGAAACNCGGG
NCCANTAAAAAAN

SEQ ID NO: 2544 GGTACAGTTAGGGGGCGGGTGGGCCAAGAAAGGCAATCATTTGGGCAGAA
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GCCACGGAAGCACACAGCAAGATGCAAGCCACCAACAAAGCCAAAGAAAGTGGCCTTAGAATGA
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AGGTAGGAGGATTGATTGAGGCCAAGGTTAAAGACGAGCTGTGCAATATACAGAAACCCCTNT
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SEQ ID NO: 2545 CGAGGTACTGATGCTGAAAAATCAATAAGATTAAACCAAGAAATGGCTCAAT
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TAAACTCCNGGGTCTTTTTTCTNTTCCANGGGGNNTAACTGG

SEQ ID NO: 2546 ACGAGCAGCTGTCTGGGAAGTAGGGGGTTAGCTTGGGGACCTGAACTGTCT
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CCTTGGCATGGGTGAGACCTGACCAGTCAGATGGTAGTTGAGGGTGACTTTCTGCTGCTGGCC
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SEQ ID NO: 2547 GGTACTGAANGGCTGGAGACAACACTTTATCAGTTTTGACACTGACAGGAG
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SEQ ID NO: 2548 ACTCAAGTTTATAATGTCCCCAAACCTTAAGACTAGAAAAATCATCCCAAGAA
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CACGGAAGATGGGGACAGTGATCCCGAAGGTTTACTAAAAATTTGACAGCTTTCAGTANTTATGA
NGAAGCNCATATNACTNNAAAAAGAAAGCNATCATTTGGAGTNNCTCNGGCCGNCACACGCTA
AA

SEQ ID NO: 2549 ACGCGGGAGCTACGGGCATGCACTGGACCTATGAGCAGAGGAAAAATCGTGG
AGTTCACCTGCCACACAGCCTTCTCTGTCAGTATCGTGGTGGTGCAGTGGGCCGACTTGGTCACTC
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SEQ ID NO: 2550 ACTGGATTTAACTACCTTTGGCTTAATTCCAATCATTTGTTAAAGTAAAAACAA
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AAACAAAGCATTTGACTTTCTGTCTGTGGAGTGGAGTAGGTGAAGGCCCNCTGTAACTGTCTT
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CTCAAAACNAANTGGGGACATNTTGTGNTGNTGCCNAGGAATTTCTGACNCTTNNNGCCN
NCNGNCTTTCTTNNAAANTTANGGCCNAGGNTNNGCTANTTGATTTTCTCTTNTCCTCTTTTGGG
GGNGAGGGNTTACTCNGTTTAAAAANTGGAACCTCCN

SEQ ID NO: 2551 ACGCGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCAG
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GCTTAAGATTTTAAAGAGAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAGATAAAA
GGTTTCTAAAAATGACGGAGGTGAGATGAAGCTTCTCATGGAGTAAAAATGTATTTAAAAAG

AAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATCCAATTTGAANGGCCAATG

SEQ ID NO: 2552 ACGCNGGGAACGCTGGGAACTCCCGCCTCGCCACCATCTTGCTTTCCTT
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ACTATTCCTGTATCAAGAATTGGTTTGTTCATTAAAGCAGGCAGTAGATAAGGACTTCAGCA
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SEQ ID NO: 2553 ACCCATGGAGCTGGGCTAAGTAAATAGGAATTGGTTTCACGCTGAGGCAA
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NGTTTNTNTTCTGNCAGCNAAAATAAANTAANACAANTGGGNAAGGNANGCNCGGCTT
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SEQ ID NO: 2554 CGAGGACAAGGCAGCTGGCAACGTTCCCTTCAAGACACAGAGGAGAAATCC
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SEQ ID NO: 2555 GGTACGGATCAOGCTTTCCCGAGGATGACCTCTGCCAGTATATCACATCAGAT
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SEQ ID NO: 2556 GGTACTTTGAAATTTGAAACTGGATCAGTGTGTGACGGGACTGTCAACTGAA
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TAAATGGTAANNCTNGGGGGCTTANNGGNNCACTTNAATNTTNGGGGNCNNG

SEQ ID NO: 2557 GGTACAGTTGATCCCACTTTGGAATAAATGCCAGAGGTAATAAGCATTAT
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SEQ ID NO: 2558 ACCACCAGCCAGCTGATTTTGTATTTTAGTAGAGATGGGATTTCACCATG
ACGGCCAGCTGGTTTCAGATTCTGACCTCAAGTGATCTGCCACCTCGGCTCCCAAAGCTGCTA
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SEQ ID NO: 2559 CGAGGTACTTTTTTTTTTTTTTTTTTGGTTIATGCAACTTTATTGAAGAAA
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SEQ ID NO: 2560 ACTATCTCTGTATTCTCACAATAGAGAAGACTAATATGCAGACCTGGTG
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ACACCTGACGTGGAGACTTTCCAAAACCCGTANGAGATTGCTTCGGCATCGCAATGGTTGCATT
GCAGTGGCCTTTCAAGTTGCCAGCTCTATTCCCTCAAAATACGATTATCCACTGTATGGCAATCA
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SEQ ID NO: 2561 ACTTTTTTTTTTTTTTTTTTTTTTTTACCAACAAACGATGAAGTCTCA
GGAGTAAAGTTGATACACAAGTAAATTTATTTGGTAATGTTTTTGTGTGGTCTTTAAGCAGAGGG
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SEQ ID NO: 2562 GGTACTTTTTTTTTTTTTTTTTTTTGGAGCAGTTGATTCCAGTTCCAGGC
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SEQ ID NO: 2563 GGTACGCGGGAACANAATCCAGGATGTTCCATCTCTATATAAATGTATTG
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SEQ ID NO: 2564 GGTACTTCCAACTCTGGGTTGGCCCCAAATCCAACTAATGCCACCACCAAGG
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CTAGATGATGGATGCCAATATAAATCTGCTGGAGTTTCATGT

SEQ ID NO: 2565 ACAGAAAGGGTATGTTAAGTAGTTCAGCCAGCAGCTCACCACAGGGATTAA
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SEQ ID NO: 2566 ACCGCGGGCTTGCCACACCTTGAAGTGATACTGGCGGGGAGCTCTTCCCTGC
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SEQ ID NO: 2567 ACCTGGCCATCTTGGCAGTGTGACGTTTCTGGCTGGCAATCGGATGCTGGCC
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SEQ ID NO: 2568 ACTATAGAGACTCAGTTGCAAAAATTAACAAATATGCTGCTTGATTAATG
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GTTGTTTGCCCAAGGACTTCNTTT

SEQ ID NO: 2569 ACGCCCTGCTGCTTCTCTGATCTGCTTTAACGTTGGAAGTGGACTTCACTTA
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GGCGCGCTGGATCACCGCCCGTGGCTCTTCGGGAGGGAGAGGATCTGTCCAAGAAAGATCCAA
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SEQ ID NO: 2570 GGTACTCCAGCAAATCCTCTGAATCTCCACAGACTATGTTACCCAGTCCCA
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SEQ ID NO: 2571 GGTACTTTTTTTTTTTTTTTTTTTTTTTTACAATAGTGTGAGGATTTTTT
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SEQ ID NO: 2572 ACGGAGAGGGTCAACCAAGCGTGGATCGTTGGCAATTGTGGAAAAGGGAACC
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CAAGAAAGGCTGCCTGCATAGTGGTTCCGGCTGCCCTTTCTAGGTGATTGGAATCAGCCATCTAA
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TTTTNCTGNGAAATTTCCCTCAAATC

SEQ ID NO: 2573 ACCCGATTAAAGTAGTGACATTGATACTAGTAATTTGATGACTTGGAAAGA
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GACAAGATAATGAAAGAAATTGGATGAAGAGGGAATCAAAGAAAGAAATCTAGAATCTACAGTAT
CTCAGATTGAGAAGGAGAAATGTTGCTACAGCATAGAAATTAATGAGTACC

SEQ ID NO: 2574 ACATCAAGTCCATCTGACAAAAATGGGGCAGAAGAGAAAGGACTCAGTGTGT
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SEQ ID NO: 2575 ACTAAAAAAGGAGAAATTATAAAATTAGCCGTCTTGGGGCCCTAGGCC
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SEQ ID NO: 2576 ACCCACTGTATTTATTTATGTGCAACAAGAAGTGTGAGCACTGCACAACTC
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SEQ ID NO: 2577 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGGGTTTTTTTTTTTTTTTT
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SEQ ID NO: 2578 ACTTTTTTTTTTTTTTTTTTTTTTTTCAGNGCCTTCTCANACTGCTGTGGA
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CCNCCA

SEQ ID NO: 2579 GGTACGCGGATGTTTTTCTGATTCCATCCTGTGTCCTTCATCCTTGACTC
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SEQ ID NO: 2580 ACTATGTCGATTGACAGAACATTCAGAAGATTCTCGGCCTTGCCTTCACG
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SEQ ID NO: 2581 ACATGCTTTTATCTTTCCATAGGACATATTTCCAAATAATGATCACAGTATT
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SEQ ID NO: 2582 ACGCGGGGGTGGTTGGTGTGCGGGTTTCGGTTGGAGGACTCGTTGGGGAGGT
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SEQ ID NO: 2583 ACAATGTAGAACTCTGTCCAACACTAATTTATTTGTCTTGAGTTTACTTCAA
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SEQ ID NO: 2584 CGAGGTACAGTGAGGGTGTTCAGAGGGAGGCACAAAGAATAGCTCTGAGAT
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SEQ ID NO: 2585 ACCTGAGCTAAATGACTGAAGCTTTAGGGGTGCATAGAAACCACCATAATT
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SEQ ID NO: 2586 GGTACTTTTTTTTTTTTTTTTTTTTTTCTACAGTNGGACTGAATCTAA
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SEQ ID NO: 2587 GGTACTGATACATGTCTATAACAGAGATGAACTTCGAAAACATGCTAAGTGAA
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SEQ ID NO: 2588 GGTACTTACTGAAGTTTITTTTTTTTTTTTGAACCAAGTCTCGCTCTGTGCGC
AGGCTGGAGTGTAGTGGCATGATCTCACCACTGCAACCTCTGCCTCCCGGGTTCAAACGATTTCT
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SEQ ID NO: 2589 ACTTGAAGTGGTAGGAAATGCATCAAAAGACTTAAAGGTAAAGCGTATTACC
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SEQ ID NO: 2590 GGTACGCGGGAACTCGGTGGTGGCCACTGCGCAGACCAGACTTCGCTCGTA
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GGTCACGTCTCTTCAITTTCCATCTTGAAAGAGAGAGGCCAACAGGACTTTATTTCAITCTGTTTT
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SEQ ID NO: 2591 ACTCTTTTTTTTTTTTTTTTTTGGGTGAGGGGACCTACTCTGTTATCCAAAT
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CCAAAGGNAAC

SEQ ID NO: 2592 GGTACAGTGGAAAGGTGGATAACGCCCTCCAA TCGGGTA AACTCCAGGAGAGT
GTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAAG
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TCCAGCTCATCTTACCTCACCCCTCTCTCTGGCTTTAATTAGCTAATGTTGGAGGAGAAT
GAATAAATAAGTGAATCTTTCCNANNAAAAAAAAAANNNNNNNNNNNNNNNGTTCCTGCCGGG
CGCCCTTCA

SEQ ID NO: 2593 GGTACAGTGGGGTGTTCAGAGGGAGGCACAAAGAATAOCTCTGAGATTAG
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SEQ ID NO: 2594 CGAGGTACTGCTCGGAGGTGGGTCTGCTCCGAGGTGCGCCCAACCGAAAT
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SEQ ID NO: 2595 GCGTGGTCGGGCGGAGGTACAGAGAAGCACCTATTGACAAAAAGGGGAATT
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SEQ ID NO: 2596 ACGCGGGATTATTTTAAATGAGACAATCATTTAAGTTTAAAGATAACAGAA
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SEQ ID NO: 2597 ACTAGAGCCAGTCATCTTAACAAATCTTTTACATTTTATTTCTTTCATGT
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TGGCTGAAACTGCCTAAAAATGCCGGACGGGGTCTCTGATCCCCCTTGGGGCNGGCGG

SEQ ID NO: 2598 GGTACTGATACATGCTATAACAGAGATGAACTTCGAAAAACATGCTAAGTGAA
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SEQ ID NO: 2599 ACTGGAACATACAACACACACACTTTTAGTAGGAGAGTCGGCCACCACTTT
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GNGAACACGCTAA

SEQ ID NO: 2600 ACTGGCTGGGATGGCTCTGATATAGCAGCCTGGTGTAGTTTCTGCATTTCCG
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TACT

SEQ ID NO: 2601 ACGCGGGAGATGAATGCCAGAGGACTTGGATCTGAGCTAAAGGACAGTATTC
CAGTTACTGAACCTTCAGCAAGTGACCTTTTGAAAGTCATGATCTTCTCGGAAAGGTTTCTTCTG
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SEQ ID NO: 2602 ACTCTTGATAAAAGACCGTGAAACCAAAATCAAGAGGATTGCTTTTGTG
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SEQ ID NO: 2603 GGTACAATAAAGGAATGGGGAAGGGGGAATGAAAGAATAGAGAAAACTAT
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SEQ ID NO: 2604 GGTACGCGGGATGTTTTTCTGATTCCATCTGTGTCCTTCACTCTGACTC
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SEQ ID NO: 2605 ACTTTTTTTTTTTTTTTTTTGGAGGNATTGAAATACAACITTTATTCTGAT
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SEQ ID NO: 2606 ACGCGGGGAGCGCGGAGCACCTGCGCCCGCGGCTGACACCTTCGCTCGCAGT
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SEQ ID NO: 2607 GGTACGCGGGCTACAACAGGCAGGCAGGGGAGCAAGATGGTGTGCGAGA
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SEQ ID NO: 2608 GGTACAGTCTTTCATTAAATAAGAATCTTACACATACATTTTCAGATATTTT
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SEQ ID NO: 2609 GGTACTTTTTTTTTTTTTTTTTTTCGCTAAATGCCCTGTTTATTCTGCAAAACA
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SEQ ID NO: 2610 TNTACCAATGGCAACCAAGTCTTTTTCTGCAAAATATTCTGATGTAATTTCT
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SEQ ID NO: 2612 GGTACGCGGGCTCGTCTGACTTCTTTATTGGTGCCATCGCCATTGGGAGACTT
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CTCTTATGTTAAACCAATGATGGTGCCATTCTTAAAAACATTTGTTGACAAATCCAGCAGCTA
AAGTTTATGTTGATGTCAAGGGTTCAAGATGATGAAGTTGGTGTGGCACTACCTCTGTTACCG
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ATCATAGCGGGTTGGAGAGAGCCAGAGGCTGCAAGAGAGGGCGCTGTTGAGTTCTGCAGTTGA
TCATGNTCCGATGAAGTTAAATTTCCGTCAGAAATTAATGAATATTGGGGGCAACATTAATNCT
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GAAANGNTTTTGGCAACCTGGANGCAATTTCTATTTTCAAGAAAGCTTGGAGGAAGTTGGCCGAT
TNTATT

SEQ ID NO: 2613 GGTACTATACTGGCAATTGCTGGAGAAGATTTTGAATTTGTTGCTTCTGATAC
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AAACAGTCATTGGATGCAGCGGTTTTCATGGAGACTGCTTACGCTGACAAAGATTATTGAAGCA

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GAAGAAGAAAGGGGGCTGTATACAGCTTTGATCCAGTAGGGTCTTACCAGAGAGACTCCTTCAA
GGCTGGAGGCTCAACAAGTGCCATGCTACAAGCCCTGCTTGACAAACAGGTGGTTTTTAAAGAA
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SEQ ID NO: 2614 GGTACTTGGAAACAGTTACAGCCCTCACCAAGCTAGGTTGGGGACATGAAAT
CCAACAGCATCTGAAATGCTGTGAAGGCAAACTTTACAAATAGCAATGTAAGCTTACAGAACTTG
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CGGCCACCTTTGCGACATTACAGGANGTCTCATTNCCATCGGAGGNCAGGAAAGGCCCCCTGCT
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TC

SEQ ID NO: 2615 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGGACCTTTCTATTTTTAA
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CAAGGGAGATTTTCTCTCNNTTTTAACTGNGTGNCCCTCAGAAAGGATAATCTTGGAAAGCCT
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SEQ ID NO: 2616 ACTTCTTTTTTTTTTTTTTTTTTTTTTTTGGAACTTTTATTNATATTTTGGNCTT
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SEQ ID NO: 2617 GGTACGCGGGGGCTCACTCTGCGCTTCAACATGGCTTCAATTGCCAAGTCTT
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CCG

SEQ ID NO: 2618 ACGCGGGGGCAGAAGTCTCTCTCAGTCAGGACACAGCATGGACATGAGGGTC
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ACTCTCACCATCAGTAGCCTGCAGCTGAAAGATGCTGCGATTTATTAAGTCAAAAGTATAACAGT
GCCCTCAGACGTTCCGGCCAGGGGACAAAGTTGGAGATCAACGAACTGTGGCTGCAACCATCTGT
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SEQ ID NO: 2619 ACTTCACCTTCCAGGAGGTGAAAAGGAATACAAATTCACAGCAGACTTCCAG
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SEQ ID NO: 2620 GGNACTTTTTTTTTTTTTTTTTTTTTTTTNGGGGCAAAGATTCATTATTIATT
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SEQ ID NO: 2621 ACAGGTTTTATGTGAACATACATTTTCATTTCTGGGATAAATGCTCAAAAG
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SEQ ID NO: 2622 ACTTTGCTACGGCAGCAACCTGCTGACAGAGAGGATCCACCTCCGAAACCC
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ATTTT

SEQ ID NO: 2623 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGNGTTATAATCCAATCTTTATTT
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GGACAAGTCCANTTTATCTGCCNAGGATTNCTTTTGGAAAGGAAAGCCGACNCTNTTTCGCAATT
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SEQ ID NO: 2624 GGTACAGGAGATCTCATTTGGGACAACATAAGGATAAATGCTGGTCATCGAA
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GTATGGAGGAGGGGTGCTGAGATATCCTGTGCCCTGGCAGTTAGCCAAGAGGGCGGATAAGTGCC
CCACCTTANAACAGTATGCCATGAGAGCGTTTGGCGACGCACTGGAGGTCATCCCATGGGCCCTCT
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SEQ ID NO: 2625 GGTACGGCTCTACTGCCACCTCTTCCAGCTCCACGGCCGGCGCAGCAGGGA
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SEQ ID NO: 2626 GGTACAAGCTTTGTCCAAATGGCACAGTGAGCACAAATGAGTTCTGTGT
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SEQ ID NO: 2627 ACATGCTCATGGCAGCAACAACCCATTGACCACTTCTCAAAGTAGTTCAGTG
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SEQ ID NO: 2628 GGTACTTT
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SEQ ID NO: 2629 GGTACTTTTATATAAAGTAATNCTGGATTGACATTCTCATTTAGAGAAACCT
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SEQ ID NO: 2630 ACGATCGAAGGGACTATGCTCTCATTTGAATTTTGTGTGAAGACAGTAAGGA
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SEQ ID NO: 2631 ACGCGGGGCTCTTTTCCGGCTGGAACCATGGAGGGTGTAGAAGAGAAGAAG
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CTTGCAAGGTTAAGGACTTACTGGCTTTTGAAAAGATGAGCCTTGTGAGGGACTAAAGATTGAGT
TTGAGGGTCATTCAAACAGATAAAATTATCAAAGCTTTGGACC

SEQ ID NO: 2632 GGTACACTTTTTTGAATGGTTTTCTAACAACCTGAAGTACAGGATCAAGGAA
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CAAGGGTAATTCTAGGCTAACCGTATGGCTATAGTTTAAAGCACATCTATGTTCACTGGCACT
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SEQ ID NO: 2633 GGTACTCTGTGACGGAGCTGAAGGACTCTTGCCGTAGATTAAGCCAGTCAGT
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SEQ ID NO: 2634 GGTACTTTTTTTTTTTTTTTTTTTTTTTTATAGGTTCCATTTTACTGNGCAT
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SEQ ID NO: 2635 GGTACGCGGGGGAAGTAGGGCGTGTGGCGTCACTTCCGGCTTCCCTCAGTCC
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SEQ ID NO: 2636 ACACTGTGTCTCTATGTGAATATGGACAGTTAGCATTTACCAACATGTATCTG
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SEQ ID NO: 2637 ACTTTTTTTTTTTTTTTTTTTTTTCTAATTATGATCAACTTTTATGATTTTACAT
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CGGGGAAAGNNGNCCCAANAATNACCCCTNTGTGTGAAGA

SEQ ID NO: 2638 GGTACAGAGGATCAGACCCCTATAACAAAAAGAGTTATGTTTGCTTATGAAC
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SEQ ID NO: 2639 ACCATGAAATATCCAGAACATACCTATATGTAAAGTATTATTTTGAATCT
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SEQ ID NO: 2640 GGTACATGACCTAATTTTACATCATAAGTAAACAGGCCCTATGGAGAGAGG
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SEQ ID NO: 2641 ACGCGGGAAGACAAAGACCCGCAAAAGATGTATGCCACCATCTATGAGCT
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SEQ ID NO: 2642 ACTTTTTTTTTTTTTTTTTTTTTTCCAAATTTGTTTATTTTATTATGGC
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SEQ ID NO: 2643 GGTACAGTTGAGTCTGTGTGTTTCTTGAATGTTTGAGACAGCTTCACCTTG
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SEQ ID NO: 2644 ACATATTTTGGTTGAAGACACCAAGTGAAGTAAACAGCTGTGCATCCAATT
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SEQ ID NO: 2645 ACCTTGATACACATAATCAGCCTTTTCAAAAATGCCTGACAAGAATTAGTCTT
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SEQ ID NO: 2646 GGTACTGGAAGCATGCTCCAAAGACCTGTAAGAAGTCTTGTGAGTCGGCTCG
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SEQ ID NO: 2647 ACAGATATCTTCAAAGGAGGAAGAAGAAAGGGAAGCAGATGGTGGAGCTG
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SEQ ID NO: 2648 GGTACGCGGGGAGACGAAGACTGAGCGGTTGTGGCCGCTTGCCGACCTCCA
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SEQ ID NO: 2651 ACAAGTATAGGCAGAGTTATTTCTGTTTACATTTTTTTTGGTGGGAAA
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SEQ ID NO: 2652 CGAGGTACACACACATGGGGAACACACCACAGCTTAGATGTGACAAAGTTCC
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SEQ ID NO: 2653 ACTTTTTTTTTTTTTTTTTTTTTTGGCAGTTTCTAAGTCATTACTTTTTAT
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SEQ ID NO: 2654 ACAGATTGCTTCTCTTACAAAAAGAAAAAAATCCTGTTGTATTAACAT
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SEQ ID NO: 2655 CGAGGTACAGTGTGATCTGTTTAAAGTTACATAAATTACAATCAGGGTAAC
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SEQ ID NO: 2656 GGTACCAAAATTAACCTGGCAAACTTTCTATTGCTGTCCCATGTGCATCTTA
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SEQ ID NO: 2658 ACAGCTTTTAGCAAAACTGCTTTCCAGAAAAGCAAAATAAAAATAATGCAAT
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SEQ ID NO: 2659 ACTTCTTCGGCCAAAGGCTGTTCCACATTCACATTTAAAAAGGCTTCTCT
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SEQ ID NO: 2660 CGAGGTACAGGTCCTTTTGAATAAACTGGTTATGACTTGATCCAAAGTGTT
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SEQ ID NO: 2661 ACGCGGGGATGCGCAGACACCTCAGGCGACTGGCGGGTTCGCGGCTTCCAAG
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SEQ ID NO: 2662 ACITTTTTTTTTTTTTTTTTTTTTTGGAAAATTATACTTTTATTGAGTCAOC
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SEQ ID NO: 2663 GGTACGAGTCAAGCACAACCTGCTGCGCAGGAAAAGACAAGGCTAATTGG
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SEQ ID NO: 2664 ACAGTTGGAGTCTGTGTGTTTTCTTGAATGTTTGAACAGCTTCTTGAACCTT
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SEQ ID NO: 2665 ACTCCTCCAGTTCTACTCAACAAAAATCATGATAATTGTGATAAAATAAGA
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SEQ ID NO: 2666 ACAACATCTACCCCGGACACGGGAGGCGCTACGCCAGGACCGACGGGAAG
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SEQ ID NO: 2667 ACATGGCAATTAGAAGTTGTCAATGGCAAAAGAAAACACAGCTGGCCTGCCA
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SEQ ID NO: 2668 CGAGGTACACAGTTTCTGTGAAATATGATGCTGTATGTGGTTGTGATTTTT
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SEQ ID NO: 2669 ACATTTTTTAAAGCCCGTAGCAAGCAAAATGTGACGGCATCCAAAAATGTTT
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SEQ ID NO: 2671 ACTGTTTAAAGCCCAAGTAATAGTTTTTACAGATCTTTTAGTTTCAACTAAG
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SEQ ID NO: 2672 TCTCCATTTAGTTTGTGGTANCAAGCAGCANNGGNGNAATTGAATGANAA
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SEQ ID NO: 2673 ACCANGTTTGGTGTCAACTAGAAAGAGGTCTTATTGAAGTTAAACAGATGA
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SEQ ID NO: 2674 CGAGGTACGCGGGTCTCTTCTGGTCAAAATGGCTGGTAAGCAGGCGGTTT
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SEQ ID NO: 2677 ACTCCTCTCAGTTTGGTGGTGAAGTCAATATGCTTATTTCCATGAGGAGGAT
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SEQ ID NO: 2678 ACAGAAAAGAAAATCCCGTTGTTTTTCGATTGCAAGAGGGTTATGATCATA
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SEQ ID NO: 2680 ACITTTTTTTTTTTTTTTTTTTGGATCTTGTCATTCTTGGCACTGTTTCTAAA
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SEQ ID NO: 2681 GGTACCTAGAAGAGAGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGT
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SEQ ID NO: 2682 ACAGTATTGGAATGGATCTGTCTTTGGTAAAGATCAGCCTATAATTCTTGTG
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SEQ ID NO: 2683 ACTCACATTCATTGTGACATATTTAGGGCCCTATACACCCCTTTTAAATGT
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SEQ ID NO: 2684 GGTACTGGAGATGATTTGATAACCAAGGTTTATAGGTAATTTTACCAGTAT
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SEQ ID NO: 2690 GGTACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTTCATGTGTGATGA
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SEQ ID NO: 2691 CGAGGTACAGCATCGTAGGGTCCCTAAACTTGCCCTGTTTTGTTTTTTA
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SEQ ID NO: 2692 ACTTCAGACCATTCCTCCCGCATGGCCTTGGTGTGAAGTTGGTATGGCAG
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SEQ ID NO: 2694 GGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGTGAAATATCAAGGC
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SEQ ID NO: 2695 GGNACTTTTTTTTTTTTTTTTTTTTTCGAANCCAACTGTATCCAGCTTT
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SEQ ID NO: 2696 ACGGATACCGAAAGGCTGGATACCTGGTTATTAGAGGATTTGGAGATGG
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SEQ ID NO: 2697 ACTTTTTTTTTTTTTTTTTTTTNGAGNCATTACTTTTTATTGGAAGGATT
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SEQ ID NO: 2698 GGTACAAAGCTTTGCAAGGGTGTGTTTGGAAATGACGCTAAACTGAAGGTG
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SEQ ID NO: 2702 ACTTTTTTTTTTTTTTTTTTTTTTGGCTTNGAAATTTANAACAAATTTTAT
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AAATGAGAAAAAGGAGCTTCCGCCNTTATTNTNGTTTAAACANACNGAAAAACAACTGGN
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SEQ ID NO: 2703 GGTACATTGTGTTTAAAGAAAAATGAAACCCACATGCCGCCATTTCTCTGA
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CCAATCAANAGGCTNCTGCTCAGCTCTCAGCTTTGGGCCAATNCTTTGCTCTGCCAGGGTANGT
NAAACNTGGGAGACTCTGGTCTTTTACCCTCCCTNNTTCCATACCTGNCNCTNCTGGGTGGCAAC
ATGGTCTTGGACAATTATAGAAACAAATGACTTTTGGGAATAGCCCTGTCTTAGGGCAAACTGT
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SEQ ID NO: 2704 ACATAGTGGTGGCCCTGATAGGACATTGTTAGCATAGAGGCTCTTCTGATG
TCAATATCACACTCATGATGCTGTTGAGGTGGTTTCATGGATGCCAGCAGACTCCATCCCGATG
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ATCAGGCACTCGTAACCTTCTCAAGGGAGGATGAGGATGGGGCAGTGGCCATCTCAATTTCAA
AGTCCAGAGCTACATAACACAGTTTCTCTGATGTCCCGGACAACTCAACGCTCAGCAGTATGTA
CGAAGGAATAGCCACGCTCAGTCAGGATCTTCAAGGTAGTCAAGTGAGATCTCNGCCAGCCAN
ATCCATACGCATGATGGCATGGGGCAAGGCATAGCCCTCATAGATGGGGGACATTTGGGTGACA
CCATCTTCAAGTCCAGCACNGATGCCNAGTTGTGCGTCCAAGAGCCATANAANAACAAACCCG
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SEQ ID NO: 2705 GGTACTGTATTTCCGCAAAAAGAAATTAACATTTAGTAACACACTAATGAA
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SEQ ID NO: 2706 ACCTAGAAGAGAGGGGGTCAAGAAGTAGTGAAGAAGCATTTCTCAGTTCA
AGGCTATCCCATCACCTTTATTTGGAGAAAGAAACGAGAGAAAGGAAATTAAGTGATGATGAGGCA
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SEQ ID NO: 2707 GGCNCGGCGGANGTACTCTATGCATTCTATCTATACAGAAACACCTATTTATT
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CATCAACTCTCCATAATGAATCTGAACCTCACAATGATTACCAAAACACTTACTTAAATTAATA
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CAACAAATACTATGATGCAATTTTACATTTATTAACCTACAGTTCAAAGCAAAATTTACACATTC
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CGATTTAATGGGGAACCAATTAATGGGCTTCATCTCCCTAAGTCATCCATTTTGGTGCATATTTA
TTTTAACGCTTAANGGTAG

SEQ ID NO: 2708 AC0CGGGGATTTCAAAAACAACCGATGAGATTATGACTTCACTCAAGTC
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CAGAGACCTGAAATTTCTGCCATCTGAACTCAAGAGTGGAGAACTAGTGGTTGACCCTAACCAAG
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AATCCTTTGAATGTTCCACGGAAACACTGGTGGACAGATTCTAGTCTGAGAAAGAAACAGTTTG
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CTGCAAAAAATAGCATTTGCATACATGGATCAGGCCAGTGGAAATGTAAAGAAAGCCCTGAAGCTGA
TGGGGTCAAATGAAGGTGAATTCAGGCTGAAGGAAATAGCAAAATTCACCTACACAGTTCTTGGA
GGATGGTTGCACGAAACACACTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAAACCCCCAAG
GCTGGGAGACTAC

SEQ ID NO: 2709 ACAATGTTGAACAAAAGACCACAGGGGACCTTTTGTCAAGTAGCACCAA
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TTTCTCAATTTAGTTACTGACCTCTCCGCAAACTCAGCCCGAGTCTCAACCTTCTTCAGCTTGTG
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NGG

SEQ ID NO: 2710 ACACTTACTGGGCTGGCCTTTTAAATTTTACTCTTTTGCCTTCCCTTCCACC
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SEQ ID NO: 2711 ACATCAAAGATTACATGAATCAATCAAAGGAAACTTGAAGAACAGAGAC
CAGANTTNAGTAAACCTTTTATGACAGGGGCTGCAGAACAAATCAAGCACATCCTTGCTAATTTT
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CAAAATGTGGCAATTTTGGATCTATCACTGTCTATCACTAAGTGGCTTCTGCTTGTCTCCACACA
ACACCAAGGACTTAAAGCAAAATGGGACTGATGTATCTTGAGCTCTTCAATTTATTTGACTGTGATT
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TTTAAACACAAAAAAGAAAAAAGTCTCGG

SEQ ID NO: 2712 GNACAGNGGAAACAATCCAAAGTTTAAATCAAGAAAGNGGTGNTCANTTG
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TGNTATCGACTACNTTGATAGTAAATTTGANGNCTACCTAAATGCNAAATCACGAATGAACAAGA

CCTCAGAAATGCCTGATAACAGGGGTGCAAGTONTGTTTATACTTCATTGCTCCTCAGGCATGGAA
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TGCCAAAGCAGACACACTCACACCAGAGGAATGCCAAGCTTTAAAAACAGATAATGAAGAA
ATCCAAGAACATAAAATTTAAATATACGAATTTCCAGAAACAGATGATGAAGAAGAAAAATAAC
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SEQ ID NO: 2713 ACTGTACATTCTCTTTTCANATTCCTTTTITTTGGGATAATTTCTCTTCTCTA
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CTGGCGCTTGAAAGGNCNAATTCACGCTAATGNOGGCTANTAC

SEQ ID NO: 2714 ACGCCGGAGCTCTTCTCTTCGCTGCTGGCGCCGAGCCATGAGTATGCTCAG
GCTTCAAAANAGGCTCGCTCTAGTGTCTCCGCTGTGGCAAGAAAAAGGTCTGTTANACCCCA
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CTGATCATCCGCAAGCCTGTGACGGTCCATTCGCCGCTCGATGCCGGAACCACTCTGGCCCGCC
GGAAAGGCAGGCACATGGGCATAGGTAAGCGGAAGGGT

SEQ ID NO: 2715 ACGCGGGGGCAGTCCGCTGGTCCGAGCAGAGCTGTGAGGGGATTCACTTG
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SEQ ID NO: 2716 ACTCAAGTCACTTAATGAGGAAGCTGTGAAGAAAGACAACTCTGTCCATTGG
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CCTCCACCAAGCACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGAGCAGCCACATTTACCA
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GAAAGTGACAGGAGAAGGATGTGTACCTCCAGACATCCTTGAATACAAATTTCTCCAGAAA
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SEQ ID NO: 2717 ACAAGTATTACGTAAATATGTAAAGATTCTTCAAGGTAAACAGGGTTGGG
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CTGGCTTTT

SEQ ID NO: 2718 ACCAAACGGGCAAGGACATCTCTACAAATTACTATGGAGTCAAGAAAAAC
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SEQ ID NO: 2719 ACTGCAGTAATAGGAATCTCTCCACAGAGGCAGCAGAGAAAGTGGTTTAGTG
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GCATCTGGTGTGCCATCTCTCCOCACAGTAGGGTATTGCCCTCAGCAGAGAAACAGAAAGCCCATCAT
AGTACCATTGGTGGCCAAATTGATTGTGTAAGGGAGGGATCGTTGCCCTGCTGTTATGTAAAG
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SEQ ID NO: 2720 ACCAGTAAAAACCAGAATGAOCCATTGCCAGGACGCATCAAAGTTGACTTT
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GGTGAATTAAT

SEQ ID NO: 2721 ACACCTCTATAAATAAACACATCAATTTTGCTCTATTACTACTCTTCCAAAAAC
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SEQ ID NO: 2722 ACTACTTGGTTCCCGATATGGATGATGAAGAAGGAGAAGGAGAAGAGATG
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SEQ ID NO: 2723 ACCAAGAATGTGCTGTGACAGGACTTGNCTCTGCTGTGGTAGCAAAATGCC
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CCCGAACTTGTCTTCAGTTTAGCATNGNAATATTTCTTTTCTCTGTTCTTNCAGNTCAGT

SEQ ID NO: 2724 ACAGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTTGAAGGA
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SEQ ID NO: 2725 ACAGACAAAACCTACAGACTTAGTCTGGTGGACTGGACTAATTACTTGAAGGA
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CCTTCNAACCTGCTGCTTTGAACCGACCAACATTAAGTCCAGANAGTAACTTGAATGGAAATACT
ACATTCAGAAAGGTTANTCATTTGAATTTCTGAACACTGGAGAAAAACCGTAAANTGGACGGGNC
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SEQ ID NO: 2726 ACTGTACAGAACTTTTACATACATTTCTCAGTCTAGTTGTGAAAGGCTAAA
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TAAAAAGA

SEQ ID NO: 2727 ACTGTGATTGAACATCCTGAATACGGAGAGGTTATTCACTCTCAAGGTGACC
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SEQ ID NO: 2728 ACAAATACGCAAAATTTTCATAGTGCCTAGAAATAGCACAGATCTATTCTACTC
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TCGCGATCTT

SEQ ID NO: 2729 CAGCTGATGGGAACGGGCTCCAATGGACTGGATTGCATTCAAAATATTATTTT
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SEQ ID NO: 2730 GTACCNNGACAGTGCATGTCACATATGATTTCAAAAAAGTTCACTTCATTGC
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GGTGGTGGCTCTGCAGAGAACCCCTTCAGGATCCGTGAGGAAGACCAAAATGAACAAGCAGA
AGACTCTGGAAACGGAGATGGTGGCAGGTGAAGTCTCTCCACAGCATGCCCTGGGCTCTCTGCT
CAGGAGAAAAAGCCCCAGTTCTACATGATTCCTGAGGTCTTCTGTTCTCTCGCGCTGGCGCT
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SEQ ID NO: 2731 ACACAAC TGCAACTCTACATAAATGCCACAGATGCAGAATACTGTTTCTTGC
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SEQ ID NO: 2732 ACCTGGGTGTTCCCACTTGGGCATCATGCACCACAACAAACAGGCCACTG
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SEQ ID NO: 2733 ACTTATTTCAACAATTCTTAGAGATGCTAGCTAGTGTGAAGCTAAAAATAGC
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TTCCATTTGATTTTAGGTTTCTTTTACATTTCTTTTATATGCAATCTGACATTACATATTTTAA
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SEQ ID NO: 2734 ACTGGTCCAGGAGTTATCCAGGATAGATTTTCAOCCACATGGGCGTCACT
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CTGGGACAGACACCTCAGCTTGGTCTCAAACTAATCCACCACTTATCCAGGAAAGCGCTGCCAA
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SEQ ID NO: 2735 AAAAAATCCCTTTGTTGAAAAATAAGGGGCTTTCTAACTAATAAAAAAGG
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SEQ ID NO: 2741 ACCAGAGTCAAGGTGCCAGGGTCTGGGAGCAACAAATGCATTCCCATGAT
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SEQ ID NO: 2742 ACTGGGAGATACAGCCATCCACCTTCAGATGTGTCTACGTGGCTCTGCCATT
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AATTTAAAAATACATTAA

SEQ ID NO: 2743 ACAGCTTAAACCACAATGGTATAAATCTTCAITTTGTAAATTAATAATTTCTG
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CAGTGACAAAACGAAAAAGGGCTTTTCTTTTCTTCTCCCGCT

SEQ ID NO: 2744 ACCAGCGATTCTGCGGCAACACGTGCACCCCTGAGGAGACAGGTGGCAGTGA
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CGGCAAGATGAACTGOCATGAGGGTGTAGTGAAAGTTCACAGATTGCAAGGGACACAGGGAAATGC
CAAGGCACCCAACTGCAAAATACGGGCCATAGCGAGCACTAGACGTGTTGTCTATTGCCTGTGAGG
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SEQ ID NO: 2745 ACACTTATAGAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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SEQ ID NO: 2746 ACTGGGAGATACAGCCATCCACCTTCAGATGTGTCTACGTGGCTCTGCCATT
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SEQ ID NO: 2748 ACAGGATGAATTTAAATGTGTTTTCTGAGAGACAAGGAAGACTTGGGTAT
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SEQ ID NO: 2749 ACAGCTTAAACCACAAATGGTATAAATCTTCATTTGTAATTAATAATTTCTG
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SEQ ID NO: 2750 ACCAGCGATTCTGCGGCAACAGTGCACCCCTGAGGAGACAGGTGGCAATGA
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SEQ ID NO: 2751 ACACTTATAGAAAAAGGTAAAGGAAACCCCAACATGCATGCACTGCCTTGGT
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SEQ ID NO: 2752 ACTGGGAGATACAGCCATCCACCTTCAGATGTCTACGTGCGCTCTGCCATT
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SEQ ID NO: 2753 ACCACTCCAGTTGTCTTCACAATTTAATGCTACAGAAACCTAAATGTTCTAC
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SEQ ID NO: 2754 ACCTGATGCTACAGACGAGGACATCACTCACACATGGAAGCGAGGAGTT
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SEQ ID NO: 2755 ACGCGGGGACTTCCGGGTCCGGTGCTTGAAGGAGTGTTCGGTGGTTCC
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SEQ ID NO: 2757 ACCAGCAGTGTGTCAGGTGCTGCAGAGCGTTCTTGGAGAAAGGCCACTGAGG
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TC

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SEQ ID NO: 2759 ACGATTGCTTCTCTGATTCCAGCAGAGGGAAGCTATCCAAAAAGTTGGCA
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SEQ ID NO: 2761 ACCCAACTGGATTGTCTCTCTGAGAAATGCAAACTGCAGACCCCATATCTTT
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SEQ ID NO: 2762 ACTTTTTTTTTTTTTTTTTTTTTTTTACAAAAAGTTGTTACAAAAATACAG
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TGTTTTT

SEQ ID NO: 2763 ACCTCAGGCGCTGGGCACCTCTTGTGCTGAAATATGGCAAGACTTGGAAAAAT
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SEQ ID NO: 2764 ACATCAAAGATTACATGAAATCAATCAAAGGGAACCTGAAAGAACAGAGAC
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SEQ ID NO: 2765 ACGAAGTTCTCAGTTTCACTTTAGTAGAAAGAGCTCTAGAAATGAGGCTGAT
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SEQ ID NO: 2766 ACTAGGAAGGTTATTGCACAGCTCTTAAGTATCGGGGTCAGGGCAGAGTG
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SEQ ID NO: 2767 ACCAAGGGATGGAAGAAATAATATAGCTCAGGTAGCACTTTATCTCAGGC
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SEQ ID NO: 2768 ACCTTGATACACATAATCAGCCTTTTCAAAAAATGCCTGACAAAGAAATAGTCTT
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SEQ ID NO: 2769 ACATCAGGGACCTGTGCACTGGGCTCAAGCCAGACACGCAGCCACAGATGAT
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SEQ ID NO: 2770 ACTTACAAAGTTACAACCATTTGCTTCCTTAACATTTTCCATGTTAAGTTTATA
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SEQ ID NO: 2771 ACGCGGGGTATCTTGATGCAGTAACCTTATAGTTGTGATCTGCACCTGGACCA
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SEQ ID NO: 2772 ACTCTTTGTTTGGCACACTTTTCTGACAAACAGCCAGTGTCTCAACACAT
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NGGAN

SEQ ID NO: 2773 ACATCTTAGGTTTTTCTTCTTTAGTGTGAAGAGGGGTTNCCACCAACCCACA
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SEQ ID NO: 2774 ACTTAA
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SEQ ID NO: 2775 ACTCCTGGTGTATTTATGGGACCCACAAATATAACATTTACCTCACAAGCACC
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SEQ ID NO: 2776 ACTTTTTTTTTTTTTTTTTTTTGTAGANANATGGGGTTTCACGATGTGGC
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SEQ ID NO: 2777 ACCTTTTATTGGTATAAGAAGTAAAGTCCAGATTAACCATGTCAATTGNTTCA
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SEQ ID NO: 2778 ACTTTTTTTTTTTTTTTTTTTTGGATAAAANATGCTTTATAAAGTTTTT
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SEQ ID NO: 2779 ACGCGGAGCGGCGAGAGACATTGTTCTTGGCGGCTCCCTACGGTGCCGTGTG
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SEQ ID NO: 2780 ACTGCAAGTCAAGGGGACTCTTTCAGGCGTGTCTTTAGAAGGGAGCTGTTT
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SEQ ID NO: 2781 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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SEQ ID NO: 2782 ACACAGGTATTTTCAAGGAAACAGTCACTCTAAAGTAATATTTTCTATAT
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SEQ ID NO: 2783 ACTATAGGAATACATTAAGTAATCAATGGAATATACCTTGCTAATATTATA
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SEQ ID NO: 2784 ACTAAATAAGACCATGGATGTTAGTAACTCTCTGCTGAAAAAGTGGAAAT
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SEQ ID NO: 2785 ACCAATATTCACAAGCAAACTATCACTAGTATCCCATTAATTTAAATTCGCC
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SEQ ID NO: 21977 ACTGGTCAACAGCATTTTTCATTCACATTTGAAATATAGCAGTATGCTTAATG
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SEQ ID NO: 2798 ACAGTTGCCTGAAGTTACTATAAATGAAGAACTGCTTTAGCAGAAAGTTAAT
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SEQ ID NO: 2799 ACAAGCTTTTGTCCAAAATGGCACAGTGAGCACAAATGAGTTCTGTGTGAT
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SEQ ID NO: 2800 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGCA
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SEQ ID NO: 2801 ACCATGACCTACATAAGGCTGGATGGCACCTCAGCCTGAGGGCCCAATGT
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SEQ ID NO: 2802 ACGCATACTAGCAAGGTAATGGTGATCTAGCAACAAATTTGGTTCTGCA
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SEQ ID NO: 2803 ACAAACCAAAATGTTGTTACTATAACTTCTGCATCACAATTAATAATCCAAAC
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SEQ ID NO: 2804 ACTTTTTTTTTTTTTTTTTTTTTTAAAAATCGCCTATTTATTTCCATTANA
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SEQ ID NO: 2805 ACCGTCCAGCGAGTTGCAGATCTACACTTGGATGGATGCACTTTGAAAGAA
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SEQ ID NO: 2806 ACTGTTATTAAGCATATTGATTATAGAGCTATTCAGATATTTAAATATA
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SEQ ID NO: 2807 ACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGTTCAGTGGCTC
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SEQ ID NO: 2808 ACCATCGCACACACTGTTGACGTCAATTGGAAGAAAGGAAGACGACTTTGTCT
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SEQ ID NO: 2810 ACAACAATTATGACATTTGATTAGGCTGGACTCTAACTTGCTTGGATGAGATT
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SEQ ID NO: 2811 ACCCCAATCTGAAGTCAGTAAATGAATACTACAAGCCTGTTATGGCAA
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SEQ ID NO: 2812 ACNNINTATNTANCAGATNTNAAGAGTCCATTTTAAAAAGTGAGCAAT
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SEQ ID NO: 2813 ACCGGATTCTGTCTTAAACCTGCCCTTGGTGTTCGCCCAATGTTTAAATGT
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SEQ ID NO: 2814 ACGCGGAGTTTATAATGAACTATCTACAATCTGTGTTTAGCACATCTGTT
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SEQ ID NO: 2815 ACAAAATCCAGTGTGCAGACCACANCTCAAAACAAAAAGATCTATTTCTA
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SEQ ID NO: 2816 ACAAGATGACTATAACAANATGCATNCTCGGTTTCCATGAACAGNACAC
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T

SEQ ID NO: 2817 ACATGAATTAGAAGCGTGCATCTAGGATTATGGCCAAACTGTTTAAAAATG
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SEQ ID NO: 2818 ACATGAATTAGAAATAAAAATGTCGAGGATTCTGAAATCTGATACCTTA
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SEQ ID NO: 2819 ACCTCTTGAACGCAATTGATTCTCAAAATCGAGAGATCATGAAACACCTGAA
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SEQ ID NO: 2820 ACACATGTCATAGTGACCACAGCTTGTGGCTCCTTGAGGGAGGAGATTCAAC
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SEQ ID NO: 2821 ACTCTTGCTTATATCATCAGAGCTGGATGAGAGAGAGCGAGAAGAGTTCT
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SEQ ID NO: 2824 ACGGGGTCTCTTTCGGCGGTGCTCGCAAGCGAGGCGCCATGTCTTATCCC
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SEQ ID NO: 2825 ACATCTTGCCTAGATGTCGATGACTGCAAGTAATAATACAGTTTATAATGAA
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GCAGACTGGATCTTAAATGATCGGAAAAATACATTTTAGGCNCCTGCCCTCCATGATNNNTGTT
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SEQ ID NO: 2829 ACAGATGTGCAGGAATGCTAGGTGTGGTTGGTTGATGCCGATTGTAACATT
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GGAATAGGGCTGAGACTGGGTGGGGCTTCTATGGCTAGGGGAGTCAAGGGTGGAGACTAAT
TGGGCTGATTGCGCTGCTGCTAGGAGGAGGCTANTAGTGGGAGGAGGCTTGGATTANCGTTT
ANAGGCTATTGTTGGGTCTCATAGTGGANTGTANGATAATCATGCTAAGCCAGGATNAAC
CGTATCCCGGTTGCGTTGATAGNATGCTTATGGGTGCNGGTTGCTGTGCGGTTCTCACTTAN
ACANANGTTTATTCTCCCTT

SEQ ID NO: 2830 ACATATTTTGGTTGAAGACACCAGACTGAAGTAAACAGCTGTGCATCCAATT
TATTATATTTTGAAGTAAACATATGTAATCAAACTTCTAGGTGACTTGAAGTGGAACTCTCTA
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SEQ ID NO: 2831 ACGCGGGGCTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAGCTGT
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AAAGCTGGGAACCTTGGTGGAGGGGTGGGACCAACGAAGGAGCAAGAGCAAGATCACCGTGA
CATCCGAAGTGGCTTTCTCCAAAAGGTATTGAAATATCTCAACCAAAAAATTTTGAAGAAATA
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ACCAGNGAANAGANGAGGAAGACGAGGATAAATTCATTATCTGGAATTTGTTTAAATCTGG
AATAAATCTGGGACCCNAAAAGAAATAAAAAATA

SEQ ID NO: 2832 ACGCGGGGAGAAAGTTAGGGGCTGCAAGCGGCGCTGGCTTAGGTGAACGAGCT
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AGATTTGGAGAAAGTTTCGGATGTGGAGATCATCACAGGAAAGATGACCAAGGAACCCAGAAAT
TTTTGATATATCATCAGTGTACAGAGCGGCTGAAAAATGNTGCTGTTTAAATAAAACAAA
TGGAAAGGGACNTTACAAATCACTAGCAAAAGAGCTTTCTGAANATGGCCA

SEQ ID NO: 2833 ACAAGTTCGGCTTTGAGCTTCTCAGGGGCTCTGGGAACATCCTTCAAAGG
AAAAATATGGGTGTGAGTACTAGTGGTGAAGGCTTTCTTTGACCCCGAGCCAGCCAACTCAAG
AGACAAAGAAAACTTTGAAGTAGTGAATCTGGTGGATGCAATACCCCTGATTTAATGGCACT
GTGCTGCTCTAAAAAAGAAAAAGTTTCTGCTGATGTTTCAATCTGATGGGCGGGTGTCTGTCT
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ACATGTTCCCGAATTTGGTCCCAAGCTGCCATTTGGCCCGCCCACTTACTTGCATGGCC
AGACAAGGTGCTGACTCAAAAGTGCATCATCANAGCATTTTATCTAAGGANTTGGCATATGGC
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SEQ ID NO: 2834 ACTTTTTTTTTTTTTTTTTTTTNNATTTTTTAAAACAACTTTGTGATATTTAT
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ATAGTTAAATATATTGACACTGAAATAGTGCACATTTAAATTAAGGAGAAATTAATAATGTGTGC
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TTNAAAGGNAATTAACAANNNTGGNGNCTATANNGGATCCAACTCGNTCCAACTT

SEQ ID NO: 2835 ACTTTTTTTTTTTTTTTTTTTTNNATTTTTTAAAACTGAAAGTCTTGNNTTTACTA
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TAOCCTTATCATCAATGATTAAGAGGCCCTGAACGAGATGCTTATCACTTAANCCATAATC
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AAAGNGGTTTTTAANACCTNGNNAANTGGTTATTGGGGNGGCCATTNTTTNAAANTTTTANG
NCCANAAGGAAAAATCCC

SEQ ID NO: 2836 ACATGTTGAAGAAGTGCCGATTGTAATTAATAATTCACATCTGATCAATGTC
CTAATGTGGAACTTGAAAAAGAGTCAAGCTGTGCAGATAAACATGAATGCTCAGGCTTCCAG
CAGCAATCATTTGGGGAAGAACTTACAGTTGCTGTGACAGAGATGAATGAGCCAAAGATA
TAGTTAAATACACACATATAGGAATACATAGTAACAACAGCAGCAGAAATCATGATATCAG
CAGGCTGGCCAGCAGGAATATGCAGGCCAGAGCCGAGGAGAACCCCGCTCCCTGAGGAGA
CCTGTCAAATCTTCAAACCAACAGCGCTGTGCCAGGATGGCTGCTGTGTTATGAGCCAGATA
AAACTTACTGCCANACTTAANGAGTCACTGGCCAAACTTAGGNAGCTTNTCATGCCAGCTNTTA
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GANAATTTTGNNTTGAANCAAGNNTTNTNAGCTTGCCGTTTGTANANGTTTNTCAATNAA
AAAAANAANTNGAAAAAATAACCTNCCG

SEQ ID NO: 2837 GTGGTCCGGCCGGGTACCTTTTGTATGCTATATTACTGCGATTAAAAAGTTC
TTGCAAGTAATGTTTATGATATGTAACGTTGTAATTTCTATGCTAATTATAACATCCCATTTCT
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NGNCCCTTTAAATTAACGGANATT

SEQ ID NO: 2838 ACGCGGATTCATTATGAGCTATTACACCAAGTTTAAACACCTTCTCGTGTAT
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TCTGCACCTTNCATATATACTCTACCTTCTTAATTACTTCTGGCAAGATGTTCTGCTTACACTCA
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SEQ ID NO: 2839 ACTGCTCTTTTGGAAAAAGTCTTGATCCCAATGCTTCACAAGCAGAGAGCA
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TCCACTTTTGTGCTATCTAAATTAACANAAACATTTNCTCATNTGCCCAANGTTTTGTACAT
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SEQ ID NO: 2840 ACGATOGAAGGGACTATGTCTTCATTGAATTTGTGTTGAAGACAGTAAGGA
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GCAITTTAAATGAAATTGATCTTTTCACTGTATTGATCCAAATGATTCCAAAGCATAAAGAACGGA
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SEQ ID NO: 2841 ACACCTGTAATCTGTCTCTTCAACAAAGGAAGCAGAAGATGCACTGAAA
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CCTTGGCGGATTAGATGCCAACATAGCTAGACTCCAGAACTCTTANGGACTGTCTCTGAGAAAT
GAATTCAGAAAGAAATCATCAGGTGCTCTTTTAAACNAGAACTTGCTATATTGAATGTGATTTCT
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SEQ ID NO: 2842 ACTACACGCGCTGGGCAACGACTTCCACACGAACAAGCGCTGTGCGAGGA
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GGANAGACANTTATGTTCTGNNGTCTCATCTGATCAGGAGATTATTGAAGTAGATCTTGACA
CTAAGGAANTGCTGAATCTTTTGGACTTCNGCAGTCTGTNANCCTTCANGCCACTNAGCCCTAC
TTTGGATGANTTTTCAAAAGCCTTCGNGACCTGNTTNAATTTTATTGNTGAGCTGNTTATTTN
TNATTNAATTCGGGACAAATNTGCAT

SEQ ID NO: 2843 ACTGTCCGTTTCAGAAATGCCTTGCAAGTGGGATGTCTCAATGCCATCAGG
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SEQ ID NO: 2844 ACTAACTGATGGGCGGAGGGGGCATTCACAGTTGCTGGGAGAGCAGTG
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SEQ ID NO: 2845 ACGTATAGTTAAGTGATGAAGAAAGGTTATTTGGTTTGTGTCGTCACTTATA
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GACGAAACAGACTGAGCAGCGTGGTTCTCAGTCCACTTATCAGAGGTTGAGCTGGAAAAACGAGA
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GCCCCATCCGCTCTTNTTTTAA

SEQ ID NO: 2846 ACGGGTAGTGGCGCACATGGTAGCATTTGAGCATATGGACAAACTCCACCTTG
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ACTGGCAGCATGATTCAAGAACTGAGACATATTCACAATGTGGTAAGGAATCCCAAGGAGCT
GGTAGAACTCTCTCGGTGGTAATCATCTCTTCAAAACATCTCCATGACTGTTGTGTCATGGGGTG
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SEQ ID NO: 2847 ACCTAGAAGAGAGGCGGTCAAAGAGTAGTGAAGAAGCAATTCAGTTTCAT
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SEQ ID NO: 2848 ACAGATTGCTTTCTCTTACAAAAGAAAAAAAATCCTGTGTATTAACATT
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AGTCTAGAGAAGCAATTGGTAAAGCTTATCGTATATATTTTTTAAAGAGAGAAAAACACCTTGAG
CCTTAAAAAGGCTGCTGCTGGGAAACATTTGCACTCTTTAAGTGCAATTCCTCTGCTTTGCTGT
TCACTGCANTCTAAAAAGAGGTAAAAAGCAAGCAAGGAGATGAATCTGTTCTGGGAATGTTCA
GCACCNANTAAAGTCCGAGCCACTGCCCGNTGCTGCTGCCCNNTNNGAAGGAAATGCTGTTTNT
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SEQ ID NO: 2849 AATAAAGAACTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
CAGCTTAAATTTCTTGAATTCATATACGCTTCTGTCAATTAACAACTTCCAGAGAAAACTGGT
CTCTATATATTTAAGTAAACAAATTTGACAAAATACATATTTATACATATATAGATCTCTAATATA
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TTTTATACATTAAGATATTTGGTTGAATATCTTCAATTAAGTTCTAAAAAACACCAATATCTGCTT
CTTAGTAATTCGACATCTTNAAGCNTGTGAACGGNTTAACTNACTCTGGCTAANTCAN
ATTGNGTNGTCTCTTAACTTTTCTTAAANATTTGCGGAGNTACAAGGAA

SEQ ID NO: 2850 ACTACTGCTGTTTCTGAAGACGCGAGGGCAAGTGCAGCCAGCCGTTCTTTT
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TGAAACCATTTGCTTCTCTATGACATCCAGATTTCTTCTGTTGATCTCTCAGTCTCTAGAGGACA
NGTCGCTCTTCAACTTGTCTCGAAGCTTCTCCCGAATACACTCGTGGGCACTCAGAGAAAGCAA
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GGTGCAANTGNGCGANANACNTCCCAACGNTCCCAATANGGG

SEQ ID NO: 2851 ACTTTTCTTTTCTTTTCTTTTCTTTTNGGANANACAAGGCTNACTATGTTG
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SEQ ID NO: 2852 ACCTGTGACCAAGTGTGGGCGAGGATGAGATGATCGACGTATCATGGGGTG
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CNAAGCCGCTCTGGANANATGACCTAAATTTGCACTCANTTTGCAATGGCGTTCAACA
TGGAGAAAAAGATTCTTGGACCTTTAAAAACNATTTTNGNAGANAAGTNTTNCCTAAAAATNTT
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SEQ ID NO: 2853 AATAAAGAACTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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CTCTATATATTTAAGTAAACAATTTGACAAAATACATATTTATACATATATAGATCTCTAATATA
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TTTTATACATTAAAGTATTTGGTTGAATATACCTCAATTAGGTTTCTAAAAACACCATTTATCTGCT
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TCTGTTNGTCTCCAAACTTTATCTCTCTAAACATNTGCGAGCTCCAAGGAANGGACATTAC

SEQ ID NO: 2854 AC GCGGGGAGTCAGTCCAGTCAGGACACAGCATGGACATGAGGGTCCCCG
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CACCTTCGCGAAGGACACGGTGNACTCAACANCTGGGCTGACATCTGCTTATTTCCGCAATTGATAG
CAGTTNAAATCNGGACTGCTNTNTGGTGCCTGTAAATCTNATCAAA

SEQ ID NO: 2855 ACACGTGTGGTGTATATGGGGATGGGGTCTCGGTAAATTTGTGTTATTTTA
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TGCTACAGTATGGCTGNCCANAAAGAAATTAACNGTATTTTTTCNNAGAAAGGATCCATGGCCTT
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SEQ ID NO: 2856 ACTTTTTTTTTTTTTTTAGTATTTTCAGCAGGATCTGCTGGCAGGGTTTTTTG
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SEQ ID NO: 2857 ACATTTAAATTTTGGTGGTGTGTTGTTTAAAAAGAAACAGCTTCCTTACG
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SEQ ID NO: 2858 AC GCGGGGAGCGGAAGTAGGAGCTCTCAGAGGCTAAGAAAGTGGAGACCGG
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SEQ ID NO: 2859 ACCAAGGGATGGAAGAAATAATAGCTCAGGTAGCACTTTATCTCAGGC
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SEQ ID NO: 2866 ACAGCAATGAAACACCAAAGGGAGCTTTTCTCCAAATTGTGTATAAGCTTG
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SEQ ID NO: 2868 ACITTTTTTTTTTTTTTTTTTTTTATATCACAAATCGTTTATTATGTGAAT
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SEQ ID NO: 2870 CGCGGCGGANGTACGCATTNCAATTTTCAGTGCTNNTACAAGGAAAAAGGTG
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SEQ ID NO: 2873 ACTTGTGTGCTTAAATACTTTATGCTCTGAACCTTCATAGAAATCCTTTATG
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SEQ ID NO: 2874 ACAGTTCACCTGCAAAAAATCTCCTCTCAGCAATTCACATTCACATTCAGCA
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SEQ ID NO: 2875 ACATCAGTGAATTTTAAATGCTAAAAATTTATGATAAAAGAAATCTGAAATC
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SEQ ID NO: 2876 ACCAGAAGTATAAGTTTATGGAACCTCAACCTTGCTCAAAAGAAAGAAAGGCT
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SEQ ID NO: 2877 ACTTTTTTTTTTTTTTTTTTGTCTGCAAGATCTAGGACGTTTTTATTAAT
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SEQ ID NO: 2878 ACGCGGGGACTCAGGGAGCCGGAGGGGACGCGCCGGAGGAAAGATGGAAG
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SEQ ID NO: 2879 ACGCGGGGATCAAGCCTCACTCCCTTCATATTACCCCTCTCCTTTTAAAAAT
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SEQ ID NO: 2881 ACTTTTTTTTTTTTTTTTTTTTTTTTNNACAGCAAGATAAAATGAATCAATTT
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SEQ ID NO: 2882 ACGCGGATCCACAGCAAAACAAAAATAAGCTTTTATTTTATTAATAATTTGG
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SEQ ID NO: 2883 ACTTTTTTTTTTTTTTTTTTTTTTNGGNAATTTGAATGTATTTTAAATTTAT
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SEQ ID NO: 2884 ACATGAATTAGAAAGCGTGCATCTAGGATTATGGCCAAACTGTTTTAAAAATG
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SEQ ID NO: 2886 ACTTGCAAGTGCTTCATGTGGTCTTTCTCCAAGTTTAAACCACAAAGGACTCT
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SEQ ID NO: 2888 AATAAAGAACCTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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SEQ ID NO: 2892 ACTGGAGATGTATTGTATAACCAAGTTTTAGGTAAATTTTACCAQTATTAG
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SEQ ID NO: 2893 ACATTCCAGATCCCTCGGCCAAGGACTGGACCAAGAAACACTTGGGAATCT
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SEQ ID NO: 2896 ACGCGGGGGGCTGGTTTCCGAGTGGCTCTCTAGAGGGATGCACGTTGCCT
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SEQ ID NO: 2897 GGTACAGAAGATACAAAAGTGGCAGCCAGCCTCACTAGCACTCTCATTTCTC
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SEQ ID NO: 2898 GGTACTTTTCTTTTCTTTTCTTTTGGAGTCTGTGTTTACTAATGGAAA
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SEQ ID NO: 2899 ACTTAAGTAATCATGAAAAATCTACTTGTAAGTATAGAAAGTGAATTGTGGA
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GCGCA

SEQ ID NO: 2900 GGTACACCTTGAAGGCGAGGTTAATTAATCCTGTTGTGGAGTTTGAAGGCC
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SEQ ID NO: 2901 ACTGTATTTTCGCAAAAAGAAAAATTAACATTTAGTAACACACTAATGAATTTT
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CTTNG

SEQ ID NO: 2902 ACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTGCTTTTGTG
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CCCGA

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SEQ ID NO: 2904 TCGAGCGGCGCCCGGGCCGNACTGNTCTGTTGGCCGANTGGANACTGGTG
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SEQ ID NO: 2905 GGTACCGCGGGGCTCTTCTGCTCTCCATCATGCGCAGGATCAAGGTGAAA
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SEQ ID NO: 2906 ACATAGTGTGCCCCCTGATAGGACATTGTTAGCATAGAGGTCTTCTGATG
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SEQ ID NO: 2907 ACACGTTCTTGTGTCTGGCTCGGCAACAACACCACTTCTCTGGCCAGTCTTC
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SEQ ID NO: 2908 GGTACCGCGGGGAGAAAGGAACACAGTAAACTGAATTGATCCGTTTGAAGTT
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SEQ ID NO: 2913 GGTACACTGACATATAAATCGCAAGTCACACACATACACACCCGGCAGG
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SEQ ID NO: 2914 ACTGAAAGAAAATGTCATGCTGCAATCAGGAGGAGGCTCTCTCTCTCA
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SEQ ID NO: 2916 ACGGGGGGACTCTGCTTCCGTTTCTGGTTTGTCTAGTGTGTTGGGTTTCTCG
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SEQ ID NO: 2917 GCGTGGCGGGCCGAGGTACCGGCCAAGCCTGGTCCCTTCTTGTGTTGGCA
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SEQ ID NO: 2918 GGGACACGTAAATCTGTTCAAGGAATCATTGTTGGCATTGAAATAGGAGA
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SEQ ID NO: 2919 ACATGCTCTGCAATCTGTATTTTCCAATGTTGTTAAACATCAGCAAGCTGGC
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CCTTGGCGGGAC

SEQ ID NO: 2921 GGTACGCGGGGGCTGACTCTCTTTTCGGACTCAGCCCGCTGCACCCAGGTG
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SEQ ID NO: 2923 GGTACATAGTGTGCGAACTCAAATGGCATTTAGATAGATCCAGTGATTTA
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SEQ ID NO: 2929 ACTTTTTTTTTTTTTTTTCTCTGTGTCCAGATTTATGAAAAATATACAGC
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SEQ ID NO: 2930 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGCGGTTCCACACCTGCCCT
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ACTTTAAGGAGGCGCTTGTATGTCAGGCTCAATGTTGATGTTGGGAAAGNGCCGCTNANTCCTCC
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SEQ ID NO: 2931 GGTACCTGCAGGCTCTACACCTACCTCTCTCTGGGCTTCTATTTGACCGC
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AAGTTAT

SEQ ID NO: 2932 ACGGGGGGTTGCCCTGGCGCTACCGGACATCTCTCAGGGTGGCGGCACC
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ACCCG

SEQ ID NO: 2933 ACTTTTITTTTTTTTTTTTTTTTTTGGCTTTTATTTGGCCAAATCCATAGCG
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SEQ ID NO: 2934 TCNAGCGGCCGCCNCGGNGNACGGGGGCCAGNNANAANCCAGCNGGGC
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SEQ ID NO: 2935 GGTACCCCTTAAACCCCTTCTCTTCAACCTTAGCAGCAAGTCCCACTTTCTA
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SEQ ID NO: 2936 GGTACTTTTTTTTTTTTATTATTTATTCAGAAAGTTTCAATCTTTTGAGCAAAAAA
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SEQ ID NO: 2937 GGTACTTCTAGCAAGTGCAACCAAGAAAAACAACGCTGGAATGGGTGGGC
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GCTTCAGAAAAAGAAAGCATTCAACAGAAAGGTGTCAAAATNACAGCTCTCAATGACAGCAGCC
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[illegible]

TTNTCCAAACCNCATACTGGCTAATTATCCTGG

SEQ ID NO: 2944 NOGCNNGNACGCAAAACAAATTGCAATATAATGTGATAAGTTCTTTAAAAGA
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ANGCCAGAAANTTCTGATGACCGGNACTTCGANGCCTCCTAGCCACTGCTGCCCTTNCCTGNA
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SEQ ID NO: 2945 ACGCGGGGCTTGTCAGTGAAACACCCCTGGCTGGGAAGTCAGTTCGTTCTCT
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SEQ ID NO: 2946 GGTACCTACATCAGATCTAACCTTGATCCAGCAATGTGGATTCCCTCTCTA
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SEQ ID NO: 2947 ACCTGCATCAGATTAGTAATCAACCTGTAAATCCAAAGGTCTTTAGAAAAACT
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SEQ ID NO: 2948 NGTACGAAGTCTCAGTTTCACTTTAGTAGAAAGAGCTCTAGAAATGAGGCT
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SEQ ID NO: 2949 GGTACCTGGCCAGCAGACATGTGCTCAGAGCTGAGGCCAGAACAAAA
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GCTTATCTGTCTGTGACCTTGCAGCTATGCAGGGAAGAAAGAAACAGGAGTTTACAGAGCCTAC
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SEQ ID NO: 2950 GGTACATCGTGCATGGCGTCCAGGAAGACCTCCGTGTGGATGGCCGTGGCTG
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SEQ ID NO: 2951 GGGTGGGTGGCGGCGAGGTACCTTAAAGTGTCTCACTAGAAGGCCTCTA
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SEQ ID NO: 2952 ACAGCATCGTAGGGTTCCTTAAACTGGCCTGTTTGTGTTTTTATGTTGT
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SEQ ID NO: 2953 GGTACCCAGTAAAAACCAGATGACCCATTGCCAGGAGCATCAAAAGTTGAC
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SEQ ID NO: 2954 GTACCGGGGAGTTCTCTGGGGGACTAACTGCAACGGGAGAGACTCAAGATG
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TTCAACAGATTTTGGGCAOCAAAGAAATACTTNGACACTGTAAAGAACTGGTNTAAAAGTCC
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CGTNNGAAGGTTTGGGNNAGCNANCTTGGAAATGTTGNAATTNNGNANGCTTTAACATNTTCC
NCANTAA

SEQ ID NO: 2955 ACGCGGGGACCCGACCTTTTTCAGTCTCAGGACGGCGCTTTGGAGCC
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CNANAGCTATTTCCGCAACCAATGAGAAATGACCGGGCAAGCATGGNGATCAGCAGGNAGGTT
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TTTGTAAATGCANGGTGAANACATTNNNTGAAGCTTTGCTGATNGGNATGGAAANCCANCC
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SEQ ID NO: 2956 ACCACCGCAAAGCCCTGTGAGCGTCTACAGACAGCTCACCATTTTGTCTGT
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SEQ ID NO: 2962 ACTTTAATAGTTTTCCTAGAAAAAAATTCACGACACTTAACATTTCACAA
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SEQ ID NO: 2969 ACGCGGGGAGCGGATAGAGGACACGACCAAGATGGCGGCGGTGTCTGGCTT
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NTGCTTTT

SEQ ID NO: 2970 ACAATGACTCATIATTTCTTTATAAAAACTGTGTGTGAAAAATCAACAACC
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SEQ ID NO: 2971 ACTTTNTTTTTTTTTTTTTTTTTTTTATATCACAACATGGTTTATTGTGAAT
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SEQ ID NO: 2972 ACTTTTTTTTTTTTTTTTGAGCAGTAAGGTATTATTTAAGATCTTAAGCC
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SEQ ID NO: 2973 ACAAAGCAGACTGCCNGCAAATCGACCGGTGTAAAGCACCCAGNAAGCAA
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AGGCTGTGATCTGGCGCTCCTTGAAATAGACGTTATNATAAGTCCANTGAATCTNCTGANTCG
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SEQ ID NO: 2974 ACTTTTTTTTTTTTTTTTTTTTGGNGCTTAAAAATATATTTAAATTTTTTAACA
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TCTANATGGAAATTTAAGCCGCTCTNTCCCTAAAAAGTTAAGGGCCNGGTTGCTTCGG

SEQ ID NO: 2976 ACTTGATTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGATTNCAACAGGATC
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SEQ ID NO: 2977 ACAGCTATTGGAATCAGATGCAAGATGGTGTCTTTGGGTAAGAAAAAT
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SEQ ID NO: 2978 ACCAACTGCCAGCATTTCTGTGGAGGGTAATCCTGCTCTTAATCGTGTGAGAT
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ATAAT

SEQ ID NO: 2979 ACAGGCTGACAGAGAAGATTCCGAGAGTAAATCATCTTCCAAATCCAGAGG
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SEQ ID NO: 2980 ACAGCTATTGGAATCAGATGCAAGATGGTGTCTTTGGGTAAGAAAAAT
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SEQ ID NO: 2981 ACAGTTTCAGGGCAAGAAAAAGAAATTTGCTAGTGATGTAACATGATGAA
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GCAATGAGATTCTTTGAATGATTTGTTCTGTTGTGTTATTTCAGATGATCAAAATACAAAGG
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SEQ ID NO: 2982 ACCCGGGTCTTGTATCCAGGGCCCTGGAGACAAAGGGGACGTGTTGACGA
AGAAGCAGACGAGTGGCTCTGGCCAGCGGGAATGGCAGAGTAACATGCAAGCAGAGTCAAA
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SEQ ID NO: 2987

ACGAGAAATACGTGCTGCTGAGCTGCGAATGCTTGTGTAAGATCTTTGAAATG
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AAAAAAAAAAAAAAAAANG

SEQ ID NO: 2988 ACTGTTTCTCAGCAGAGGAGAAAACTCAACCTAGTTATGAGACCAACCAC
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AGGACCTGT

SEQ ID NO: 2989 ACTACCAAGCCTTTAAGTGACATTGATTATAAAGTTGGTCACAATTCAGTGC
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SEQ ID NO: 2990 ACCAAGAAAAATAAGAGAGGCTGCAGAAATGCTAAACTTTTGGCCAAAG
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GATCAGACTCTGAAAAA

SEQ ID NO: 2991 ACATCAATAACCGGGGATTTTCTTTTGTCTATACTATTTTCACAAACACGG
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SEQ ID NO: 2992 ACTTTTTTTTTTTTTTTTTTTTNGAAGGATTTGTGAACTCTTCACATCATG
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SEQ ID NO: 2993 ACATCAGTGAATTTTAAATGCTAAAAATTTATGATAAAGAACTGAAATC
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SEQ ID NO: 2999 ACCTTTT TTTT TTTT TTTT TTTTGGGAANAATCANAATTTATTTCTACTATGTG
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SEQ ID NO: 3000 ACTTTTTTTTTTTTTTTTTTTTTTTTANATGCTAANTTNANTNTTTATTNN
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SEQ ID NO: 3001 ACTACAGCAGTCAAAGAGATCTCCACTAGAGATCAGAAAAGACCACTAT
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SEQ ID NO: 3002 ACTGGCATTCTCCAGGACATCCCCCAAGGTGTCAAAATTTAGCCAAAGCAA
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SEQ ID NO: 3003 ACTTTTTTTTTTTTTTTTTTTTTTINGGTTTTATAGATTTATTTCAAAAGGTA
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SEQ ID NO: 3004 ACTGAATGGAAGATGAGCATTCTAGTTCTACACTTCTTTTTTCCCCCTCAT
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CGAAAGCGC

SEQ ID NO: 3005 ACAATCAATAAGTCTTAAATCTCTTCCATGGATTTCGCCCATCTCCCACTT
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SEQ ID NO: 3006 ACAGCTCATCAGGTTGCCAGGATGGCATCAGTGGCAAAACACATTCCCTGA
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SEQ ID NO: 3007 ACGGGGGGGGCTACCTCCCGCCCGGGGCTCTCGGTCTGTCTGTGTTA
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SEQ ID NO: 3008 ACATGGCAATTAGAAGTTGTATGGCAAAAGAAAAACCAAGCTGGCTGCCA
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SEQ ID NO: 3009 ACGGGGGAGTCCAGTCCCAAGATGGGGCCCAACATGAAGAAAGCGGCTGCA
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SEQ ID NO: 3010 ACATGGAGTGTTCAGCAAAAGACCAAAAGATGGAGTGAGAGAGGTTTGTAAAT
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SEQ ID NO: 3011 ACGCGGGTGAACAACTGCTGAGCCCTGTGCTCCCCAGATCAGTGCCCGGC
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GTCACT

SEQ ID NO: 3012 ACCATTATTTGTCTGCCGCTTTAAAAAATACCATGGCTATGCCACTTGA
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CCTTGAACCTTTGGGCTCAAGTATTCTCCCTCTCACTCCCGAGTACGTGGAAACGAACTATAGTT
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SEQ ID NO: 3013 ACCACAGTATCTTCTCTCTCTGCGGCTCTCTGTTTTGTCTTGCTTATGCTTC
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SEQ ID NO: 3014 ACGCGGGGCTGTGCTCAGTGAACACCCCTCGGCTGGGAAGTCAAGTTCTCTCT
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SEQ ID NO: 3015 ACAGGTTGTGTCTGCCAGTTCACTCCACAGCTCAGAGTATCACCTTGTCTCTCA
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SEQ ID NO: 3018 ACTACTGCTGCAAGAAGGACCTGTGTAACCTTAAAGCAAGCTTGAAATGG
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SEQ ID NO: 3019 ACGGGAGCTGTGGACAGGAAAAAGGAAACACTTTTAATATGGCAGATCATGT
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SEQ ID NO: 3022 ACTGTTTATTAACCAACAGCTTAGAAAAAATATCATGGTAGACACCTTAGTT
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SEQ ID NO: 3023 ACTGTTTGTGCTGTGTGTGATGTTGCTTATTAAATACATTCOCOTCAGGGACA
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SEQ ID NO: 3029 ACTTGATTGGTCATTTGAAAACTGCAACAGTGAACCTTTGTCATCTCAAGAA
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SEQ ID NO: 3030 ACCATTCTGAACGATGTTAAAGCAAGTGTGGTTATTTATGACATGAACCATG
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SEQ ID NO: 3031 ACAGAGAGCATAGAATAAAAGCAAGATGTGAATGTCTCTACCAGACAGAG
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SEQ ID NO: 3032 ACTTTGGATTAGAGCCCTCATAACATCTTTGAAAAAATCTTTTGTCTCT
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SEQ ID NO: 3033 ACGCGGCCACAGAGAAAGGAGGAAAGACCTAAATGACTCCCTAACACCAAAATTAAGAACTAGAGAGCAAGAGCAAAATTCAAAACCTAGCAGAAAGCAAGAAATAACTAAGATCAGAGCAGAACTGAAAGGATAGAGACACAAAAAACCTTCAAAAAATCAATGAATCCAGAGCTGCTTTTTGAAAAGATCAAAAAATAGATAGATTGCTAGCAAGACTANTAAAGAAAAAAGATGANTCAAAGAGACACATAAAAAATGATAAAGGGGATATCACCACCTGNTCCACAGAAATACAAACTAOCATCAGAGAACTATAAACTCTACACAANTAACCTAGAACTCTAGAAGAAATGGATAAATCCCTGGACATGTACGCGGGGTATGGTTAAACAGCCAAATTTAGGGGAGGGAGGGATTTAACTTTATCCAGCNAAGCATGGGTGTGTCGGGCTGTTANAAGAAATGTAAAAAGGCCGTGNAAGCTTGGGGAGAAAGCATCAGGGAAACTTAGGCTGNTTANAATTTGTAAGCTACAAATTCATTGNTGTCATC

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SEQ ID NO: 3035 CGCGCGAGGTACTGTTGTGTAAATTGAACCCAGTGACCACAGATGAGGATCTGGAAATAATATCTCTAGATTGGGCCAATAAGAAAGTTGTGAAGTTATCCGAGACTGGAAGACAGGAGAGTCCCTCTGTTAGCTTTTATTGAAATTTGAAAAGGAAAGAAATTTGAGAAAGCAATTTCAAAAATGGACAATGTGCTTATAGATGACAGAAATACATGTGGAATTTAGCCAGTCTGGTGC

SEQ ID NO: 3036 ACATAGTGTGCGGAACCTCAATCGGCATTAGATAGATCCAGTGGTTTAAACGGCACGTTTTTGCTTATAAAAAAGTGCAAAAAAGATGTGGTTTACAAGTTAAAGCTACAGAAATCCTTTTGCTGTAAATGCAACAGTTTAAAGCCTCTGGACAGAGCAGTATTCGTTTAAACCTTGT

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SEQ ID NO: 3038 CGCGGCGAGGTACACCAATCAAACGTAGATTGGTCTTTTCACATAGTCTCATTTTTTGGAGACTTTGTCATCTCTTTTCACTTTTCTCTAATCTGTGCTCATGCTTTATTCATTAATTCATCTCTGATATCTTTCTTCAGCTTTATCAATTCAGTACTGATCTGTGATGCTCTCATGCTGCTTTTTCAGTTCCATCAGGTCAATTAATGTTTCTCTAACTGGTTATCTAGTAGCAATCCCCCAACCTTTTCAAGGTCTCTAGCTTCTGTATNGGTAGAGAAC

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SEQ ID NO: 3039 GTTCGGCGGAGGTACAAGTGAATATCTTAACAGACTTGCCGCAGAAATG
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SEQ ID NO: 3040 ACCTTGTGGAGATGCCACCTCAGAAAGTTCACTGTGACGAAAAAGGTTT
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SEQ ID NO: 3041 CGCGCGAGGTACTTTTTTTTTTTTTTTTTTTTTCOGATAGNAAAAATATCT
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SEQ ID NO: 3043 ACAAGGCGATATTTAACGGATTCTCAGTTACACTTAAAGAGGATGCTGTCG
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SEQ ID NO: 3044 CGCGGCGAGGTACGCTTCTCTGTGCAGACCTGCCGGGAAGAGCACAAGAG
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SEQ ID NO: 3046 ACAATTGTTATTTGCTTCTCTTCTCTTCTTCAGACAAACACCAATAAAAT
GCAAGTGAAAAGAGATGAACCAAGACTAGAGGCTGACTTAGAAATTTATGCTGACTCGATCTAAAA
AAAAATTATGTTGTTAATGTTAATCTATCTAAAAATAGAGCAATTTGGGAAATGCTTTTCAAAGAGGG
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TTTTCAAAAACCCACAATGCGAGCTTANTTTTCTTTATTTATTTGNGGCAATGAAGACTNTCCCAAT
TNTCCATAAAAACTCTCCCTCATCTGCTCAATTATGNGACAAAAAAGCTNTTATGNTGCCCAACAGAA
NCCCAANTTTCTGATTTTAAACANGGCTNGGTATGGTTAATGAACATTGGTATNGTNGNCAA
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SEQ ID NO: 3047 ACTTGAGCTGTGAGGTCAATGGAATCCGACACCTGTCTCATCTGGAACAA
GGTAAAAAGGGGTCACTATGGAGTTCAAAGGACAGAACTCTGCTGGTGACGGGGACAACTGG
CCATTGAGACCCGGGTGGCCAGAAAAAGCATGAAGTAACTGGCTGGGTGCTGTTATCTCTCTA
AGTAAGGAAGATGCTGGAGAATATGAGTCCATGCAATCCCAATGCCAAGGACAGGCTTCAGCATC
AGCAAAAAATTACAGTGGTTGATGCTTACATGAATAACCAATTGAAAAAGGTGAAGGTGCCGAG
CTATAAAGCTCCAGAAATATTATGCTGCAATGTTAAAAAGTANTCATGGATAACTACATTACCTG
TTCTTNTAATAAGTTCTTTTATCCAAATCCACTACACTTATTTTATTTCACTGGTTTACACAGAG
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SEQ ID NO: 3048 ACTTTTTTTTTTTTTTTTTTTTGGTNATATTTTTATTTTCANAAAAACAGAGT
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TCTGG

SEQ ID NO: 3049 ACTTTTTTTTTTTTTTTTTTTTAACTNAAAAAGTGACATTATTTCAA
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TTTTCTGTCCACCATGTTAATAGCCACAACCTTTACGGCCAAACCGTCACNTATACCGATTTTGAGG
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SEQ ID NO: 3050 ACTTTTCTTTTTTTTTTTTTTTTTTGGACAGAGTTTGCTCTGTCAOCC
AGGCTGGAGTGCACTGGCATGATCTGGCTTACTGCACTTCTACTTCTGAGTTTAAAGCAATCT
TGTGCTCAGCTCCANAGTAGCTGGGATAACAGGCATGCACCAACCGCCGACTAATTTTGTGA
TTTTATGATANAGATGGGGTTTCTCCATGTTGGCCAGTGGTCTCAAAATCTGCTGAGTGTATC
CTCCACCTAGGCTTCCAAAGT

SEQ ID NO: 3051 CCGGGCAGGTACCGGGGAAATTCAGAAAGGAAATGTGCCAGCCTGC
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CAGGCCACTCTCTGGGCTCTGCTGTTCATGCACTCTGTGTGGCTCACTGACTGATGGAAGCA
CTCGAGTCTACTACTGGGCATCCGGGATGTGAGTGGAACTATGCTCCAAAGGAAAGAAATGTC
ATCAAGAACCAACCTCTGGAAGTGAATGAGTCTCCAGCTTCTTAAAGTCTGCAAGAACCG
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GTGGCCAGCTCTGCTGTTGGGCTTCTGGGGCAAGTGTGCAAGGTGAAAGTGGGGATGTCTTCT
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SEQ ID NO: 3052 ACCTTGCTCACTAGAGCAGCTAAAGGAGGAAGAGCTGAACCCCTGATTTCAT
AGAAACAGTTGCAGAAATTTGTTCTCATCTCAGCCATTCCAATGTCAAGATCTTTCAGGTGG
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GGATCTACCTGCAATGGAAGCAGTCTGCTGGCTTGGCCAGATAGAGAACTCAGCCGCAAGTGG
AAAAAGCTATTGCCACTATGAACAGCAGATGGGCCAGAAAGGTGAGCTGCCACGGAAACCTCT

SEQ ID NO: 3059 ACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTCCAGGAG
CTCCAAACTGGCACCACCCCAAGTGCTCATGGCTGACTTTATCTCCGTGTTCATTTGGCACA
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CACAATCTGCTTAGCCGAGTGCAGCCTCAGCATACTTCTGCTGCTTTCAGGACCAAGTCCAA
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SEQ ID NO: 3060 ACATGGAGTGTTCAGCAAGACCAAGATGGAGTGAGAGAGGTTTTGAAAT
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TNTTTANAAGCCAACTATGANTATTACGATGTNCACCTGCTGGGCCACAGGGTCTTTTGACA
CTGCTNTAACANCCCTCCTCTGNCCTCCCTGACACACCCNGGCGCTAATTCNAGGAATTTCTAA
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SEQ ID NO: 3061 ACCTCTGCATGATATCTTACGTGGGGCAAAATGATTCATGTGTGATGAGAT
GGAGCGCTCTTACATGATGCACTTTGTGTAGTGAAGAGAGTTTTGGAGTCAAAATCTGTGTTC
CGTGGGGGTGCTGTAGAAAGCAGCCCTTCCATATACCTTGAAAACATGCAACCCAGCATGGGT
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CTGCAATCANCAATTTTCUNATTGNGATTTTAAATCTNTCAGAAAG

SEQ ID NO: 3062 ACOCGGGGGAGGTGAGGTTGTTACCCGNAATTCGAGAGGTGGGCTTTTGT
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TNAAGTCAATCCACAGAGTGTGANTGNTNACATCATAGAAATGCTGATTNTCAAGAAACAG
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SEQ ID NO: 3063 ACACCTGTAGTCTTCTGACCTGTATGTATCTTGAGGTGGGTCCGAGGTTGC
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CTGGTCAGATGGGCTTTGAACTCTGTGTGAAGAAATGCACTCCTTGCCACAGTTACAGAGATGCACA
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SEQ ID NO: 3064 ACTTTTITTTTTTTTTTTTTTTTTTGGCTGCTTAAATGTTTATTAAGTATGAA
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GCCTGCAAAATGAGGCCACGCAATNCCCTGTGCTTGTGGACTGGATTGGAGACCACTGGGTGTNA
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SEQ ID NO: 3065 TCGCGCGAGGTACTTGGCTTTTGTGCACTCTATGACATGGAATATTG
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AANTNTCAAGCAGAGCANNTTTGNAAGGACTTTTNTCTGGAGTATTATAGGTGTTTNAATANA
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GTCAGAAAAATTTACTNATTG

SEQ ID NO: 3066 ACTGCGCCTTCCTGCACTGAAGCAACCCCTGCAGGGCTCAGTGACCAAGGAAG
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AGCTCCTGCATCCAAATGGATGCTGCCAGANATGCCAGCATATCAAAATCGTGCAATTGAGGCCAT
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CTCCCANCTCTTGTGCTTTTGGGGAAANAATTAGAACTTGGGGCAACTTNAACAGAAAT
GGACGGATTAAATGATGNNTTTNTTAACTGGANNTTTATGGGGATCTTTTNGTTNACTACTC
TAGGTNGTGGCA

SEQ ID NO: 3067 ACCAACCTATGCAGCCAAGCAACCTCAGCAGTTCCCATCAAGGCCAAGCTCCA
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CAAAAAACAGACTCTACTAACACAGAAAAACAGAACTGAGTGTGAANNNTGGTGAATACAA
GGGAAATGCAGTAAAGCCAAGGAATTTACATANCATTCCGTTTCAATTGAAATAAGTCTTATTC
AGNNTCNGGGAGGTAAAGCAATAATGATTTTGGACNTGTATTGNANTGATCTAAATACTGG
TTGGNGTAAAGAAATTTGGCATTAGGNGTTAAGTGTATTGGATTTTTCTAAANTTANTANGAGT
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SEQ ID NO: 3068 CGCGGCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGTGTTCAAGTTA
ATACAAACTACAAAAAGATTAAATGGTTGCTCTACTAATACATACATACAAACCAAGTGCCTGCCA
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ACTTNTGTTGNANAAANATNTTGTGTTTGAATNAGGCTTGAATGATNANTGNANGT
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NAATCCAAANGGCCACAGGNGGTATTTNANGATTGCGGAAAAATCCCTTTATTTAAANAA
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SEQ ID NO: 3069 ACAGCAATGAAACACCAAGGGACGTTTCTCCAAATGTGTATAAGCTTG
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GCAAGCCATGCTCATTGAGTTTATAAATTTTTTCAGAAAAAANACTTCATCAAGAAGCTTTGTG
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GTCCAATAGCTTCCATGGCATAATCAACTTGTATANCNGACCTTTGGANAAAAATAGNGGTCC
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CGGACTNGCGGAC

SEQ ID NO: 3070 ACCTCTGTTCTGGATCTGGGCACTCAGCACTCTTTTATGATCTTTGTGTGGCTC
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ATTCT

SEQ ID NO: 3071 GTCCGCGGCGAGGTACAGTTCAGTTATTTACACTCAGATATTACACCTGT
GTAATACGTAGAACTAGATCACTCACTGAAATCAGAAAGCATTCACTCAGTCTGATAATGATCA
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AATCTGGGAAATCCGTCTAAATGTTTGTGACACNCTGGCACTTTGTAAGCCACAGAGAAAT
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G

SEQ ID NO: 3072 ACTTCTTTTTTTTTCTTTTTTAAATGGCAGCTAAAGATATACAGATTACTG
TTAAATTCAGTCTCTTTTTTTTAAAGATATTTCTTGAGTTATTAGAACATGGTAAGCTGGTA

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GGAAATGTATGTCTGGAGTATTTCAAACTTTACATTGAAACATAATTCCTTGGAACAAACCATAA
CCTGAGGAGGTTTATCAACTGGAAATGCTTATATTAGTTGGTTTCACTGNCCTGGCCGGACCAAC
TAAGGCN

SEQ ID NO: 3073 ACAACACCGAGGTGGGAGACAAGTGATCTGGCTGAAGTGAACGGGCCGCC
TTCTGCTCCAGCTGCATCAGATGATGGCCAAGCTGCATCAGCCGACTCTCTGGGACGCATATA
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AAGCAAATCCATCCTGTAGTATAGCTAATGGAGTTGGGGAGAGCAAGCTTCCATTCTGGATGTTTGA
ACCTTTAGCTTTGTGGAAATGGGCCACCAATCTCACTGGAAACAGTGGTCTGTCTGTGAAAG
GCCAGCTCTCGGAGCCCTGTGGTTTCAGCGCTGCGCTCTGTGTCTTCANGTTGTGCACATTG
TTTTTTCTGACTTCANAAATAAAATGTTTCCATGGGAAAAAANAATAAAAAATAAAN
TCTNGGCGGGANCA

SEQ ID NO: 3074 ACAACCTTGTCAACATCTCAGGGGAGAGCACTCACTGATGATGCCAA
TGTGAGAACACACAGAGAAAGAAATGCTGTAAAGTCTGGTCACTGGAAAAACCAATTCACAAA
AGACAAACATTCAAGCCCTTGGAGGCTCACTCAAGAGATGAACCTTAGGGCAAGAGCTCTCC
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TNNTGATCTCTGACAAACAGAAATGNAATGTTTCTCTGTCTCAAAAGTAAAAACCGTGTAAANAAC
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CGTTATAGGTCC

SEQ ID NO: 3075 ACAGCAGCAGTTGTATCTTTATTAGCTTGGTAGATCAATTTCTCTGCTCTT
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GTTTATTGGAANAGGGNATGGTGGAAAAANNTTCTTTCTNNAGGGATTAAAGGNACTTAAAC
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SEQ ID NO: 3076 ACTTGGTGAATATGAGGATATATTACTAACTTTTCACTACCAAAAGTTC
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GGGATTCGACATCAATCCCTATAATGATCTGCCGCACTGGAGCGTGCTCTCAGGATCCAAATGTTG
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SEQ ID NO: 3077 ACCCTTAACTGGCAGGACATTTTGAATACAAATTTGCACATAAAGAAAT
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CCAAGCTTATGAATCTCAACCAACTTGAATTTCTGT

SEQ ID NO: 3078 ACGCGGGAGCAGCAGGAGGAGGAGCAGCAGCATCTCGGGACCAAGACT
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ACCCATCTCAGAGCAGAACTCTCTAGCCCCACAGAAATGCTGTGCTCTGAGGAAAACCAATGAC
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TGATGGCCGANTGATAGTGNGGTTATGGACTGAGGNCAAAATCTAANAAGTTCOCANACCTGA
CATCCAGCCCTCGGCCGGAAC

SEQ ID NO: 3079 ACCACGCTGGTCTAATGCANAAATGGAGATTGCTACAAAGGACCCCTTTAAAC
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SEQ ID NO: 3080 ACAAGTGCCAGAGAACACATTTATGATTTACGATCCAGGAAAAATCCACT
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ACTTCAAGGGCTACANNAAGTC

SEQ ID NO: 3081 AATAAAGAACTCTATCAGTGAGACTTCTCATTTTATAGCAAAATACATTTTG
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AATATTAATTTGAAAAAATCAAAATGTGAAGCAGAAACTGCTATACAGATATATGNATAATATT
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GGGAANGGCCATATACAGAGCACTATAACATGCTTTGGACAGTAAAAAAGATTTATCTTCTAC
ACTCTTGGATTTTCCAATCATATCTTCTCAAGGCATGTTCTTTTGGCCCATTTGGGGCACTAAAC
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SEQ ID NO: 3082 ACAAGATGTTGTTACTATGCTTTGGACAGGTTTACACAGAAGCCAAAGCGTCC
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SEQ ID NO: 3083 CCGGGGTATTNATTCGCCCCNACCCGGANTTGGGTGGGGTCTTGTGTTGT
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NCCCTCAAAA

SEQ ID NO: 3084 CACITTTGTACAGTTCATATATGAATAGTTAGCAGAGGGGAAAACTCCTCG
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GGGGGCTTAATAATGCATAAATTTATANAATAAATTTAGGNTTTNCANAATTTTATGGGG
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SEQ ID NO: 3085 ACTCACACAAGTTGTTCAAAGATGATATTCTGTGACAGAGAGGCCATGG
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GTAAACCTTTCTTAGTATGTTCAATACATCAATTAATTTTAAAGTTATCCTGAAGAAAGGAAAG
GCCTTAATTTATATAGTCAAAACAAATTTATAAGATTACTGTTTGAAGTAAATAACGAGTGAAAT
ATTTTCAAAATGTGATAAAATAGCACAAGTGGCTGGTGAATAAATTTGAAANTATGGTTAACTCA
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SEQ ID NO: 3086 ACATGTTTGAAAAAGAGTATGATACCTGAAAAAGTCTAAACACACTGATTAG
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SEQ ID NO: 3087 ACTTGCCCTCTCCAGAAAAAGCGGACTTGCTGCTAAGGGTGAAGGACCA
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SEQ ID NO: 3088 ACAGATGTCAAGTGAAGAGAGTCTTACTGACACTCAAGTTGTTTCTTTACGG
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SEQ ID NO: 3089 ACTTNTTTTTTTTTTTTTTTTTTGGGATTAGTGGGCTATTTCTGCTAGGGG
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CAATCCAAAAAANA

SEQ ID NO: 3090 ACTTTTTTTTTTTTGGGTTTGTGTGANACAGNCTGCTCTGTACCAAGG
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SEQ ID NO: 3091 ACTGTTGGCTTTTCGGAGCAGAGTNGGAGAACTTGTGAACCAAGGCTGCNT
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SEQ ID NO: 3092 AC0CGGGATTTAATCATTATTTTGCCTGTCATAAGAAAACTCTTAGCTGAA
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SEQ ID NO: 3093 ACTGGATTCTGTATCTTCTGATCATCAAGAATGGAAACAGACTGTAAATCCC
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SEQ ID NO: 3094 ACTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTT
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GCTGATGGT

SEQ ID NO: 3095 ACTCTNNANGTGACANTNNAATGATCANTGAGNGGTGTNATANATGATGAA
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AGCGTAAATCCAAAAAGTAGGT

SEQ ID NO: 3096 ACAGAAATATCTGGTGAGGGGCCCGCATGGTCCGGGATGTGTCCGCCCTG
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SEQ ID NO: 3097 ACCACCAATCAATGCCAGGAAGAGAGTAAATGCACCTTAGACTCATTTTGGC
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ATCTTGTGACTGAAATGCCACTGAAGCTACAGAAATTTGTGCACTTGGACCCCTGAGCTGCTTTT
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CTCAAGAACAAAGGAAGC

SEQ ID NO: 3098 ACCTTAACAGCTCTGAAAGCTTCTTCGATTTTGAGAGTCTTCTGTATTCCA
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SEQ ID NO: 3099 ACGCGGGTAGCATTGAATCTCTAAATACAAAGATTGCTTTTGAACAGCAGAG
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SEQ ID NO: 3100 ACACAGATATTTACATTTATTATCCCTTATATATACGTTTATGTATTTNTGA
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TTCTGGGTT

SEQ ID NO: 3101 GTACCGCTGAGGGAAGGAACGGGACTCCGACCTCCAAGATGCAAGGAT
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SEQ ID NO: 3102 ACGCGGGACAGACGAGATCTCGATCGAAGGCGAGATGGCGGACGTGCTAG
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GGAACTTCTGCTGTTTATATTAACT

SEQ ID NO: 3103 ACACAATGGGTTTGGTTCTTCAAAAATGTCGCCCTTATTGGAATCATGGTTG
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ATGT

SEQ ID NO: 3104 ACAGACATGTTGCAAACTGACTTTTAAAACAATTTTTAAAAATATACAAAC
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ACTTGGAGAAATTTG

SEQ ID NO: 3105 ACANCCAGTGTGGGATGTGATGANGGCCCTGGGCCAGAACCTCAACCGC
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SEQ ID NO: 3106 ACGCGGGAGTCAAGCCAGTCAGGACACAGCATGGACATGAGGGTCCCCG
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SEQ ID NO: 3107 ACACCTTCCAGTTTCGAGCTTCTTCTCCAGTTGAAGAGCTGCTTACTATGA
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[illegible]

SEQ ID NO: 3119 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGTAACTTAATGGATCATCAATTTGT
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TGCCCGGGCCCTCGAAAAGGGCG

SEQ ID NO: 3120 ACCTTTGATCTCAAAATACTTTGTGAATTGGCCCCGGATTGATTGGATGGGT
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SEQ ID NO: 3121 ACGCCGGGGGGCAGGGGAGCTTGAGGAAACCGCAGATAAGTTTCTCT
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SEQ ID NO: 3122 ACAAAACCGGATCTGTGTCAGAAACACATGTTGAGACTCTCCATCTCTC
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SEQ ID NO: 3123 ACATATTTTGGTTGAAGACACCGAGCTGAAGTAAACAGCTGTGCATCCAAT
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NGANGGGTGGGGGAGANACNCTTGGG

SEQ ID NO: 3124 ACCTATTCTTTGCACTCAGGAATTTGTGACATGCTCACTATCTGTCAGC
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CAAAACNCCCTTTGANNNGNTNAAAAAAGAAATNANAOCANATANGNGANGGNCNAAATATC
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[illegible][illegible][illegible][illegible][illegible]

SEQ ID NO: 3130 ACACGTTCTGTTGTGTCGCTGGGACACCAACCACTCTGGCCGAGCTCTTC
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TCTGACATCAATGGGANAATCTTTGACCTGAGNCTCAAGGTTATGGCAATATCTGATTTTCTG
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ATCTCCATCAAGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGAT
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TCCAAGACCCANCANCTNAAAANCCACCCCTAAAGCTTT

SEQ ID NO: 3131 ACTGGTTCTTAAACAGCCCATAAAAACCCATTGGGCTGAAGCTTATATCTCAG
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SEQ ID NO: 3132 ACTTTTTTTTTTTTTTTTTTTTTTTTNNAGGCTGAOCATTTATGGGACTT
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SEQ ID NO: 3133 ACTTTTTTTTTTTTTTTTTTTTGGGAATGCAACAACCTTATGAAAGGAAAGTG
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SEQ ID NO: 3134 ACCAAGTCCCTTCAACCATCCTGGGAGAAAGATGGAGGACAGAGGAAAGG
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SEQ ID NO: 3135 ACGGGGGGACCGACCTTCAGCAGGGCTGTGGCTACCATGTTCTCTGGCGG
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AGTCTGACNGCATGAT

SEQ ID NO: 3136 ACCCATTCACCTAAGAAGCAGAACTTTTTCACAGCATTTGTAATAGGAATGG
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ACACANTTCAACCTCACCACAAACAAAAAGTAGTGGAGGTGCCACCAACACAACCCCTTTTNNNT
ANAAAGAAAGACTTGTAAACCNCAANAGGGTGTAGACCTGCCCAACACTGGATTGTCTCTGAAC
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SEQ ID NO: 3137 AOCGGCCAAAGCTGTGCTCCCTCTTGTGGGCACTGTGTATGGCGGAGAAA
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GCCAGCTGGGATGGCTTGGCTACCCAGATTTCTGGCTTCCCTCCTCCTCATGTCTGACCTAAACTTA
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SEQ ID NO: 3138 ACTGTGTAGTGTATCAGTGTAAAAATGGAAGATCATTATGAAGAAACAAT
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CTAAGGGCGAA

SEQ ID NO: 3139 CCCCAGGGCTCTGCCAGGGGTTCTCGTGGGAANTGANATCTGCTTTTAA
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TCCTTTGGGCTG

SEQ ID NO: 3140 ACAAGTCCAAATCTTACTTTATGGATGTAAAAATGCCAGGTGCTACAAGA
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SEQ ID NO: 3141 ACGCGGTGGGGCAGAGTTTTCATGGAGGCATGCAGAGGTTAGGCTTTT
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SEQ ID NO: 3142 ACOCGGGGGTCAACCTGAAGTTTATATTCTTATCCTACAGGCTTGGGAATAA
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SEQ ID NO: 3143 ACACGGGTGGCATTAAAGGGTGAAGATGTCCCTTACGGAGCAGACCGTG
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SEQ ID NO: 3144 ACCTCTTTTTCATTAAGAATCTGCCTGGAAGTTTAGGTCAAAGAGCTCCT
TGGAGCAAAATACAGTGGTGTCTCATCCCAATATTCTCCAGGGCTTCTTCACTCTTCCAGGAT
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GCCACAGAAATGCAGAAATGCCCTTGAATTGGCCAGAGAAAGACATTCAATGTCCTCCCTGGAATGCC
TTTCAAAGAGT

SEQ ID NO: 3145 ACCCTGCTGTTTGGCTTTGGTAATGTGATGTGTGATTTCTCCCTACCCCA
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CGGCTCTGGTGGGTGAGCATGGGGCAGTTGAGCTGGTCTTGAAGAGTCCGGAGTGACAAAGCT
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CTGTAAACAGAAATGGTGGAGTCCAAAGAAACAGCCTGTCTGTGTGAATGGGACTTCTTTGGTG
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GCCGCGACACCTT

SEQ ID NO: 3146 ACAGAAATGGCACAGGGAATGCATATGAAGAGGAAGCCAAACAGAGTCATG
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SEQ ID NO: 3147 ACAAATCTAGGCAATAAACCGTTCACCTGGGATCAGTTCAGATGAGACAGTA
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GAAAAAGAAAGCTNCTTAGCTATTCAACTATTGCCCTTAATTTTAAACATAAAGATTTGGTT
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TTAACCCAC

SEQ ID NO: 3148 ACGAGAGGGTCAACAGCGTGGATGTTGGCATTGTGGAAAAAGGAAACC
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SEQ ID NO: 3155 ACATAAAGTTTATTAAATTTCTGATTCTGTCATAGCTTTTATGGCAGGA
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SEQ ID NO: 3156 ACCAAAGGGCAAACCCCACTATGGCTTGTGATGGCTTACAAAGAAAACT
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SEQ ID NO: 3157 ACTGTGTGTGAACCAACCACTGATACTTTGCAGAAATGCACATTAGAATA
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SEQ ID NO: 3158 ACGCGGGTATGCTATAAATCAATAACAGAAAGACACTGGAAAAACCCAA
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SEQ ID NO: 3159 ACGGGGGCTCCTCTCTCTCTCTCCGCCATGGTGTGTCTTGAACCTGCTG
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SEQ ID NO: 3160 ACAAGGAGCAACTGCAATACTCAAGGTTAAAAACATTAGAAAAACATTGTG
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SEQ ID NO: 3161 ACTTGGCCCTTCCCGAGAAAGGGGACTTGTGTGAAGGTGAAAGGACCA
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SEQ ID NO: 3167 ACGCGGGGACTTTGTTCATACAAACTGGCAGAGAAATTTGTGAAACAAG
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SEQ ID NO: 3168 GGTACGCGGGCTGAACGGGAAGCTCACTGGCATGGGCTTCCGTGTCGCCAC
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GCACAGAGGGAAGAGAGAGCCCTCACTGCTGGGGAGTCCCTGCCACATCACTGCTCCGCCACCA
ACTGAATCTCCCTTCTNCACTTGGCATGTTAGACCCCTTNAAGAAAGGGGAGGGGCTANGGAGCC
CANCTGTTATTANCTTGNCCCGNGNGCTCTAAAGGGGGAATTCACAC

SEQ ID NO: 3169 ACGCGGGGATCACAGTTTGAAGGCACAGTGGACCAAGTGGAAAGCGATGCA
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SEQ ID NO: 3170 GGTACATCATGGCTGGACTTGGTCAAGCTCTTGGCAOCAAATGCTCGCAT
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SEQ ID NO: 3171 ACACCTTGAAACCAAAATTTCTAAACTTGTTTCTTAAAAAATAGTTGTGTA
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SEQ ID NO: 3172 ACGCGGGCTTTTCTGCTTTTCCCGGTGCTGCTGCTGTGAGTGTCTAG
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SEQ ID NO: 3173 ACTGAAACCATAGCTAGCCACAGAACTTAAAAAATACCTTTCCAAATGC
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SEQ ID NO: 3179 GGTACA GCTTTTCATTAATAAGAATACTTACACATACATTTTCAGATATTTCTACCTTCTGTATGTGTGTGGAAATGTATGTAGGTAGCCACTGAAAGAATTTGGGCCCTTGGGAGGATGGCAGTGGGAAGTCCATGAAGTAAAGAGCAJTCTTTAAAAAGCAGATTGTGTCATACCTTT

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SEQ ID NO: 3181 GGTACACTGAAACCAAAATTTCTAAAACCTGTTTCTTAAAAAATAGTTGT
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SEQ ID NO: 3183 GGTACGGGGGGAGTGGAGAAACCGGGAACCATGGCCGCTGTGTTGCTGTT
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SEQ ID NO: 3184 ACACAAACCATGGAGGAGAGTAGAGAAATAATTAACAATGCTGTGG
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SEQ ID NO: 3185 ACAGTTGTTGGGCTACCTGATGCTATCTCTAACTCTTTAAAAATGAAGAC
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SEQ ID NO: 3189 ACTACTTGGTTCCGATATGGATGATGAAGAGGAGAGGAGAAAGAGATG
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SEQ ID NO: 3191 ACATAAAGTAAGTGTATATGTGCACAAGCATATTGCAATTTTTTTTAAAC
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SEQ ID NO: 3198

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SEQ ID NO: 3204 ACTTCATAAAATCTCTTATAGAGTTACTCTTGGCTAGATTGTAAATTAAGT
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SEQ ID NO: 3206 GGTACCACTGGAGGAAGCCCTCCGGCGGAACATGGCACTGAACTGCTCCGA
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SEQ ID NO: 3213 ACGGGACACACATGCAAGCTTTAAAGAAAGTGTGCTGAAAATAAAGAA
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SEQ ID NO: 3215 ACACCTTGAACCAAAATTTCTAAACATGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3216 GGTACTGCTCCCCAOCCTTAGTCTTCACTAAACATAGAAAAATGTCGAAAA
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SEQ ID NO: 3218 GGTACGCGGGCCATCCATCCCAAGGAGAACTTCAGTTGCTTGACTGTTGG
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SEQ ID NO: 3220 ACGCGGGGGCCAAATGTGCCAGCAGATCTGAGCTGAGAATCATCTGTTGGG
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SEQ ID NO: 3222 ACCCTCAACTCAAAAGGAAAAAGGTTATTTGGGAATTTAAATATCTTTT
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SEQ ID NO: 3224 ACGCAGTTTTCATGTCTTGCCTTAAAGAGCTCTCTAGTCTAAAGGCTTGTGA
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SEQ ID NO: 3225 GGTACAAAGGACGGAGCACCATCAACCGGTCAAGGCCAGCACAAACCCAG
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SEQ ID NO: 3226 ACAAGGAGAAATTCAGGAAGTAAGAAGTAAGAGTGACCTATTATGCTTC
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SEQ ID NO: 3228 ACCTAGAAGAGAGGCGGCTCAAAGAAAGTGTGAAGAAAGCAATTCAGTTTCAT
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SEQ ID NO: 3229 GGTACGGGGGGGCGCTGGAGCGCTTGCACGCTGCTCTGTGAGCTTCTCT
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SEQ ID NO: 3230 AOCACAGAAAAGCCTCTCTGTCTACGGGTGTCAATTTGACACCCCTCCCA
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SEQ ID NO: 3231 ACGCGGGGGGTGAGCTGACGGTAAACGGGCAGAGAGGCTGTTCCAGAGC
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SEQ ID NO: 3232 GGTACGGGGGGGAAGGTGGCGTGGTGAAGTGCAGGCCGTTGGGGCGGC
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SEQ ID NO: 3234 CGGTACAAAGATGACTATAAACAGATGCAGCCCTGGGTTCCATGAACAGC
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SEQ ID NO: 3236 GGTACAAAAATTTGAAAGTGTGACAATTGAAATGCTGTGACTGA
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SEQ ID NO: 3254 GGTACGACAATAGCAATCTTTCTCTCGTAGAGGACAGGGGAGGAGTCCCTA
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SEQ ID NO: 3257 GGTACCGGATCTCTCTTTAAACCTCCCTGCTGTTTCCGCCAATGTTTAAAA
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SEQ ID NO: 3258 ACAGCGGGGGGTGGAGCTCGTCTGAGGGCCAGGTTGCCACACT
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SEQ ID NO: 3260 GGTACTTTTTTTTTTTTTTTTTTGTGCTGNCCTAAATGTTTATTAAGTATGA
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SEQ ID NO: 3261 GGTACTTGTACAGTAAAAGAGGTATAAAGTCTGTTTCCAAAGTCCAAACCA
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SEQ ID NO: 3263 GGTACGCGGGGATTGTGGAAGAGACGAAGACTGAGCTTGTGGCGCGTGGC
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GGCC

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SEQ ID NO: 3300 AACTGCTGGAGGCGCTTCTGTGTGTTAGTCCCTGACTTCAACTGGGGTCT
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SEQ ID NO: 3302 ACAGCGGGGGCGGTTCTGAGGACCTGGGTTTGGGTGACAGCTTGTGCTTGGG
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CAGACAAAATCCACTATAGGAGTCATGGTAACAGGCTGCCAATCTGTGAGCAAGACAAATGGTGT
AAATTTGGTTGATCTTGGGTGAATGTGGCACCATCTGGGAGGAACATGCCACTGTTTAGC
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SEQ ID NO: 3303 ACATAGGAAAAATGATTGAAGCATTTCTCAAATACATGGCTCTGAGGGTGA
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SEQ ID NO: 3304 CCCAAGCATCTAGTCTGGAAGTACAGAGATAAGTACAGAAAAATGTTCCAAA
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SEQ ID NO: 3305 ACATTTAAAAATAGTCCCTTTATGCAATTTACTCTACATGTGTTATCCTTGCA
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SEQ ID NO: 3306 ACATCCATGTGGCCAAAAATCATCAAGCCTGTCTGACACAGGAGTCCAGCCAC
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OCCATGAGCAAGACTGTGGACCTGACGATGACAGGAAAGCTGTGGAGTTGGTCCAGTATGCTTA
CTTTAAGAAAGTTCTGGAGAGGAGAGAAAGCTTAAGAGGCAAGTGAAGGATGAATCAAGAGACA
GAGGATGAAGAGGAGAAAGCCAGAGGACAGGAGCAAGAGGAAAGAGAAAGGAAAGACTCNC
CAGCCAGATGCCAAAGATGGGGATTACATACGACCCCTATGACTCAGTGACACAGAGGAGGAAAT
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SEQ ID NO: 3307 GTTACAAAAAGAAAAAGAAAAAATCAACCCCAAAAGCTTCTAAAAAAGG
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SEQ ID NO: 3308 ACACAATGGTTTATTAAGGAATGTATGCCCCACATCAACCTAGCAAGGATT
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SEQ ID NO: 3309 GGTACGGGGGGGCTGATGTGGCAAGAATGTCTCCACATCTCCCTCCTGCAQ
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SEQ ID NO: 3310 GGTACTATGACTGAAAGATTCTTCATGGCTAAAAAGCTCTGCACTCAAACTCA
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SEQ ID NO: 3311 GCGGNGGCCGNGCNGGNGCCNGGNCNTCTTANGACGGGGGCTNTGGAG
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SEQ ID NO: 3312 GGTACACAGGCTGCTACCCAAGTTGTTGGAATGTTCTGAAACAGAGTAA
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SEQ ID NO: 3313 GGTACATGGGCCACAGATCATAAOCCAACTTTTTTTGTGAAATCATGAACAA
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SEQ ID NO: 3314 ACTAAAAATACAAAAATTAAGTGGGTGTGGTGGGCTGCCCTGTAGACCCAG
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AAAAACAGATTGTTGANGGGACAAAACCTTTGGNTAAAAAQQCNITGNCATTAAANTTTTTTTT
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SEQ ID NO: 3321 ACGCGGGGGAACGGAAAGTGAGCGGCGGGGTGCACTGACGGTAACGGGGCA
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SEQ ID NO: 3322 ACTGCAAGCCTGGATTACAGAGACTTGTCTCTTAAAAAACAACCAAACT
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SEQ ID NO: 3323 ACTGATTCACCTTCAGCTCCCAAGTCCAAAGCGGTAAACATCAAGAAAGCGA
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SEQ ID NO: 3324 GGTACCTACATCAGATCTAACCTTGATCCCAAGCAATGGGATTCCTCTCTA
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SEQ ID NO: 3325 CGAGGTACTCAGGCCAGCATCGCCCACTTGATTTTGGAGGGATCTCCCTCC
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SEQ ID NO: 3326 ACAGCTTCTTAAATAAGAACTTACAGATACATTTTCAGATATTCTAC
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SEQ ID NO: 3327 ACOCGGGGGOCCTCTTGTCTTGCCTGTGTGGTGTGTTAGTTCTGGCACTTG
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SEQ ID NO: 3328 ACOCGGGGAGTGGACACCATGCACTTCTGCAAGCCACCTGGGTGCAAGCTGA
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SEQ ID NO: 3329 CAAGACACTACGGGAACAGTTTGCCTCCCTCCAGCTCAACCCAAATCTTC
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SEQ ID NO: 3330 ACOCGGGGGTTGGCGGCGAGGCTTTGGCAGCTGGGACTGAGTGCAGAA
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SEQ ID NO: 3331 GTTACCCCAAGATTACAGAGCTTTGAACAAGTGAACCTATGGTTACCAAC
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SEQ ID NO: 3332 CGAGGTACCCAGGTATCTGCTAGAAAAGAGAACTAGGGACACCTGC
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SEQ ID NO: 3334 GGTACAAATAAAATCAAAAAGAGCAGTGTCTGTTGATTCATTTCTGCATGT
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SEQ ID NO: 3335 GGTACTTTTTTTTTTTTTTTTTTGGCTGAAAGAGTGGACAAATTTATTTTC
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SEQ ID NO: 3336 GGTAGGCGGAACTCAGAGCTTGGACGGCATCTAAGCCGCGAGCTCAGACAA
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SEQ ID NO: 3337 GGAAGGCGGAGCTCCGCGAGCTTATCGCCAGAGTCCCTGAACCTCTGCTT
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SEQ ID NO: 3343 GGTACTTTTTTTTTTTTTTTTGTATGAAAAAGGCTAAACGCTTCTGAT
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SEQ ID NO: 3344 ACGCGGGGCAAGGAGGTCTGTGTCCAGTTGTTTCCAAATTCACCGGCTC
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SEQ ID NO: 3379 CCGACTGAAGGAGACAAGAAAGCAAGCAAAAGTTCAAAAGCTGTCTAAGAATGAAGTGTCTATGGTGAACATAGGATCCCTGTCAACAGGAGGGAGAGTTAGTGTGTCAAGGCCGATTTGGGTAAAAATGTTTGGACCAATCCAGTGTGCAAGAGGATAGGAAAGAAATTTGCCCTTAGCCGAAGAGTTGAAAAACACTGGGCTTTAAATGGTTGGGTCAGATAAGAAAGGAGGTGACAAATCAAAGCAACAGTAGATGATGACTGAAAGATACAGTTTAAATATACATTGGGATGGATTGGAAAGTTGGAATTCCTCTTAACCAACCAAGGGTTTATTTCAAAGCAATATTGGGGAATTGATTTCAAGAGTCTTTAAGCTTACTAGGTAAAGGTATTCCTTTTCTTTTCTTGGGTATGAAAACTTAGGGCTAAATATATATAAAATTTGGCATAATGTTGGATTGAATCTCAITTTGGCAGAAAGTTNAACATTNCCACATAATGTCTNAAAANTATACATCATGCTGAGTTTGGTTTGGTTTGGTTTAAATTTGGTTTGGNTTGAAGCTGGCTTTGTCAACCCAGCTGGANTGCAAGTGGGTTGATTAAGCTTTGGCC

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SEQ ID NO: 3381 GGTACCTTTGGATTCAACAGTAACATCGGATGTAACAAACTTAGTTGCTTTTACTCACTGAACAACTCAAGGGCTCTAGTGAACAATCTGAAATCTTTTCAAGAGTTCACTAGCTTADGAAAGAGACCTATGCAAGGAATTTGAAACTGTTGACTTCAAGATATAATTTGGAAGAAAGGTCAGATCAACAACCTCAATTAAGGATCTCAGATGGCCACTTTGAGAACTTTAGCTGACAAACAGTGTGAACGACGACCAAAATCCTTGTGGTTAATGCTGCTACTTTTGGCAAOTGGATGAAGAAATTTCTGAAATCAGAAACAAAAGATTCCTTTCAAGATCAACAAGACAGACACAAACAGTGCAGATGATGAACATGAGAGGCCCTTCTGTATAGGAAACATGACAGTTCAATONAGATCATAGAGTTNNTTGAATAAGGATCTCAAACTGTTCAATCTCCCAAGGATGTGGAGATGATCCANGCTTGGAGAGATGAATAACCACTCACTCAAGTCACTGNCACAGGGGCTAATNCAACCCATGGCCATGCCANGNCAACTTCTTCNAAATTAAGGGA

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SEQ ID NO: 3396 GGTACATCTTAAAGTTTTTCTTCTTAAAGTGTGAAGAGGGCTTTCCACCAACCC
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SEQ ID NO: 3403 ACOCGGGGAOCGAGCGGTAGCTGGTCTGGCGAGGTTTTATACACCTGAAA
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SEQ ID NO: 3404 CAGGCCACTGAATAACACCCAAAAAGCAAGCAGGCCCTGCCATCGCACCT
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NAAAGGGGACTTTNCCCTTTTCAAGGGATAANANATTNTTTTTTCCAAACCCCATNGGCGCTNGG
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SEQ ID NO: 3405 ACTTTCCTGGAAATAAGTGAAGTCAAAGCCACAAGCTCTCCAGGAAGCTCTG
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SEQ ID NO: 3406 ACCGGCAGCTCTCTGCTCTOCAAGGGCTCCCGGCCACCCGGGCTGATAAA
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SEQ ID NO: 3407 ACCAGTGAAGGAAGGCTTCCGGCGGAACATGGCAGTGAATGCTGCTCGAGAT
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SEQ ID NO: 3408 CCGGGCAGGTACTTTTTTTTTTTTTTTTTTTTTTTNGGATTTGTCTGCCAA
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SEQ ID NO: 3409 ACAACCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCAACAGTGTCTTA
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SEQ ID NO: 3411 GGTAONCAATATAAGCAAAATCTCAAAATCAAACTACTTTGTAATTAGAACAC
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SEQ ID NO: 3412 ACGNCGGGGGGATGTGGACCTCCAAATTCACGCCCCGGCTCAGCTCTT
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SEQ ID NO: 3413 GTACTTTCTGCAGAGCTACATTCACGTGATAGCGCATAAACTCATTOCTGGA
CCTGAGAACAGAAAGGCTTTCTGTGGGCTTTGGATACATATCCCTGAAAAGAGCAATGAGAAAGAC
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SEQ ID NO: 3414 ACGCGGGTTTTTGTCCCTGTCTGCTGCAAGCATGCAGGACTTGACTCAGGAA
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SEQ ID NO: 3416 QGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTGGGAGTTTAAATATCGG
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SEQ ID NO: 3417 GGTACACTTGAACCAAAATTTCTAAACATGTTTTCTTAAAAAATAGTTGTT
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SEQ ID NO: 3418 GGTAGCGGGGACTCAAAAGCTTGGACCCGACTNCTANCCGNCAGTCAACAA
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SEQ ID NO: 3419 ACCTAAAGACGCCCCACCTGGCATATACTGGCTGGGCTCTCTCTGTCAAG
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SEQ ID NO: 3420 AGGAGGGGCTGACTCTCTTTTGGGACTCAGCCGCGCTGCAACCCAGTGAAA
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SEQ ID NO: 3421 GCGTGGNCNNGGCCAGGNNCACTCTATAACTCCAACAGTCTCCACTGT
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[illegible]

SEQ ID NO: 3432 CGAGGTACAGGACACATTGGAGATCTTTATCOTATCCOCTGAACTAGCTGC
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SEQ ID NO: 3433 ACACGAGAAAGCTCCGAGGATGGCTGAAGTCCAAGTCTCTGATCGGTGGCT
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ATCNAAN

SEQ ID NO: 3435 GGTACACTTGAAACCAATTTCTAAACTGTGTTTTCTTAAAAAATAGTTGTT
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SEQ ID NO: 3437 ACGCGGGGCTAAATCTGCTCATTATTTAGAGGGGAAACCTAGCAAACTAA
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SEQ ID NO: 3438 A C C T G G C C T A T T T T T A A A C T A G T G T A A T C A C C C T A G T C A T A C C A T T C A G T A T G
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T G A A T G A A T T C T C A G C C A A A T T A A G T C T T G T C T C A T C T G A T T G A T T A A T T C C A A A T T C T A A A
A T G A T T C A A G T C C A C A A T A G C T C T A G G G G A T G A A A A A T T G C C T A C T T T G C C A A G T T C C T A A A A
C T G T G A A G T T G C C A A T C C T A A A C T U T A A A G C T C T T C A A G G G A G C A A G A N G G C G C A T T T T C T T C
G G T G C A T G T A A T T T T C T A A A G T G T T G G C A A C A C T N T G G A C C T T G G C C N G A N C A C C C T T A A G
G C G A A T T T C A A C A C A C T T G C G G C G T A C T A A G T N G A A T C C A A C C T G G A N C A A C C T N G G G A A
T C A T T G G C A A A C T N G T T C T T G G N G N A A T G G T A T T C C G T T A C N A T T C C C A C N A C A T T C C A A N C C
G G A C A T T A A A T G T N A A A C C T N G G G G C C T A A G N G N G C C T A C C T A C A A T T A A G G T G G C C T C C
T N G C C C N T

SEQ ID NO: 3439 A C C G A C C A T A G A G C A A G A A T C A A G A T T C T G C T A C C T C C A C A C C C C G T C
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A G T G A A A G G G C C C T A C A C T G C C T T T T T A G G C T T A G A G A C A G A A C T T T A G C A T T G G C C A G
T A G T G C T T C T A G C T C T A A A T G T T G C C C G C C A T C C C T T C C A C A G T A T C C T T C T C C C C C T C C C
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A T C T G A T G T C G A A T C T G A A C C G G A G A A T C T T G C C G T C A G C A G A G T C A G G G A T G G G T C C A T T A T
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T T G A A T G T G C T N G T A A C T G N T T G C T T C T T G A T A G A A C C A C C A C C T T A C C C A C C A G A T A N
T G C T T T G A A C C A G C C T A A C T T A A T G G G A C C C A A A N C C C A A T T G C T T T N T T C A N A A A C C
C T G C A A A T G G A G G A C A T T A A T T G A G C C T G G T T G C A A G G A T A T T A A C T T C T T G T

SEQ ID NO: 3441 A C T G T G C A N A C T C A T G T A N A A A C C A G T C T G C T A A T T G C T T G A A A A G T T G C A
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T T C A T C T C T G A G C T T G T G C T C A A G A T C T C C T G T G T A G T T G T G A G G A A G G G A A G T T A A A A A
A C T C G A G A A T A C A G G T A T A G A G G C T A A T G T T T G T G T T G G A A A G T G A G A T T C T G A A A A T A T T C T
T G A A A A A G G A G T G A T C A T T G G A A A A G C A A G C C A N A T A T C T G G A C T T T C A A T C A G A G G T A A
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SEQ ID NO: 3442 G G T A C G C G G G A G A A G C T T G G A C C G A T C C T A G C G C G C A C T C A C A A A G C C
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G C C C T C C T A C A C T C T G G C C A G A G A T A C C A C A G T C A A A C C T G G A G C C A A A A A G G A C A C A A A G G A
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G C A G A N C A G T T T G T C C T C C A A T C T G G G T T A T G A A A C A A C T G A C A A A C A C C T T T C T G T A T G N
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SEQ ID NO: 3443 G G T A C C C G G G A C T C A A A G C T T G G A C C G A T C C T A G C C G C G A C T C A C A C A
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T C C T C C T C A A T C T G G T T A T G A A A C A C T G A C A A A C A C C T T C T C T G A T G C C A G T A T G C C C A
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T A T G C T T A C C A A C C T G C A G A T C A G C T N T G C T T G A C A C A T G A A A A A A G C T T T N A G T T C T G A A A N T G

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SEQ ID NO: 3445 CCGGCGAGGTACAGGCTCTTCTGTTTCATGAATGAGCATGCTGAAGGCTATT
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SEQ ID NO: 3452 GGTACACAAATGTTTATTAAGGAATGTATGCGCCACATCAACCTAGCAAAG
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SEQ ID NO: 3453 GGTACTGAGACTATTGGAGCTTGTGGCCAGCATCCCATCTGCA0CGTGTGTC
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SEQ ID NO: 3474 GGTACGCGGGGGGTCCCGTGGTCTCTATCTAATACCATCGAGCTCCCTC
CAGAAGAGGAGTGTGAATTTAGACACTTCTGCAAGGATCTGCTGCACTCTGAGCGGTGCCGTG
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CAGCTGTGCTCGGCTCACAACAGATTTGACTGCTGACTTTGACTCTCAAAATGGCGCTAAA
AATTAAGAGATGGATACANAANAAGGAAAAAAAAAAAAAAAAAGTACCC

SEQ ID NO: 3475 CGAGGTACTTTTCTTTTCTTTTCTTTTCTTTTATTTGGAGCTTGGACAAAAT
TCCACAGCTGTAATCTCAGGATCACTTTGCACTCTCAAGATTGATACAGAGGAAAGCTTCAAT
TCAACCTTTCAGAGAAAGACATTCAGCTGCGATCTCATCAACCAAGAGAAATGTTGGTGGCAAT
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CAGCATTTGGCTCACTGTGTTTCAGGTGACACCCCAAGCTGACCTGATTTCTGAATGTTCTGCTG
AATTTTAAGTAAATGTTTCTGAAAGNCAAAACAGAGTTCTGAGCAAGAACTTGGGAAATATGA
GCAATGCTACAAACAAATGCTTGGACTCCAACTGNGGCTGCTTTAGACTGGGCTTATGTTAAT
CAAGGCTTNTGCAATGCGCTTTCACGGGCCAGCCCTGGAACACCAAGCTNATNAATAGCATTTT
GAAGCTNAANOGNCTNACTGGATTTTGAAGTGAAGGAGGGGGGCTATTGGGCTTGAACAANA
AGNGACAAACCANGGGTGGTCANTTTTNAANAAGGGAATTTNTTTTCCAAAGGTACTAATACAAA
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SEQ ID NO: 3476 GGTACTGTTGTTGCGCAGCAGAGGCGCTGGGTGGTGGAGCGAAATGGGCCGA
TTCCACCGGATCCTGGAGCGCTGGTTTGAACATCTCATCTCCCTGTGTTAGACCGGATCCGATATGTG
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GGACCTGAGATATGCGCTGACCAAGCTAAGCTAAACAAATGAGTCAAGAGCTGGCAAACTCT
CTCTGGACAAAGTCTTCCGGGAAGGGAATCCCTGAATGCGAGCATTTGGATGGCATCAACCA
GCTGCTGACTGCTGGGATATCCCGCTGCTGCTGATGATCAAGGATATCCATGTGCAACCC
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ANTCTTANGGACCAAAAGTGGCATTAATGTGNCANANOGGAAAAACAGGCCAAATCTGGCC
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SEQ ID NO: 3484 ACGCGGGAGGGACGAGGCGAGCAAGATGGCGCANAGCGCANOGCACCC
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TTGAGCCGATATATCAGTTTCTACAAGTACAGCTCTAAACATAAAATGAATATCTGAAAGAAAT
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CAAAATANTTTCAAGACTTANNCCANATTGGGTTTNGAAAAGAGATAACATGGGAAGAAATCANAA
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ANTTTTCA

SEQ ID NO: 3485 ACGCGGGGGCTGTTGCCTTCAGGTGACCACGGATTCCGCATCGTGAGTTCCA
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CGTCGTTGAACAACCCATACATCATCCGCTGGAGCGCTCTGGAAAGCGAGGATATGCACTTCATC
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SEQ ID NO: 3486 GTACGCGGGGGGAGGTGGGAACGCTGTGGCCATTCCGATTGCGCGGAGCG
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AACCGTAACCTGGTTCTCCTCGTGTAANCCCTNCCTNTCANCCCAATGAAAACGCTCTGGGCGA
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GGTTCCCCTCACTCACATACACTTANGGGAATAAAATGNTATTTGANANATNANTGANANTN
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SEQ ID NO: 3487 ACTTTNTTTTTTTTTTTTTTTTTTTTTTAAAAAATAAAAAATGATTTTTATTAGTT
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SEQ ID NO: 3489 ACGCGGGGGAGGCGAGCCATGTCTTATCCCGCTGATGATTATGAGTCTGAGGC
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TNAT

SEQ ID NO: 3490 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGNCCCGTC
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GTCTCTGGCTGTCTCGAGCAGTCTAGAAGAGTGCTCTCCAGCCTATGAAACAGCTTGGGGTCTTT
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SEQ ID NO: 3491 ACACTTGAAACCAAAATTTCTAAACCTGTTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3492 ACTTTTCTTTATTATTACTTTTNTTTTCTGCAAGTCANTAAAAGGATTTAAG
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SEQ ID NO: 3493 ACTTTGTAGGCTATACGTTTTAAACTCCTGTAAAGAACATTACAAGCTATTTT
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CTG

SEQ ID NO: 3495 ACCATTTGGAAGAATGGAAGCTGATGCATCTGTTGACATGTTTTCCAAAGTCC
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SEQ ID NO: 3496 ACCTCTCAAATTGCTCATCAATATAGGAGATAATTGTCTTAAAAACAATCTCTG
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SEQ ID NO: 3497 ACCTTAACATCTGTTGAGAAAAATACAAATAAATATGATGCTAATAAATGGCC
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SEQ ID NO: 3498 ACACTTGAAACCAAATTTCTAAAAACATGTTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3499 ACTTTTTNTTTTTTTTTTTTTNTNTTTTTTTTTTAAAAANTTGCANATCTTTAATA
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SEQ ID NO: 3500 ACCCCCATGCAATATATGGCTCTACAATCCTCANCATGTTAATCGAANCCTTG
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SEQ ID NO: 3501 ACAAATATCCATTGCTTCATAGGTTCAAGTTACATAAAATTAAGTCAAATAAT
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SEQ ID NO: 3502 ACTCCAGCCTAAGCAGTAATTCTCTAAGTTTCGCAAAAACTCCTTCCTTTGG
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SEQ ID NO: 3503 GTACACTTGAAACCAAATTTCTAAAAACATGTTTTTCTTAAAAATANTTGTGT
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SEQ ID NO: 3504 GTACAACGCTTCAGCCTACTGCAAAATCCAAACACAGGTTTGGTGGAAGATT
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ACTCTNNTG

SEQ ID NO: 3505 ACTGGAAGCATGCTCCAAAGACCTGTAAGAACTTTGCTGAGTTGGCTCGTCG
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SEQ ID NO: 3506 ACCATAATAAGTTTGTAGTAGTATAGGCTAGGCTTAAAACTGCACTCCTCCTG
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SEQ ID NO: 3507 ACGCGGGGAAAAACAGAGTAGCAGCTCAGACTGCCAGAGATCGAAAGAAGG
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SEQ ID NO: 3508 GTACTCGGGACTGTGTGAGGAATGATGGAACCAAATCAGGGAGAGTTTCTT
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SEQ ID NO: 3509 ACTCATGTATTTTTTTTCCAGATCTCTTTCCCAAGTTGCTATTGTAAGAGTAT
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SEQ ID NO: 3510 ACGCGGGGACATGTGTATGTGCCAGCTCACACCTAGGGGCGGGCTGCCTCTC
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SEQ ID NO: 3511 GGACGCGGTGAATACATTTCTACTTTATTTTGAACATTTGCCAAACTAAAT
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SEQ ID NO: 3512 ACGCGGGTGAATACATTTCTACTTTATTTTGAACATTTGCCAAACTAAATAC
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TCCATGGTGCCTGTTGGCATTAGCACTACCATTTG

SEQ ID NO: 3513 ACATTTACATTCAAGTTGATAACACCGGTGGTTTTCAATTTCAATACAAATTATG
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TCTTGATTGAGAATCTCTTGATGATNGANGTGCANCTAATTCGTCCCGAAACTCATGAAGATCATN
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 GGTGATATTTGCGTCAAAACACNNATAGNACGANACNAGCNAACTACAATNACNAAGATNTCNNA
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SEQ ID NO: 3514 ACCACAAAGGAGAAGTTGATAGGGAATCTAATTTTAGAATGTGCCAAATGGT
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SEQ ID NO: 3516 GNGTACGCGGGGACGCGCGGGGGCATTGCTATTGCGCGGCTAGAGGTGAA
 ATTCTTGACCGGCGCAAGACGAGCAGAGCGAAAGCATTTGCCAAGAATGTTTTCAATTANTCA
 AGAACGAAAGTCGGAGGTTTGAANACGATCAGATACCGCGTAGTTCNACCATAAACGATGCCNA
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 TTCCGGGGGGAGTATGGTTGCCAAAAANAAAA

SEQ ID NO: 3517 GTACTGCAGCATGCACTGGCATACTATAGCTTGGTCCAGCTCTTCCANAGCCC
 CAACCACTTTNCAAATGAATCCTAAAGTTTTTGGTGCAGGACCCAATTTAAATCCATGTTTCTTCA
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 AGCATTGTTTGACCAAAAGGAACTACCCCTTCAATTTGTGCCAATTTGTTGTCCATGATATAGGC
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 AAGTTGGATATAAANTGGCNGNNNAAAAATTTNCATGAACCTNNAACTGGANANCTTGAAAAAN
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SEQ ID NO: 3518 ACGCGGGGATAACCATGCACACTACTATAACCACCCTAACCCCTAACCCTA
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 TCCATTGTGCGATCCACCTTTATTATCAGTCTCTTCCCCACAACAATTTATGTCCTAGACCAAG
 AAGTTATTATCTCGAACTGACACTGAGCCACAACCCAAACAACCCAGCTCTCCCTAAGCTTCAAAC
 TAGACTACTTCTCCATAATATTCATCCCTGTAGCATTGTTGCTTACATGGCCATCATAGAATTCNTC
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SEQ ID NO: 3519 ACTGGCGTGGATTCTGCATAATGGTGATCACACGTTCCACCTCATCTCAGTG
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AAT

SEQ ID NO: 3520 ACGAGATCCTTATGGAAATCGTCCCTTATGCATTGGTCGTCTTATTCCAGTGT
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SEQ ID NO: 3521 ACCTGAAGCTCAGGAGGAGATGAAAGAAGTAGCCAAACACCCAAAGAATCC
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SEQ ID NO: 3522 ACGCGGGGAGATGGCAGATGAGATTGCCAAGGCTCAGGTGCTCGGCCTGG
TGGCGACACGATCTTTGGGAAGATCATCCGCAAGGAAATACCAGCCAAAATCATTTTGGAGGATG
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TGTTAACACGTTTGGGGATAATTTCTCTTTANGCATGATTAAGTAGGCATTCAGTATGTTAA
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TNTNACTCAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 3523 ACTTTTTTTTTTTTTTTTTTTTTTTTAACTANATTTTGAACCTTTTTATTAT
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SEQ ID NO: 3524 ACTTTTTTTTTTTTTTTTTTTTTTTTGGATAAATACATGCTGATTTATTACA
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TTNTCTGGCANTNCTCAACTTTTGCTGGNCCTCTTGCTGGNNCAAACACACCGGGACCCACCAN
GATT

SEQ ID NO: 3525 ACAAAATGTAGATCTATTTATTTAGCACTTTGTTCACTCAGATAAAATTTATAT
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GGGCATTAACAGTACGCGGGGACTGGANACACTGAAGAAGGCAGGGGCCCTTAAAGTCTTGTTG
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TGCNCTCTACATCTCAGGGTAGGAAGAAAAGGNTTCCAAACATGCGGTGNTCNATTGTTGACT
CCTGCCAAAACAGGATNCTGG

SEQ ID NO: 3526 ACGCGGGGGCTTTCCACTATGGCTTCCAGCACTGTCCCGGTGAGCGCTGCTG
GCTCGGCTAATGAAACTCCCGAAATACCGGACAACGTGGGAGATTGGCTTCGGGGCGTCTACCGC
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TCCTTTTGTTCTTGATCCACGCANAATTCATTCTCTGGTCACAACAGGCTAACTAAAGNTTGCTCTA
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TGAAAAATTTANT

SEQ ID NO: 3527 ACAATTACCCACCACTGGATTGACTCAGAGAGGACCCCCAGAGGGTGTCTC
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GGTGACATACTCCTGGAAGTTCACCTCCTGGTCTTGTTCGGTCCAAGTCTTCCATCAGCCTTGCA
ACCCGCGT

SEQ ID NO: 3528 ACGATAATCCACACCATATCTTGGATTCTTGGAAATTGACTCAACTCTCCA
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SEQ ID NO: 3529 ACTTTTTTTTTTTTTTTTTTTTTTACCACATATTTATTAAGACAATCATTTAT
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SEQ ID NO: 3530 ACTCTCTCAGCTCAGGTCTCTTAGCTTTTAGTGTGGTGTGACGCAAGTCATTTT
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TAGTTAGTCTACT

SEQ ID NO: 3531 ACTGCTTGTCTCTGTGGAGGAGATGATTAATAAATAAAAAATCCAGAAAGGACA
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TCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCCCGATATATGTTCTCTA
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SEQ ID NO: 3532 ACTTGAAGTGGAGGGCAAGAAGTGGAGAGTGGAAAAATCAGGAAAATGTTTN
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TGTTGATANCCAAGTGCCCTGGGTCTTGCCCTCCCTCCACNATGGGTAAATCTGTAAACGGTCTTT
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SEQ ID NO: 3533 ACTTAGCATTGATCAAAGAAATTTCAAATTACGATCAATTGGGTGGGGAGAA
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SEQ ID NO: 3534 ACATGTTTACAATACCAAAAAAGAAAAATCCACAAAAGCCACTTTATTTTAA
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SEQ ID NO: 3535 ACGCGGGGTGTATNATGCCTGTACTANTATTCACATGGAACAAATTGCTGCC
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SEQ ID NO: 3536 ACAAAAAAATTAGCTGGGCATGATGGCGTGTGCCTATAATCCACCTACTCG
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TGNACTATTTGCCCCGCTCACTCTGAAAGCANAGGAGATGTTGTTTACTTTGTTCTATCCCTTTGC
TGAGATAATTTGAATGAAAGTTTCTCTTATGCTTCTGGTCTTTCCAANCTATACAAGAGATAG
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SEQ ID NO: 3537 ACACTTGAAACCAAATTTCTAAAACCATGTTTTCTTAAAAAATAGTTGTTGTA
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ATAATCCTGGGGACATACTGGCCATCAGGAGAAAGGTGTTTGTGAGTTGTTTCATAACCAGATTGA
GGAGGACAACTGCTCTGCCAATTTCTGGATTCTTTATTTTACAGCAAACTTCTTTAAAGCTTG
CTGGTGGGCACTCTTCAAGTGATGATATCATCAAGGGTGTGTTGCTTGTCTGGATTATAGAGCTC
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SEQ ID NO: 3538 ACACTTCTCGAAATCTAATTGGGGGCGCTGACATCATTGTGATCAAATACAA
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SEQ ID NO: 3539 ACCATGGAGAAGGAGTCGAAAACCAACCCGATTCTGTCTTATCTGTAACATAG
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SEQ ID NO: 3540 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTCGATTTTTANAAAAATCAAATAATCTT
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ACTGATTTCTATTNAATTTTATGAATCCTAGCTTTTTTAAAAACACAAAACATNCCAACCTCAGAGT
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SEQ ID NO: 3541 ACAGACAAAACAAAATCTGCCTTAGGCTGTGTGATAAACCTATCATACCTCC
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AGATTGATGGTCTGACAAGTCTTCAATGACTCACTGGACAGTCTCTGCTGAAAGTCTGCTCTCATA
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TTNCATCCACT

SEQ ID NO: 3542 ACATTTTCATGACTGGGGAATGGATTTTCTGAAGTCATCTTCAATAGGGCAAA
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CTCCTCCTTCACCGAGAGAGCTTCTAGCTTTTCCGCCACTTTTTCGGCATGATCATTTTTCCTGA
TCCTGCTTTCTTTTCTCTCTCTNCGAACTCTTTCCTGCATTCTTCAAACCTTTGTTTGAATTTCTGN
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TACAAGCGNNGGGTGTCCANACCCAGGCANCGGNNNTACTGNNTTGGGCTTACCTCCATCTT
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SEQ ID NO: 3543 ACGCGGGGAGAAAGCTTGGACCGCATCCTANCCGCCGACTCACACAAGGCAG
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CTCGACCCAAACTGCCCCAGACCTCTCCAGAGGTTGGGGTGACCAACTCATCTGGACTCAGACA
TATNAAGAAGCTCTATATAAATCCAAGACAANCAACTAACCTTGATGATTATTCATCACTNGGAT
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GAGCNTTTTGCCTTCTCAATCTGTTTATNAAACAACCTTGACAAACNCTTTCTCTGATGGCNTGAAT
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AGCT

SEQ ID NO: 3544 ACGCGGGGGTCTGGAGCTGCCTGAGGATGAGGAGGAGAAGAAGAAGATGGA
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GGCTGANGCCCACAAGAATGATAANGCAGTTNATGACCTGGTGGTGTGCTGTGTTTGAAACCGC
CTGCTTCTTCTGCTTTTCCCTGNGGATCCCNAGACCACTCCACCGCATTTTTCGCATGATCAAGCTT
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SEQ ID NO: 3545 ACATAATCGTTTTGTGGAGTCGGCACAGTTTCAGGTTATGGAGGCACGTAATTC
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CATGGTAATGATACTCCCGTTAGGACCTTAGGGATGAACCAAGGCCCAAGATCCGACNANCCC
ANACCGCTCTCCATGAGAGCCAGTGAGGCCGTGATCCCNCTGNCCCGCTGACGCCCCCGNTCTGC
CGGCGGCG

SEQ ID NO: 3546 ACAGATTGCCTATTTGAGGACCTTGCCGCTCTGTAAGCATCTGACTCATCTC
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SEQ ID NO: 3547 ACGCGGGGTTGAGGCTTTGCAATTTCACTTGTGTTAAAGGCTCTGGCATTTTT
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TNTANTCGGNGCGNACCNCTAGGCGAATCCACTCATGGNGNCGTACTANGGNCCACNTCGGTCA
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SEQ ID NO: 3548 ACAGCCTTGTGGCCAGCCTTGACAACGTTAGGAATCTCTCCACTATCTTGAAA
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CTGTTCTGGGAAGAAGGAGGAGTGGTGACAGTCTGCAAANTCAATACACAGGAACCTGAGGAGA
CCCTGGACTTGATTTCTGCAGACCAATGTATTAATAAAATTATCTGCAGTCAGANGGGCTCCGTG
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ACTTTGGAATGCAGAGTTCCACTN

SEQ ID NO: 3549 ACGCGGGGACTGCGATAGAAATCATGTCTGGTCGCGGCAAAGGCGGAAAAG
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SEQ ID NO: 3550 ACGCGGGGACTCAGAAGCTTGGACCGCATCCTAGCCGCGGACTCACACAAGG
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SEQ ID NO: 3551 ACCACAGTTCACAAGTGCAGGAGAGAATTTTGATAAATTGTTAGCTGGAAAAG
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SEQ ID NO: 3553 ACTTCAGACAGGATCCCAACCCCAACCAAAATCAATGTCGACCGTCTGAGC
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SEQ ID NO: 3562 ACACTGAAACATAAATCCGCAAGTCACCACACATACAACACCCGGCAGGAA
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SEQ ID NO: 3565 ACCATAAGGAGACACAAGAAGAAAGGTGACACTAAGGCTACAGTGACACAGA
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SEQ ID NO: 3568 ACCCACCACCATGCCTGGCTAATTTTTTGTATTTTAGTAGAGACAAGGCTTC
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SEQ ID NO: 3569 ACGCGGGGACAACATGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTGTAA
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SEQ ID NO: 3570 ACGCGGGGATCCCGGAGTTGGAAAAACAATGAAAAGGCCCCCAAGGTAGTTA
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SEQ ID NO: 3571 ACAGGCTGAACAGAATTGAGAATGCCTTGAAGACAATAGAAAGTGCCAACC
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SEQ ID NO: 3572 ACTTCTCAGAGGTATTTGCAGCTTGATGCAAAGTAGTCTCTAATGAGTAGGCA
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SEQ ID NO: 3580 ACTTATTTCAAACCTGGGACAATTGGAATCACTGGTCATCTAAGAGGAATATT
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AANC

SEQ ID NO: 3581 ACGCGGGGAAGATGGCGGCGCACAAAGTCAGGTCCGGCACATGTTTCCGCGG
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SEQ ID NO: 3582 ACACATGGAAAAGACATGATCACCAAGTGAAAACAATCTAACCAGAAAGCT
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GCCATG

SEQ ID NO: 3583 ACAGAAAAGTAAAAATGCTGTTACAATCTCAGTGTAACCTGGTAGCCACAGACG
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SEQ ID NO: 3593 ACGCGGGGGGGGCCITTTTCTCTCTTTCAGCGTGGGGCGCCACAATTTGCG
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SEQ ID NO: 3597 ACGCGGGGAGCAGCAGGAGGAGGCAGAGCACAGCATCGTCGGGACCAGACT
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SEQ ID NO: 3598 GTACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCG
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SEQ ID NO: 3599 ACCGTTTTTTCAGGCACAAGGAAGGTTTACCCCCGTTGCCGAAAGACTAAGC
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SEQ ID NO: 3600 ACGCGGGCGGGAAGGGCCTGTCCAGTCGGCTTTACCTATCGACGCAGCGT
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SEQ ID NO: 3601 ACTGAACTCCCATCACAAATCATCTTCTCTAATAACTGTAACACAACACCT
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SEQ ID NO: 3610 ACGCGGGTGCTTTTGTACCTTTGAAAAGCCAGCAGACGCTAAGGATGCAGC
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SEQ ID NO: 3611 ACAGAAATTTACAAGAAGTCAAAACACAGTGATGCCATTTGCTATGTTTTATT
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SEQ ID NO: 3612 ACGCGGGCTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGA
AGGGGAGGCAGCCGGCACCCACAAGTGCCACTGCCCGAGCTGGTGCATTACANAGAGGAGAAAC
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SEQ ID NO: 3613 ACAGCCTGTCTCCACCCAGGAACACCCTCTGCCTAATGACAGGACCTTCCT
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SEQ ID NO: 3614 ACTATTTACAGCTAAACCAGCTATACAGGATCATAAAAAGTGAGAACATTTT
TGAGCCCTGAATCAAAGCTTTCATAATCTTTTTTATAATTTCAACTTTTATTAGATTCAAGG
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SEQ ID NO: 3615 ACGCGGGGCAGCAGGACTCGGTCTAGCAAGGCCATCTTGTTGCCGGACCTTT
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TGNCAGGACAGTCTTNGAANGAACANNAACCTNGNTTCTATTCAAANCAATTTTCCNTAAAA
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SEQ ID NO: 3616 CGCGGCGAGGTACGCGGGGTCTCGCGGCCGACTCGCAAGATGGCGCCGCGAG
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ANCAGTCTCTAANAGGTATTTGAAATCCTTACTAAGAAATCCTTAAGAAGAACAATCT

SEQ ID NO: 3617 ACTTTTTTTTTTTTTTTTTTTTTTTTTTAGCANATTTTAAGGGTTTTATTTAA
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NTGCCACANTTATTTCTGTCNTGAGANCTCCNTGANCNACTGGTCCGACTTTTCTTTNGGAGGGGG
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SEQ ID NO: 3618 ACACAAGATGGTGGCCTTGGCGGTTACTCTTCCAACCACTTCCACAATTCCAG
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SEQ ID NO: 3619 CGCGGCGAGGTACTGGAGATGTATTTGATAACCAAGGTTTTAGGTAAATTTTC
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SEQ ID NO: 3621 ACCAAGGCTTTAACGTGTCTGTGCAGGGTATTATCATCTACCGAGCCGCCTAC
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SEQ ID NO: 3622 ACAATCTATCGACAAAACAACTCCAAAAGAAGGTGTGAAAGTTAACAAGG
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AATAC

SEQ ID NO: 3623 ACGCGGGGAGTGAGGAGGAACGCGAAAAAGGTAACGCCACTCATGGTCAAAG
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SEQ ID NO: 3624 ACAAAAACCCAAATTGATAAATCTGCAAAATCTTAAACTTCTTAATCCATTGA
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CAAGAAGGTATATATATGCAATTCTNAANANAGCTTANAANGTTACAGTTNACTTCTATTTCAGNATT
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SEQ ID NO: 3625 CGCGGCGGGTACAGATCTCACAGGGACACTCCTTATCCCTTGACAGAGTTCCA
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SEQ ID NO: 3626 ACGCGGGGCAGGACAGCATTTTCATATGTAACCATTTGAATGTTTTGCTGTTT
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SEQ ID NO: 3627 ACAAATAAAATCAAAAAGAGCAGTGTTCTGTTGTATTCTATTTCTGCATGTATA
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SEQ ID NO: 3628 ACGAGACATGTCATGCTGCCCAAGGACATAGCCAAGCTGGTCCCTAAAAACC
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ATGATCCATGANCCATAACCTCACATCTNGCTGTTCCGGCNCCTACTACNCAAGATNCCAANGAA
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SEQ ID NO: 3629 ACCACAGTTCACAAGTGCAGGAGAGAATTTTGATAAATTGTTAGCTGGAAAG
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SEQ ID NO: 3630 ACAGATACTTATGAGGCCAGCTGGTCTTTAATTATGTGGGTCCGAAGCAAATT
CCTTGTATGGGCATCAATTGGAGGGGTTCCTNTCTTTGAATACAGAATTCAGGGGAGCCAGGAGGG
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SEQ ID NO: 3631 ACGCGGGGAAGTATGGAATAAACTACTGATGCAGTGAANACAGTTGAAAA
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SEQ ID NO: 3632 ACCTTTCCTTTTCCAAATCTAGCTGAAATTTCTCACTTGTTTTCTTTTGATGA
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SEQ ID NO: 3633 GGGTACCAAAGTACCAATGGGCTGCAAGAGGTTTAGATTATTGCTACCCAC
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TNCATCAAGTAATNCTCAGGAACCCAAGTANCTTNTCNTTGTCTTTATCCTTCATGAAATAATTTA
ACCATTCTTCNACNTANATNTGNTTTTTGCTNAAAGCCAT

SEQ ID NO: 3634 GGGTACAGGCGGCAACTTCCAGAGCTTCCCCTCAGTGCTTGGTGACTGGCAC
AGACACGATGCCATTTGCTCATGTTCCCCTAATACAGACTGGTAGAGCTGTGGTGGATCCATTGTC
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SEQ ID NO: 3635 ACAGGGAAAGGAAAAATTTTACCAACAGAGGCAGTCTCTCATAGAGTATAA
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TNGAAATNAAATGANTTCCAAAGNTAACCTATTATGAANTATAAATTTTTTCTTGG

SEQ ID NO: 3636 AGCGGCGAGGTACCTGCAGGCCTCTACACCTACCTCTCTTGGGCTTCTATT
TCGACCGCGATGATGTGGCTCTGGAAGGCGTGAGCCACTTCTTCCGCGAATTGGCCGAGGAGAAG
CGCGAGGGCTACGANCGTCTCNTGAAGATGCANAACCGCTTGNCGGCCGTNCTCTCTTCCAGGA
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SEQ ID NO: 3637 ACGCGGGTATTCAAGTGATAGTTTGTGGCTTGTAANAATTCTATGCTCCATGG
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GNCGAAACCTNTGTNGATGCTGCTCTGAATTGCTTN

SEQ ID NO: 3638 ACTTTTCTTTGAAGTTTGTAGCGGTCAATTTGCCTTTTAAATGAACATGTGAAG
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NGGCNAAATTCCAAGACATTG

SEQ ID NO: 3639 GCGGCGAGGTACGCGGGGGCTGTGCGCGGTGGACTCGTCGGAGCCGCGGGC
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TGGCGG

SEQ ID NO: 3640 CGGTACCCATGCACAGCAGCTGTGGGGTGTGGGCATCTTCAGGTGGTGTCT
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SEQ ID NO: 3641 TTACACATTGCCTCACTTTATATTTTAAATGAGAATCTTGTTTATTGTATTTGA
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NATTGATTTTTGTAGCATAT

SEQ ID NO: 3642 ACACTTGAAACCAAATTTCTAAAACTGTTTTCTTAAAAAATAGTTGTTGA
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TCTGGTTTCAAGTCTCAAGGCCTGACAGACAGAAGGGCTTGGAGATTTTTTTCTTTACAATTGAG
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SEQ ID NO: 3643 ACGCGGGGGCTGACTCTCTTTTCGGACTCAGCCCGCTGCACCCAGGTGAAA
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SEQ ID NO: 3647 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACCTCAGTCTTTTANACTCTCAGCTG
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CGGTTGGAGGGT

SEQ ID NO: 3648 ACGCGGGGGGTGGAGGTGGTAACCGTGATAGTAGCAGCTCCGGCGGCAGCA
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SEQ ID NO: 3649 ACACTGTTGGAGAGATGAGACAGTCACACCAGCTGCCCCTAGTGGGGCTCTT
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SEQ ID NO: 3650 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGCCCTTATATCAGTTTTATTGGTGGGTTT
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CCGGCCTNNGCTGA

SEQ ID NO: 3652 ACGCGGGGGTTGTGAGTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCC
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SEQ ID NO: 3653 ACGCGGGGAGCGGTAGCTGGTCTGGCGAGGTTTTATACACCTGAAAGAAGAG
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SEQ ID NO: 3654 ACGCGGGACCGAATAGAATCGAATGGAACAATCATCGAATGGACTCAAATG
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SEQ ID NO: 3655 ACGCGGGGAATCTGCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCCAAAT
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SEQ ID NO: 3656 ACGCGGGGGACACAAAGGACTCTCGACCCAACTGCCCCAGACCTCTCCAG
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SEQ ID NO: 3658 ACAAACATGTGGCAGGTAAACATCAGGCATAAAAAGGACAAATACTGAAA
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SEQ ID NO: 3659 ACGCGGGGTGTCATGGCCGGCTCCTACCCTGAAGGTGCACCTGCAGTCCTC
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SEQ ID NO: 3661 ACAGTCTTTCATTAAATAAGAATACTTACACATACATTTTCAGATATTTCTAC
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SEQ ID NO: 3662 ACCACCCTGAGTTCCTGTCCAGGCCTATCAAGCCCTCCCCACCATACTTTGGC
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SEQ ID NO: 3663 ACTTTTTTTTTTTTTTTTTTNTGGGAATGAGAAAATAACTTTATTTCATTGNGGGG
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SEQ ID NO: 3664 ACAAATATCCCCACTTCCCTTGAGAAAGAGTATATCTAAAATACACTTTGAT
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SEQ ID NO: 3665 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 3666 TTCGGCCGAGGTACGCGGGGGAGGGTTCCAACCTTTCTGCTTATCTGGGAGGT
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SEQ ID NO: 3667 CGTNCGCGGGGACGCTGAGGGGTCCGAGGAGACCGTGAGGCTNTGGCCTG
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SEQ ID NO: 3668 ACAAATAAAATCAAAAAGGGCAGTGTTCTGTTGTATTCTTCTGCATGTATA
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SEQ ID NO: 3669 ACTCTTGATGAAAGACCGTGAAACCAACAAATCAAGAGGATTTGCTTTTGT
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SEQ ID NO: 3671 ACCCTTGGAAGATGGGAAGGTGAGGGAAATATTTGAAGCAGGGTCAGAAC
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SEQ ID NO: 3672 ACAATACAGAAATGCTGATGTCTGAGCTGAGTCCTGAAGACCAGAGAGTATT
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SEQ ID NO: 3675 ACTCCCTGTCGTCAAAGTGCTTCCCTCTGGTAAATACACGGGTGCCAACTTAA
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SEQ ID NO: 3697 ACACTTGAAACCAAATTTCTAAAACCTGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3703 ACAAAGCATTCTGCTTCCAAGAGAAATATCATTGCTACAAAAAACTGGCAC
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SEQ ID NO: 3705 ACGCACCTGGGNTNAAAAATGCAGGCGATTCTGAGGACGCCATCCCTGAGGA
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SEQ ID NO: 3706 ACCTGTATTGGGGAAACATAGCATACAAGCAAGAAGCTTACAGCCTCAGTGG
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SEQ ID NO: 3707 ACGCACCTGGGGTCCAAATGCAGGCGATTCTGAGGACGCCATCCCTGAGGA
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SEQ ID NO: 3708 ACGCGGGGGGAGCCAGGGCCGGAAGTAGAGCGGAGGTGGTGGCGGCGGAGG
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SEQ ID NO: 3710 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 3712 ACTTGCTGGTCTCAAATTTCCACAAGGAGATATCAATGGTGATACCACGTTC
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SEQ ID NO: 3713 ACACAATGTGCTTCCTTGTATTATAACACATTTCAAATAGGGACCTTTG
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SEQ ID NO: 3718 ACAGAAAGTAAAAATGCTGTTACAATCTCAGTGTAAGTGGTAGCCACAGACG
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SEQ ID NO: 3719 ACTCCAAGCTGCAGGATTTCTAACTGGGGCAATTGTGGTTGGATTTCATCCC
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SEQ ID NO: 3721 ACCACGAAGTCAATACTTCTCAGTGAGTAGGGAAGGCAAAATACTTCTCAA
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SEQ ID NO: 3724 ACTGAGACCTATTGGAGCTTGTGGCCAGCATCCCATCTGCACCGTTGGTCAGG
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SEQ ID NO: 3725 ACGCGGGGTGGCGATGGATATGTGGTTCATCTGGCCCTCCAAGTGAGGTC
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SEQ ID NO: 3726 ACTTTTAATGGAAACAACTTGACCAAAAAATTTGTACAGAATTTTGAGACCC
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SEQ ID NO: 3727 ACGCGGGGATATTGGAGCAGCAAGAGGCTGGGAAGCCATCACTTACCTTGCA
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SEQ ID NO: 3728 ACTTCCTGTTCTGGCTTCCAGAAAGTGACCTCAGCTTCATTCCGGTCTTCTGGT
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SEQ ID NO: 3730 ACCACCTCAGGTGTTTGTGCTCTTCTTTCAGGTTCTCTACTTCTTCTCAGAC
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SEQ ID NO: 3731 GTCGGCCGAGGTACCAAGAAAAGGGTGTCCGTTGCTAGAGAACTTGGTGTG
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SEQ ID NO: 3732 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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CAANT

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SEQ ID NO: 3734 ACATAGACAAGTTTCTTGTAAAGACAGAAAAACAGAGAAATCCACAGTAACTCT
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SEQ ID NO: 3736 ACGCGGGATCCCAAGTCCAGCGTGAAGGGCCACAGCCCCTCTTGGCTGCCAA
GCACGCAGATCCCATGGACATTTGGGGAAGGGCTCCTTGGGCTGCTGGTGAACCTCTGTGGCCA
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SEQ ID NO: 3737 ACAGCGGGGGCTTTTGTGTGTCCCTGGCCATGGCGCTGCAGCTCTCCCGGG
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AATTGGTTATACAAGTGTNAGNTCANAAACCTGGTTGTANTTATCTCAAAATTGAAAGTAGGTG
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SEQ ID NO: 3738 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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NTTCAAGCTTNTACACCCTTNTGCCCTCTTTCATTGGCTGCNCCNCCANCCAGCCTCTCAACTCT
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SEQ ID NO: 3739 ACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGG
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SEQ ID NO: 3740 ACCATTGGTGGTGGTATCTTTCAAGCAATCAAAGGTTTTGCGAATTCTCCAGT
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CTGGTATCTTGTGACAAGATTGCCCTCTGCACAANTTTCCCCAATGGTCTCANTTTGCAAAAAA
NCCCTCCAGTTGCCCTCAACTCANTTACCTTCTCACCTTTTGGAACTANTCGACAATNTCAGT
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SEQ ID NO: 3741 ACAATTCCTTGTTTTCAAGGGTAAGTTCCAAGACTTCCAGACTCAGGTTTGAA
GTCAGGTCCTGGTGAAGGTCGTCATGCTGTTGTGATAGCGTTTAGGTCCTNCATTAGTCCTTCCAG
GTGGGCCATCTCTTGGTCAGCTCATCTGGTTCATANCTACTCTCNGAGTCTTNCACATCATGTGG
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CCCNNTGGAATGCTTGTCTTANNCTAGANCTGAANTGTGNATGGANCNCAACCTTGCTGGGACAA
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SEQ ID NO: 3742 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGNCANCTATTTAATTAGGTTCT
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NCCCTTTTCCCCNGTGGCG

SEQ ID NO: 3743 ACTGTATTTATTTCTTATTTTATACAACTCTTACTCTTTACAAAAATGGTTATA
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ANCAGGCTTGGAGTTCTACAGCAGATTCTTCTTCTCTGGACTCTGAATCGCTTTCAGAATCATCTG
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SEQ ID NO: 3744 ACTGGAGATGTATTTGATAACCAAGGTTTTAGGTAAATTTTACCAGTATTAG
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SEQ ID NO: 3745 ACACGAGAAGCTCCGAGGATGGCTGAAGTCCAACGTCTCTGATGCGGTGGCT
CANAGCACCCGTATCATTTATGGAGGCTCTGTGACTGGGGCAACCTGCAAGGAGCTGGCCAGCCA
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AANCCCACTAACTGCCCTTCCCTGCATATGCTTCTGATGGTGTCTGCTCCTTCTGTGGCCTC
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AAAAACCANTCCTCTTCTTCTNAANCNGNNGAGGCCAANAATCCCNTAAAAAAGGCNAGGAAN
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SEQ ID NO: 3746 ACTTTGTTTGTGATACAAGGTGAGCCAAAGGGTGGTGAAGAAGACACACN
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SEQ ID NO: 3747 ACTTTCTTTTTTTTTTTTTTTTTTGTGTTGTCCAGATTTATTGAAAATAATA
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TNCTGGGGGAATATNGCGAATNTCCTTCNNNAACNCCCTTGTTCNNNTGNAATTTANTTGCCCA
AGCCCCCTGTANTANCCTTGGGCCCGGAACCCCCCNTATGGGNGNAATTTCA

SEQ ID NO: 3748 ACTGGCCAGGAAGGTGGAGTAGGTTTCAGGCCCTGGGGATTTCAAGTGCAGA
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ACTTTCAG

SEQ ID NO: 3749 ACGCGGGGGTGCCAGGCGATCTTCTGGAGGGTCATTAGCAGCATTGAGCAG
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GCTGATCTCCNNTTTGCTGNAANACAACCTCACCCCTTGGACGANCGACCAGNAGGATTAAGANG
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SEQ ID NO: 3750 ACGCGGGGGCATCCTANCCGCCGACTCACACAAGGCANGTGGGTGAGGAAA
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SEQ ID NO: 3751 ACACCTGAAACCAAATTTCTAAACTGTGTTTTCTTAAAAAATAGTTGTTGTA
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SEQ ID NO: 3752 ACTATAAGANTAAAGAAAATTGTGTTGTGGATAACATCAAAGTGTGCAGTAA
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GACNTGCCNTTTTACTTGANAGTGGGATGGTCCCGACTTTCTGTTNAATCCNANTGGTTTTNCATC
ACTNGAGTNACCATTGCNATGTAA

SEQ ID NO: 3753 ACTCATTCCTCTTCAAGAGCACCACTGGAAACATCTTTGGAATTGATGGGACA
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SEQ ID NO: 3754 ACGCGGGGAATCATCGAATGGAATGGAATGGAACAGTCAATGAACTCGAA
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SEQ ID NO: 3755 ACAGATGCAGCCGTGCAGGAGCCGAGCCAATTAATTTTATTAGAGGAAGAAA
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SEQ ID NO: 3756 ACGCTGGCAGGGCCAGTGGCAGGAAGGGAGGGACAAGTGGACAGTGGTGTG
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SEQ ID NO: 3757 ACTTCTTGCCCTGTGAGAATTTCTGAGGTTTTCTTTCTGAGTCTGGNTAATAA
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CTCCTGNTTCTNTTNCCTGCGAAGGATCTTNANCCTNGATCTTAGCNNTTGCTAGNTCAAGCCTN

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SEQ ID NO: 3758 ACTAAAAATTTAAACGTCACCTTGGTGTCTTTTCAAGACTAAGTGTGATAC
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SEQ ID NO: 3759 ACGCTTTGCCAGTGTGGCTGGGTCCACCTGCATCTAGAGAAAAAGAAAACAC
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SEQ ID NO: 3760 CATCCTNCTATTGATATTANCTANTGTCTAATTAAGCCNTANCANACAGTAANGC
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SEQ ID NO: 3761 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAAAATCACTCCTTTGTCTTTATTA
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SEQ ID NO: 3762 ACCCTTTGGATTTCAAACAGTAACATCGGATGTAAACAAACTTAGTTCCCTTT
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AGGTGGA

SEQ ID NO: 3763 ACCTTCTGGGGCATACAACATGGCAGCAGGGCCTTGGGAAGAGGGGTNGGA
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GGGTTGTCCNTGAACAGAAAGGGCAGGTGGGAGAGGTTCCCTNTGNTACTTAANANAAGGCACCACT
TNGCATAGAGCNCAATGNACAGGATGATGATNNATAACAATCCACNGATAANGGACAATNTCTT
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SEQ ID NO: 3764 ACCANATACTTGCATGTAGAAGGAGGTAATTTTCATGCCAGTTCACAGCAGT
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ATGGCTACATCCATTATGGACAAACAGTCAAACCTGTGTGCTCAGTTACTGGCATGGCACTCCCAA

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TTC

SEQ ID NO: 3766 ACGCGGGGGCGGNCGGCGTGTGTTGAAAGCGAGGCCAAAGTGGGTGGGAGCG
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SEQ ID NO: 3767 ACGCGGGGGCTGACTCTCTTTTCGGACTCAGCCCGCCTGCACCCANGTGAAA
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SEQ ID NO: 3768 ACGCGGGGGAAAAATGGAGGTATGAATTTGGGGTAAGAGGAAGTGAGATCTC
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SEQ ID NO: 3769 ACACTCCCATAATTTTAATAATATTTTAGGCAAGTCCATGACAATTATACCA
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TACACATCGGAGGCTGGGGTGAGAAAGTGCNCANGATAACCCCNCANCAATTGAACATTTCATTT
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SEQ ID NO: 3770 ACGCGGGGAGGCCCCAGCCAGCTCAGGCTACACTATCCAGGATCAGCATGG
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SEQ ID NO: 3771 ACCGGCTTCTTCTCTGGGGTAGGGGTAGCCTCGCCCGGAAGCAAGGCCTCTG
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SEQ ID NO: 3772 ACCTCATAGTCAATNTNATNTNTNGCCGCGTTTANATGATNTAANGCANGAC
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SEQ ID NO: 3773 ACGCGGGGCTTTTGTCTGCGGCCACGCGCGCTGCGGTGCTCAGGAACAGCC
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SEQ ID NO: 3774 ACCAGGTGTTAGCTGTGACCTTCAATGACACAAGTGATCANATTATTTCTGGT
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SEQ ID NO: 3775 ACCACCTGAGTTCCTGTCCAGGCCTATCAAGCCCTCCCCACCATACTTTGGC
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SEQ ID NO: 3778 ACACCAACAGCAGGTACACATTAACAGTTGTAACCTAAGCACTGTGACAAAT
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GGGC

SEQ ID NO: 3780 GTACACGCTTTTGGCCCCNACCAATGAGGCCTTCGANAAGATCCCTANTGAG
ACTTTGAACCGTATCCTGGGCGACCCAGCAANCCCTGANAGACCTGCTGAACAACCACATCTTGA
AGTCANCTATGTGTGCTGAANCCATCGTTGCGNGCTGTCTGNANAGACCCCTGGAGGGCAGCACA
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SEQ ID NO: 3781 ANTGANTCTCNGCAAANAAAAATCTTGCANAGTCTCCAAACCAACAGCTGGT
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SEQ ID NO: 3782 ACTCCAATATCTTTGTTACCTCCCCAAGCCCTGATAACCTCCATACTCTGTTTG
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SEQ ID NO: 3783 ACTGATTAAATCAGTATAAAATCGAAAGAGCTTTAGATCTGTAATAAAAAATC
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SEQ ID NO: 3784 ACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACTCACTGAA
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SEQ ID NO: 3785 ACTCCCTGTCGTCAAAGTGCTTCCCTCTGGTAAATACACGGGTGCCAACTTAA
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SEQ ID NO: 3786 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 3787 ACTTTTAAATCATGTTCCTTAAACATGGCTGTTAACCCACTGCATGCAGA
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SEQ ID NO: 3788 GNACTTGGCCANGCGCTCANATCGGCAAGGGGCACCAGNCTTGATCTGCCNA
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SEQ ID NO: 3790 ACAGGGTTTTATCAGTCCACCTTCCCTCCAAGGAGATAAAATAAATGAAATC
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SEQ ID NO: 3792 GGTACGTTTCATGACCAAAATTTATCATCCTAATGTAGACAAGTTGGGAAGA
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SEQ ID NO: 3794 GGTACAGCTGACTATCCAACATGATTCCCTATGGAAAACAGAAGGGGCAGAGTC
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SEQ ID NO: 3797 ACGCGGGGGTCTTCGCTGGACACCATGAATCACACTGTCCAAACCTTCTTCT
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ACGC

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SEQ ID NO: 3803 GGTACGCGGGGGCTCTCTGCTCCTCTGTTTCGACAGTCAGCCGATCTTCTTT
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SEQ ID NO: 3804 ACGCGGGATGACAGGGAACAGGTTAAGAAAATATGTAAATGTAGGAAAGA
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SEQ ID NO: 3805 ACCAAGCTGTTGGTGAAGTCCCCAGGCCAACAGGGACACATTAGCTTTCTCCT
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SEQ ID NO: 3806 ACCCTATGAACCTGACTCTGTGGTCATGGCAGAAAGCTCCTCCTGGGGTAGAG
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SEQ ID NO: 3807 ACAACACAAAACTAATTGAAAATTCTCTCCACCTTTCCCAATCAACCACTG
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SEQ ID NO: 3809 ACAAGTATTTATATCAATGAAAATTTCCATTGGTGATTTTTTGGCAGAAATATT
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SEQ ID NO: 3810 ACGCGGGGTTTTGACCAATCCAGTGTGCACAGAGGTAGGAGAAAAAATTGCC
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SEQ ID NO: 3811 GGTACACAAGCTTTGAGGAAGTGCAAAGGACTGACCTCTAGGCCAGAACAA
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SEQ ID NO: 3812 ACGCGGGGCTTTCAACCTTGTCAACCCGTCGGCGCGGCCTCTGGTGCAGCGG
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SEQ ID NO: 3813 ACGCGGGCCAGAATCTCTGGGACACATTTAAAGCAGTGTGGAGAGGGAAATT
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SEQ ID NO: 3814 ACGCGGGGGAGCTCCAGAGGTCTACCCAGAAGGACCCAGTTTCTTACCAGC
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SEQ ID NO: 3815 GGTACTGGAGTTGAAAGAGAAGTGAAGATCACCTAGTTCAGAGACTAACGGGA
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SEQ ID NO: 3816 ACCTGTGGAGCGAAGGAGAGGTTGTCTATCTGGGCCCCGTGTTTACCAGTCAA
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SEQ ID NO: 3817 ACCCATGATTTGGACACTTTGTGCGGGCCATTACTTATACTGCAAAGCGTCC
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SEQ ID NO: 3822 AACTAACAATTTGGATAACTCGGAAAGATGGATTAATTCCTACAAACATAT
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SEQ ID NO: 3824 GGTACAGTATGGGGGTGTAAATTGGCATGGAAATTTAAAGCAGGTTCTTGT
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SEQ ID NO: 3825 GGTACACATANTGCTTCTGCCACATGATAACGAGCGCGGTGAAACCGATGAA
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SEQ ID NO: 3827 GGTACAGCGTCCTCGAAACCACNAGCAAGTGAGCAGATCCTCCGAGGCACCA
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SEQ ID NO: 3828 ACCCAAATGCTACCACTGGAGAAGGAATGAGAGATAAAGAAAGAGACAGGT
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SEQ ID NO: 3830 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATGTTTCTTTGGTTTTATTATTACA
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SEQ ID NO: 3832 ACTAAGTTGTAGCAACCACGTGTCCGTGCAGTGCCACAGGAGCTAGAGCAGT
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SEQ ID NO: 3834 GGTACACCATATAAACAGCAGATGAAGTCGGAGAGATAGTCTAATACACTTA
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SEQ ID NO: 3835 ACCGCGCTTGGCGGTAGCTGGCCCCAGACTTCTGTCTTTTCAGCTGCAGTGAA
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SEQ ID NO: 3836 ACTTGTTGACTAGAGTTCACCTCTAGGGTGATCTATCTGTGTCATTTGCTGGGG
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SEQ ID NO: 3837 GGTACTACTTCTCCAAACTCATAGAATTTATGGACACTTCTTCTTCTCATCCTGC
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SEQ ID NO: 3838 ACTCCTTCTGAACTGCCTCCAGGTCAGCCCCTGCCACGGCTGGATGTCTTCC
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SEQ ID NO: 3839 GGTACATGTCACATATATAGTCAATGTAAAGCAATTCTACTTTGCATCCCTTA
GCCACAGGCATAAGGCAGAACACAGATATTTCTGTGTTCTGTGAATATCTGTGGAATGATACTTGA
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GGGATACAGGGTCACTTGCAGTATTCTCTAGCCATCTGCCAAGAACTACTTTGAAATTATACCCAT
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SEQ ID NO: 3840 ACACTGGCTGTCCACAAGGCCGCACCTCACAAATCCGGGTTTCTTTCACAAG
GCGGCACTCAGGGTTGTCATTGGTAACTCGTGTGGAGATACCAGTTCACAGGTCTTTGAGCACTG
GGACCATGAAGTTGTTTGAACAATACATTTCTGGCCTTGTAAGGGTTGTATAGGATGCGAGGCTC
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GGGGTCTTGATACTATCCTCGTCACAGACCCACTCCTCGCAGCACTGCCCGTAACTTTGACCAG
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SEQ ID NO: 3841 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGNATATAAACTATTTATTAAC
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CTTGCCATTTCTTGATCAGCTGGACCCCTACACACTTCCTAATGGGCAGAATTTGGGCTGTTTGGCTT
CAACTCCTAATTTTCCAGCACGATTNCTTTTGCAATTGAAAAGCACCCCTTCAAAAAGGGTTGGCCC
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SEQ ID NO: 3842 ACTTTTTTTTTTTTTTTTTTTTTTTTGAANAATCAGAATTTATTTCACTATGTG
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SEQ ID NO: 3843 GGTCGGCCGAGGTACTTTTTTTTTTTTTTTAATGTTGCACTTGTAGTTTCATT
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TGTCAGTCACATGATGATTATGTTTTTGTTTAA

SEQ ID NO: 3844 ACTCTGCCAGGCATTTAACATACATTATTTCACTTGTTTTCATGATTAAATTCA
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TGATCATCTTCTGAAATTCTTAAAAAGCA

SEQ ID NO: 3845 GGTACGCGGGGCTTGCGGTGCTGGGCAGCAGACCGTCCAAACCGACACGCGT
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SEQ ID NO: 3846 GGTACTTGACAGGAAGTGTGGCGCTTGTTGCATTGTTGCTGCTCCAAGTT
AAAAAGTTGTTATTGGAGCTCATCTCAGCACAGTGTGTTTCCACCCATGGACTTGCCAGACCAG
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SEQ ID NO: 3847 ACATAATCGTTTTGTGGAGTCGGCACAGTTCAGGTTATGGAGGCACGTAATTC
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SEQ ID NO: 3848 GGTACTCTGTGAAGAACAGAAATGATCATATTCTTATGCATCTATCTGTATGG
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SEQ ID NO: 3850 GGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTA
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SEQ ID NO: 3851 ACTGTTGTCCATTTTCATGAGAGTAGGCTTGAGGACACCATGGGCAAGGATCT
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SEQ ID NO: 3852 ACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGTGCT
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SEQ ID NO: 3853 ACATCCAAAACCATAAGGAAATATTCTGATGCCAGATGATGAAGACTGGGG
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SEQ ID NO: 3854 GGTACCTGCTACTTTTATGCTTGTGTCTTTAGATGAAGGTCCAGGTCCCTCCAA
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SEQ ID NO: 3855 ACACCTGTGAATTCAGAGGATTGAGATACCAGACAAACTTCCCATTTACAAG
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SEQ ID NO: 3856 GGTACTTGCCCTTCCCCAGAAAAGCGGGACTTGCTGCTAAGGGTGAAGGAC
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SEQ ID NO: 3857 ACGCGGGGCTCTCTGCGGGGCTCACTCTGCGCTTCAACATGGCTTTCATTGCC
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SEQ ID NO: 3858 ACGCGGGGTCTTCTGCGGCTGAACCGCCCGGCTGAGCCGACATTGCCGGCG
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SEQ ID NO: 3860 ACTTTTTTTTTTTTTTTTTTTTTTGGGCATTACTTTTTATTTGAAAGATTGT
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SEQ ID NO: 3861 GGTACTTGCTTTTGTAGCTGTTTTTTGTAGGACATGTGATCATCTTAGATGTT
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SEQ ID NO: 3862 ACACCGTGGGCACCAAATACCGCAGCGAGTCCTATACGTGGTTCCTCTTCATC
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SEQ ID NO: 3863 GGTACTGGGGGTGGAGGGGTCCCCTCTTGCAGTGTGGGGTTACTGTTTGGGT
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SEQ ID NO: 3864 ACGCGGGGGCCCCATCCATGGACTCTTGCCCTCGGTGCAGTTTCCACTCTTGAC
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SEQ ID NO: 3865 GGTACAACCAGCCAGATTCCAAGCGGCGCCAGACCAATAATCAGAACTGGG
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SEQ ID NO: 3867 ACGGCAGCCACGAGGATGCGATGTATGGGACAAAACCTGGAGACCATCCGGA
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SEQ ID NO: 3871 ACCAGGGCGGCGCGTGGTCTACGCCGAGTGACAGAGACGCTCAGGCTGTGTT
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SEQ ID NO: 3872 ACGCGGGGAAGTCAGTTTCAAAGGGCTGACCCTTGGCCTATTATGTTTCTGA
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SEQ ID NO: 3873 ACATGAAATTTTGCAATACTACATTCACTTTATTGTTCTTGTGTTTTGCATTTA
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SEQ ID NO: 3874 GGTACTTTTTTTTTTTTTTTTTTTTTTTCATGTTNGATGTTCCAAGATGAC
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SEQ ID NO: 3875 ACGCGGGGTCTCGCGAGATCCCTACTGGCTATAAAGGCAGCGCCCCGGAGAG
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SEQ ID NO: 3876 ACGCGGGTATAGGATTCTGTGTCGCGTGGTGGCCGAAAACGCCAGTTCTCT
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SEQ ID NO: 3879 GGTTCTTTTCTATGTTTAGATACACAAATACCATTGTTAAAAATTACCTACTGT
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SEQ ID NO: 3883 CTCGGTCAAGTCTGCACGAGACAGCTTCTCTGACATTCTCACTGGGCCCCCTCCA
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SEQ ID NO: 3884 CCCGATGTTGCGGACAGTATGAGGCAAGCGCAGGGGGACGGGGACCAGCA
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SEQ ID NO: 3886 GGTACTACACTGAAGACAGGTTGCTCACATACTCTAAAGCACATTCTTGATAC
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SEQ ID NO: 3887 GCGTGGNCNCGGCCGANGTTNNCNGGATCGANATGAAGGTNCAAGACCNGA
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SEQ ID NO: 3888 ACTTTTTTTTTTTTTTTTTTTTTTTTGACCACACCTGCCCTTTATTGGTCTCTCT
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SEQ ID NO: 3889 GGACTTTTAATCACTTACTGAGAATATTTCAAATTTATATTCTCATCAGGAAA
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SEQ ID NO: 3890 ACTTGGGGAAGCCATCTCTATCATTTTTTCTTGTAATCTTTTCGGGTCCATGC
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SEQ ID NO: 3892 ACTGTGCATTTCTCTACTTGCATGGCCAATAAATACAGCTACGACCTGTTTG
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SEQ ID NO: 3895 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTNGGAAATNG
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SEQ ID NO: 3896 GGTACTGTCTGTCTTTCACATTTCATATCCAGATTTATATTTTCTGGAGTTAAAT
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TTTTAGGTCG

SEQ ID NO: 3899 TACAAATATTTAAGAGTGTGATTGGGAGTAAGGGAATGTCAACTGCCAATA
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SEQ ID NO: 3900 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGAANAATGTCATTGGTATTTTT
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SEQ ID NO: 3901 ACATGGCCGCGCTCCTGGAATACCTGACAGCGGAGATTCTGGAGCTGGCTGG
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SEQ ID NO: 3902 GGTNCTTTCCTGCCTTTTAGTTCCTGTGCACAGCCCTAAGTCAACTTAGCATT
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SEQ ID NO: 3903 GGNACAGTGATTGGCTATAGACTCTCGCCCTTCAGGGCANACTGTCCTCAG
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SEQ ID NO: 3904 GGTACTTCTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTTTTTTTTTTTTTTT
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SEQ ID NO: 3905 GGTACACTGCCAGGCAAAGCGTCCGGGCAGCGTAGGCGGGCGACTTAGATC
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SEQ ID NO: 3906 ACTTTTTTTTTTTTTTTTTTTTTTTCAGNCTTGATGTGTGATCTTTATTTGTA
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SEQ ID NO: 3907 ACACAGAGTAAAATGTTTTTCTTTTTTTCAGGACCTTGAACCTGAATCTTGCAC
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SEQ ID NO: 3908 GGTACTTTTTTTTTTTTTTTTTTTCATANAAAGGAGGAAAATATTTATT
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SEQ ID NO: 3910 GGTNCCATCTGCGCCATCTGGAGAACTACCAGACAGAGAAGGGCATCACTG
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SEQ ID NO: 3911 ACACAAAGAGGGGGTGGGTGTCCGATGCAGAGTGTGTGGCCTGATGCTCCAC
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SEQ ID NO: 3912 ACCTTTGGGGCATGGGGGCATTACATGGGATGCTTGTGTAATCGACCACCTA
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SEQ ID NO: 3914 GGTACAAAATTCAAATACCAACAAAACCTGATCTGTGATGATAGAAAGCATAT
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SEQ ID NO: 3915 ACAGTGTTCCAGCCATCCTGCTGTTTTTCCCTCCAATACCTCCAGAACAG
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SEQ ID NO: 3916 GGTACTTGGGATCCCCAGTTCCAAAGTGTCTTAAAGTGTGCACTTCTCCAC
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SEQ ID NO: 3919 ACATCTTCCAGAACGTAATGGTCATGATCCTGGTCTGGACACCAAGATCTTG
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SEQ ID NO: 3920 GGACCTCTGGACCCACTCCTGCTTGGGGTCGCCACAGAAGCTGCTGGCCCTTCT
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SEQ ID NO: 3921 ACTTTTTTTTTTTTTTTTTTTTTTGGGGAAACCATGATTTTATTAATTTTATA
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SEQ ID NO: 3922 CTTAGCNTGGTGC GCGCGCCGNGGNC GCGGGTATCANANCCATGCGNAGAGT
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SEQ ID NO: 3923 GGTACGCGAAGGATATCGGTTTCATTAAGTTGGACTAAATGCTCTTCCTTCAG
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SEQ ID NO: 3924 ACAAAGCTAAAGAAAAATTGTGGTCATTGATGATGGAATATATGACTTGCAG
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ATAAAGCCAACCTTTGATTAAAAACCACTNGTTTTCAAAGCTCAAGTCTTTGATTTTGAAGAAGAAC
CAAGATATCCCCCTATGATCCTACCATCTATTTTANGNCTTTTGGACCATTCTTGACAGCTTNCAG
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SEQ ID NO: 3930 ACATCTCCGCTGCAGATCGTTTCACACCTGCTTTTCCTCGGTTCACCTTNTGGCT
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CCAATGAATACACGGGAGTTCATGGAGCGAGGATCTGTCTTGTGGTAACGTTGCTGGCCATCGTG
TTTGATGGTAAGGTTTCTCACAAGCCCGAAAATGTAAGTGAAGATCAAAAAAATCTNACAAGAA
GGGGAGGGGAGAAGAGATTNGNTTCTGAGTCTNCTACTCCCCGGGTCTGCNTNAAAAAACCTCT
GCTGGTTGGAGGCCGNAACGGGCCCAACGGTTANNTTTTNGCNTTTTAAAAAANTNCCCGGG
NCCTTNTTTTNTTTNTTNTCTTTTAAAAAACAGG

SEQ ID NO: 3931 GGTACTTTTTTTTTTTTTTTTTTTTTTGGTCACTAAATTTATTTTAAAAATCATA
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SEQ ID NO: 3932 GGTACACCCCAACCCCAACCTCAGTGGAACAATGCCAGGGATTAGGCT
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ATGTCCTTAGCTGGTGGGGGAAAGGTTGGCGATCAGGAATACATATGTGTAGTTTTTGTAGAAAGC
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AACAAAAACAAAAAACAAGAGTAGAAAAATTTATGCTAAAAAAGATTTCGAATGAAACAA
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SEQ ID NO: 3933 GGACAGACTGTTTTCCGGATGGACTGGTTTGGGAACACTGTGCTGGGGGAAG
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ATGTCAACTCTACATTGGAGGAGGCAAAACACAATCTAGAGGCACTGTCTGAACTTTCCCTGGCC
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AGCGGGAGAGGACCACGGGTGAGGATCCTGTACCACCAAGCCTGAACAGACAGTCCCATCTTTGT
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SEQ ID NO: 3934 GGTACTTTTTTTTTTTTTTTTTTTTTTAACTTTCAATCTTTTATTTAAATGC
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SEQ ID NO: 3935 ACCTGTGAACCAAGTGTGTTGGGCAGGATGAGATGATCGACGTCATCGGGGTG
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TTCCAAATTTNGGCCATGGGCGGTTTCAAAACATGGANGAAAAA

SEQ ID NO: 3936 ACAAGCTGAGTATCCCTTATCCAAAATGCTAGGGACCAGAAAGTGTGTTGGAT
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SEQ ID NO: 3937 GGTACAGATATCTTCAAAGGAGGAAGAAGAAAGGGAAGCAGATGGTGGAG
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CACTCTCATGAGNGCAACTGTGGCTTACCTAATATTGCAATGNGGTTTGAATGTAGGTAGCATCCT
TTGANGCTTCTTTGAACTNGTATGAATTTGGGTNTGAACAGATNGCCTGCTTTCCCTTAAATAAC
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CTTANAAAGGGTTTTNTATATTGNTNCTTTTGA AAAACC

SEQ ID NO: 3938 GGTACATTTAAGAATAAACTTTTGTAAGAAAAAGAAAAATCTTACAGTGGCTC
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TCATCCCAATGAAGAAAAAGTCTANGNCATCAACACCTTTTATCACCCCTCCTTGANCCTGGTNANCC
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SEQ ID NO: 3939 ACATCAGCAGCAAACCTCCTGTGCATCCCGGTAATCACGGTTCTCCATCTTCCG
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AAAATGCCATTGCAATGTTTAACTGTTCTGAAAGCTTTCTTTCTTANAGCTCTGGTGTGTTGCT
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SEQ ID NO: 3940 ACTGTCTATATTGCAAAAGTCTTGATTGAGGTGGTGGCATTTACAGTAGTTC
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CTGTGGCCCTTCTTTGCACCATGGGAAGGGGCTTCTTCTCCGAATTACAAGCTTTTTCGAAGAAG
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SEQ ID NO: 3941 ACTGCATGTTCTGTTGTGGTGAGGGAAAGAAACATGCTTTGAAGGTTTCCCT
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CCTTTCANAAATCCTCAGGTTGGGAAGACCCACACCTTCTTTAAGGATCATTGTCTCGCCATC
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GGCATCTGTNCCCGAAGGCGCCGACCTTTTAACCGGAACTTTCCCAACTANGGAATGGGANC
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SEQ ID NO: 3942 TGTACGCGGGGCTTTTTCTAACTCCGCTGCCGCCATGGCTCCTGTGAAAAAG
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SEQ ID NO: 3943 GGTACAGAGAAGCACCTATTGACAAAAAGGGGAATTTCAATTACATCGAGTT
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CTANAACACTGGCTTNGGNTNGATTAATGAATNCCCTGGTTTNGCCANANAATANGAACNCCAT
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SEQ ID NO: 3944 GGTACTTTTTTTTTTTTTTTTTTTTTTCTGGAAAAGTGACTGCTTTAATG
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SEQ ID NO: 3945 GGTACGTGCAGACGGTGGTAGTTCTGGAGTCTGGAAGCCACGAGGTGCTCA
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CCGCGT

SEQ ID NO: 3946 GGTACAAAAACAACAAAGGTTCAAAACATCGAGATGTTCCCTTAGCAAGGCT
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SEQ ID NO: 3947 ACCAAATGTCACACTGGCTGTAATCAAATCGCCCAAGAATAGTCACATTAGA
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SEQ ID NO: 3948 GGTACCTTCAGTCTACACTTAAATCCCCTGAGTTAACTTGCAGCTCACAGCT
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SEQ ID NO: 3949 GGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGA
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SEQ ID NO: 3950 ACAATAGAGTTAGAGCCAAGGTCTAGAGGCGGATAGGTGGATTCTTGAGGG
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SEQ ID NO: 3951 CGAGGTACGCGGGGCTTGCAAGCAAGAGTGCTGGAGGGCGGCAGCGCGAC
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SEQ ID NO: 3952 GGTACGAAAAGCGGCAGAACTAGCTCTGAAAACCTGAGCAAGGTCTGTGTG
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SEQ ID NO: 3953 GGTACGAGATGGCAGCCCTCCAGAGCCCCTTCTATGGAGATAAGATGAATCT
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SEQ ID NO: 3954 ACGCGGGAGCTCATGTAGGTCTTGATTGGACACAGTGAGTTTCAGATGACAG
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SEQ ID NO: 3955 ACAGACAGGCCTCTCTGCTATCCTCCAGGCAGTGTAAATAGTCAAGGAAAAGG
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SEQ ID NO: 3956 ACNNGGGGGCNGCCGAGGCGTGACATGCTCGCCCAGCCACCCCCAGGACG
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SEQ ID NO: 3957 ACTTTTTTTTTTTTTTTTTTTTTTTTGGCAAAGTGCTTTATTTACACAGAGC
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ATTATTGGCANNACTTGCNNTTGCNCCCTGGATTGGACACTGNTTTTCTTGGCCCCACCTTTG
GGGGCNCANCCCCAANANTGAGGGAAATTTTTTGAAGGCCANAGGAGCNCNTCCAGGNCCTTACA
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SEQ ID NO: 3958 ACGCGGGGGCTGACTCTCTTTTCAGACTCAGCCCACTTGACCCCAAGTGAATT
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CCTANCTGGACGATTAGTNCNTGNNAAGTCTGAACCCCTTAAACTCTACAGCCTCAATGGGACA
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SEQ ID NO: 3959 ACTGNTTACAAACACAGCTACTCTTCTCAAAATAGTCCTTTTCTTTCTTGAG
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GCTTGTTNACTAGCTGCTCCAGGGGGAAGATGGGCAGAGGCCAGAACTGAGGTGCTGTTAGCA
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AGNTCCGNTTCAGGTCCTCATAGGATTGGGGTNCCTCCANTTGAANGGATNNCAANNCAAGAAC
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CGCCTTTGGGATNGGCTTNGANGATTCTNTGTGNAANGGTGCTGTNGCCTTTNTTCTTNTCTG
TGGNNTGTTTACNAANTCACAANAAGATCTGGTNCNTNGANATTTANNTGGACACAANAATCTTT
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SEQ ID NO: 3960 ACGGCACCTGGCGTAAAGCCGCTTCCCTCAAGAGTAACTACAATCTTCCCAT
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TTNTTCCGGCNAAAAAACNAAAAAAAAAAAAAAAAAAGNTCTTTGGCCGGGACCCNTTANGGG
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SEQ ID NO: 3961 ACGCGGGGATTACGAGATTGGCTTGGATTCTGTGCGGATGGACTTGGGGCTAG
CTGCGGCGGGGCTGGAGGAGGCCAGATAACCATGTCAGCCACAGTTGTAGATGCAGTTAATGCTG
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SEQ ID NO: 3962 ACTTTTTT1TTTTTTTTTTTTTGCCGTTTCCACACCTGCCCTTTATTGGTCTCTTCT
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TGTCTTTAAGNAAGCCAAAAAAGAAANNCGTCTNTGCCATTANCTCAAATTTTGGCAAGGGGAAAG
GGGNTNGNTTCCCCCAGACGGAATNTTANATNTAAGATNTC

SEQ ID NO: 3963 GGTACTTCCCAGGAAGTGGGGACCTACGGGATATCGGGGCTGGCAAAGGCAA
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GCCCGTCATGTCCAAAGTAATGGAGATGTTCCAGCCTAGTGCGGTGGTCTTACAGTGTGGCTCAGA
CTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTAACTATCAAAGGACACGCCAAGTGTGTGGA
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SEQ ID NO: 3964 CGAGGTACATTTCCCCGGGAGAACTCGTCCATTGCGGTGGTGGCGGCCGTTATT
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CCCCGCGT

SEQ ID NO: 3965 ACTTGTGACATTAGAGGAGAAATGCCAAGGAATTTAAGAGAATACATGGTT
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TTGGGAGACGCATATAATATGAGGCATCCACTTACTGGTGGAGGAATGACTGTTGCTTTTAAAGAT
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SEQ ID NO: 3966 GGTACATGACAAGGTGCGGCTCCCTAGGCCCTCCCTCTTCAAGGGGTCTA
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CNTTCGACGCTGCTTCAACACCTTCTTGATGTCTATCATATTTGGCAAGGTTTTTCTAAGAANGGCA
GGTCAAGGTCCACCACTTACACGTTGGCAGTGGGGACACCGNAAGGCNATGNCAATGAANCTTNC
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GAAAA

SEQ ID NO: 3967 GGTACTTTTTTTTTTTTTTTTTTTTGGCAAGCACGTGCACTTTATTGAATGACAC
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SEQ ID NO: 3968 GGTACTGCAAGTCAAGGGGACTCTTTGCAGGCGTGTCTTTAGAAGGGAGCTG
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SEQ ID NO: 3969 GGTACACTGTAAATGCTCAATAAATATTGATGATGGGAGGCAGTGAGTCTTG
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TAAATTGGGAAATATTGGCCCTTTTGAATAATTGTCCCAAATATTACATTCAAATAAAGTGCAAT
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CNCNCTGCTGCCTTCTTGGATGNGGNANACGTTTTNAGGCTNCCTTTCCGGAATCNAACCTG
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SEQ ID NO: 3970 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCACCCTCCAGC
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GTCGTCTGGTCCCTGTTCAACACCCTCTTCTGAACCTGGTGTCTGTGGGCTTCATAGCA'TTCGCCT
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ACCGCCAAGTGCCTGAACATCTGGGCCCTGATTCTGGGCATTCTCATGACCATTGGATTCACTCCTT
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GGTTCTAGTAACCGGCCATAACCTTGNAACCTTTGGATTCACTGGGCAANNNTTGNCCCTTGNCT
TGGGT

SEQ ID NO: 3971 ACACTGCCCAGGCAAAGCGTCCGGGCAGCGTAGGCGGGCGACTCAGATCCC
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CAGCCTCCCCCGTTGCCCTCTGGATCCACTGCTTAAATACGGACGAGGACAGGGCCCTGTCTCCT
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ATCCTCCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGGTGAGGATCCCCAGGGAGAT
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SEQ ID NO: 3972 ACCTGCAGGCCTCCTACACTACCTCTCTCTGGGCTTCTATTTGACCGGAT
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CTTTGGAN

SEQ ID NO: 3973 GCCTGTGCAGTGGGACTGATTGCCGTGGGTGTGGGGGCACAGCTTGTCTGA
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SEQ ID NO: 3974 ACGCGGGGAGAGGACGAAAAAATAACCGTCCGCGACGCCGAGACAAACCG
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TCAGCCGCATTTCTGGAGCCTCTGTATCTTCCCATGGCCCAATCTGTGGCTGTGGGCCCTTAG
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TNCTTCANCTTCTGGANGGCCCTCCCAATGCTGGTTAACTTGNAAGCATTGCAGGGGAGCCAACGT
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SEQ ID NO: 3975 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 3976 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCATCAAAAAGCTTTATTTCCAT
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SEQ ID NO: 3977 CGAGGTACGCGGGGAGATGGCAGATGAGATTGCCAAGGCTCAGGTGCTC
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SEQ ID NO: 3978 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTAGTATCGATCTCTTTAATTTTAGGCC
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SEQ ID NO: 3979 GGTACGCGGGCCTTGCTCCTGTGTGCTGTCTAAACCACTGGTGGATGAATACT
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SEQ ID NO: 3980 ACTGTTGTCCATTTTCATGAGAGTAGGCTTGAGGACACCATGGGCAAGGATCT
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SEQ ID NO: 3981 GCGTGTGCGGGCCGAGGTACAAAGAAAGTTTAAAGTCAAGGCCTCACCAATT
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GCTAGCACCTTTGAGTTTTCAAAAAAGCACGTCTCCCCAGTGTGTTCACTGTGATGTGGTGAAA
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GAACAAC

SEQ ID NO: 3982 GGTACGCGGGGGTGGCAGCTTCGGATAAACGCAGGACTCCGCCCGGCAGCCC
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SEQ ID NO: 3983 GCGTGGGTGCGGGCCGAGGTACTGTTTATTAACCAACCAGCTTAGAAAAATA
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SEQ ID NO: 3984 ANTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACCTCACTGAA
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CCGCTCTGCAGGAAGCCTGGTAGCTCCTTCTCCATCAGCACCTTGAGCTCCCCCTTGGTCAGGGTC
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SEQ ID NO: 3985 ACTTGTGACAGGCAGACGTGATTGCAGCCACGAACACGATGAACCTCACTGAA
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SEQ ID NO: 3986 ACCGACGTTGAGGTGGCTGCTGACCTTGGGTCTCATCTCCTTGATTTTCTTTAT
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SEQ ID NO: 3987 GGACGNGGGGTCTCTCTNCGGTCCGTGCCTCCAAGATGANAAAGAAAAGAA
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SEQ ID NO: 3988 GGTACTTTTTTTTTTTTTTTTTTTTTTTTACTTCTTATGGCCAAAAGACCCAGC
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SEQ ID NO: 3989 ACTTTAAGGGAACCTACCCAACTATGTTGTGATAGAAGAAAGAGAAACCTTCA
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SEQ ID NO: 3993 ACGAAAACAGAACCAATCTAAAAATGGCTGATGTTACTTTAGGAGCCTGAAA
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SEQ ID NO: 3994 ACATGGCAATTAGAAGTTGTCATGGCAAAAAGAAAAACACAGCTGGCCCTGCCA
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SEQ ID NO: 3995 ACGGGCTCATGAAAGTGTGTGAAGAGCGAAGACTTTTCGCTCCAGCTTAT
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SEQ ID NO: 3996 GCCGTGGGCGCCGNCAGAGNCCAGACATTTTCAAAGTTGCCAGTGTTACTT
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SEQ ID NO: 3997 TTTTTTTTTTTTTTTTTTTTNTACTTTTTCTTTAGTTTATTGAAAGAAATGTTTA
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SEQ ID NO: 4005 ACTGCTATGAAGCATCCCTTCCACATCAGATCAAAGACATCTTAAAGCCAGA
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SEQ ID NO: 4007 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCACCGTCCAGC
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SEQ ID NO: 4009 ACCATCCTTTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACA
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SEQ ID NO: 4010 ACACTGCCCAGGCAAAGCGTCCGGGCAGCGTAGGCGGGCGACTCAGATCCC
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AACTCAATCCAAATAATTCCACTGCTATGCTGAGAAAAGGAATATTGTGAATCCCATGAAAAAAA
CTATGCTGCTGGCCTAGAAACCTTTACANAAAGACAAAAAATTGATAAGACGGGGTTTATCGGGT
GGCCNAGCTNGCNTTNAACNTTGACTCNAGGGAACCACTTGCTTTGACTCCAAAGTGCTTGGGAT
ANAAGTGCCAAATGCTTATTTNNATGGNTGGGNTNAAAAGNGGNAANAACTTAAATNGNTNT
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SEQ ID NO: 4012 CGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGNTAGGAAGAAGAAT
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AGAGAAAAAATATTTNTGTAAAGGGCCAAATAGGTGTCAGCCGAACTAGACCTAATCTGCCTGG
AACTAAATCCAGATCTAGGCTCTACTTTTATTATTCCATTCTTGCAATGATTGAATGACCTTCTCT
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CCCCACCATGAAANACCATGTCCCTGGCAACCNNTCCCATNACCTTCCCTGGGAGGTTCTCCTNTT
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TGTTGCTGGAACCCAGGANGGAATCTANTTCTGGATTCCAGGAATCCTCNTNCCGGGGTNTTGN
TTTGAAAANNANTAACCTAAGGCTTGTTNGAANNNTANAAGGGANT

SEQ ID NO: 4013 GGTACAAAAGCTTTTCTGATGCTTTTCATTATCACAGAACACACCACCTGTAA
TGTGTGCAAAAAGGAAATGAGGGGTGGAAGGAGAGGAAGTCTAATTGGGAAAGGCTGGATGGTC
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TTTCAATAATGAGTTGAGTATCAAAAAGGACGAAGGCCACATGACCACAGTCCACATCAGGT
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CAGGGCTGACATCAAGATACCTTCCAGAAAGAGGTACTACGGCCCTGGCATAAAGTGCACTTANG
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NAGGCCCCCTGATGAAAGAGNGCNTNTGGCCTAGGCCCTCCNCCCCNA

SEQ ID NO: 4014 ACGTAAAGTTAACCTTCCAATTGTCTGAGCTGTCGTCAGTCTGACTTCATGACAG
TCTGGCCCTCCAGACAAGAGCAGCGCTGGCATCGGGCAGGTGATTCTTGACACCTGCTGCCTGCA
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CGTGCACCTCTGTTTCAAAAACGCAAGCAGAAAATAGGTCTGGACAAGGGCAAGCTGCAACTCA
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ACCTATTCTTCCATTTTATTCTCAATTTGTTCTTGAGGTTCCGAAGTCTTAACGATGTCATGGATNA
ACATCAACAGCAAAGGAAAAAGTAATGGCCAACACAAAAGAACATTGACTTCTTCAACATGGAG
AAAAGGGAANNCTCCNCCACCTGACCNCTA

SEQ ID NO: 4015 ACGCGGGGAAACGACAGGGGAAAGGAGGTCTCACTGAGCACCGTCCCAGCA
TCCGGACACCACAGCGGCCCTTCGCTCCACGAGAAAAACCACTTCTCAAACCTTCACTCAACAC
TTCCTTCCCCAAAGCCAGAAGATGCACAAGGAGGAACATGGGGTGGCTGTGCTGGGGGCACCCCC
CAGCACCATCCTTCCAAGGTCCACCGNGATCAACATNACAGCGAGACCTCCGTGCCCGACCATG
TCGNTTGGTCCCTGTTCAACACCTCTTCTTGAAGTGGTGTGCTGCTGGGCTTATANCAATTCGCTACT
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NCGNCCATANNNTNNAACTTTGNNTTCACTTNGCAANGNTGGCCTTGNCTGTTGGGNTGNTGCCN
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SEQ ID NO: 4016 GGTACCATCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAG
CAATGGGGCTGGACACAAGGTGCGTGGCCAAAAAGAGTGCTGAATTTTGTGTCACATGCTTAA
AAACGCAGAGAGTAATGCTGAACCTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCA
AGTGAACAAAGCACCTAAGATGCGCCGCCGACCTACAGAGCTCATGGTCGGATTAACCCATACA
TGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCTTAAACCAGAA
GAGGAGGTTGCCAGAAAGAAAAAGATATCCCAAAAAAACTGAAGAAACAAAACTTATGGCCN
GGAGTAAATTCAGCATTAAATAAATGTAATTTNTTGGGAAAAAA

SEQ ID NO: 4017 ACGCAGCCCCTCACACACTGCTTCATTTTGTGATTTCTGCATTTCCAGCTGCC
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ACTGGGTCAACTCTTCTAANTGGGCACTGANGCACTGCAATATCATAATGGGGCATGCAAAAAA
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ATGGATCTCCCCNCC

SEQ ID NO: 4018 GGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACTGGCTAACAGAATTTTATTGT
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ACANACAGCTTCCAACCCACACCCAGCATCCAATCCACACCCAGCANACCCTTCGGCATGCC
GCCCTNTACCAGGAAGCCAGAGGCCTAGGAGCTCGCCATCCATATTTATTGAAAAGGTCAAAAG
GAGCATNTATGANACAAGGGAGGGGTGCAGGCTGAAGCAGCGCCTNAACAGCCAGGGACATGTA
GGCAACACGAGCAGGCACAGCGGGCCACCACTGTCCACACGCTCACACAAGCCAGGCCCGCAG
GGCCTTCGGAGAGCTAGCAGGTTACATTACAGGCAGATGGNCTNTTCCACCCAAACCCACAGAAC
CCCAACAANGGNTNACCAGGAAGACACNGGAAACCAATTACAATTTGAACNNGGNGAGANA
AACCTTGGGCCCTTGNTGTCCAAGCACAAAAGTTGTTTCA

SEQ ID NO: 4019 ACAATATCATATATCTGGTATACAAAAAAATCGCTCATTATTTTAGCCCTAC
CCTCCATTGTCTCTCTTTCTGGGACTCCTATTGATTGCATGACCTTCTGAAGGTCCTGTGTGTG
TCTTACCTTTTTTTCATAACTCTCTTAATTTTTTTTTTTTTTTTTTANAGTCTTCTCTGTACCC
AGGCTGGAGTGCAATGGCGTGATCTCAGCTCACTGCAACCTCTGCCTCCTGGGTTCCAGGTGATTCT
CGTGTCTCAGCCTCCTGAGTGGCTGANACTACAGGTGTGCACCAAGTGTCCAGCTGATTTTGT
TTTTATGTANAGATGGGGTTATGCCATTTTGGCCGGGCTAATCTCGAACTCCTGAGCTCAGGGGAT
ACACACACCTCAGCAAAANTTTTAAATATACANTCNGGNGATATTTCCCTTGACTTTTCTTAACC
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ATGGAAAAATCCAACTTNC

SEQ ID NO: 4020 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGGCCATATCATTCATGACCAAAAAA
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TTTCAATAATAGGCTAAGGAAANACATGTTTTCTCTTTTAAATCTCTGCAACTCCAAAGTAAACT
CCTTCGAACGTATTTAATTTGGCCTTTTCAAGCTTTCTTCTGCCCAGCTCTGTGCAATTCATGGGNG
TGTGTGCACATGTTGGTTTCACTCACCAAGTAATTTTNGAGCATGCNTGGGCTTTTAATTTCT
GCTTGAATGTTGNCCTGCTNGGTTGCAGCTTCTAAAGANATTGC

SEQ ID NO: 4021 ACGGAGGAGTTCCTGGAAGCCTTCATGGATCTGAGCCTCCGGAATCTCCGTG
AGGTTGAAATTCAGGCCCTCCAGGATTTTCATCGTGAGTGTGACGCTTGGTCCCCAGGGAGAGCATT
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CTGGCGGTATAGGCTGAAGGCGAACTCAGCCAGGTTGGGGGTGATCTTGTGAAGGTTGGGTGAT
CCTGATCATGGTGGGATGTATCTTGTCTTCTGGGCANNATCTNCNTGGGGATNCTTCATCCANGG
ANACATGNACCAANTAGNCTNNGCCTGCCTACTAANAGGATGCCCNCCAGANNGATATCGGNTTT
GTNGTTNTCTTTCTCA

SEQ ID NO: 4022 ACTGATTCATCACTGTCAGATTCTGTTCCAGACCCTGTCTCAGCCTGGGGCTG
CGGCAACTCCTGCTCTGTAGCAGGGACGGTTTCTGTGGCTTCGCCGGGCATTTTGTGCAGGGAACG
CGGAACCAAGATGGCGGCCCCCGCTACTCTGATTTAAAACTTTGGACATCCTGTGATCTGTTTTA
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GTNTTAAATGTCCCNCTTGAATANCANTAATTCTTCATAGNTTTTNTAATCAANGGAAAAANTGGAA
ANCTAATTATTTGTAATGAATTATNTTATAACANTTCTTAGCCCTTGCTTTNGGG

SEQ ID NO: 4023 ACAGACATGGCGGCGGCTTTTCGGAAGGCGGCTAANTCCCGGCAGCGGGAA
CACAGAGAGCGAAGCCAGCCTGGCTTTTCGAAAACATCTGGGCCTGCTGGAGAAAAAGAAAGATT
ACAAACTTCGTGCAGATGACTACCGTAAAAACAAGANTACCTCAAAGCTCTTCGGAAGAAGGCT
CTTGAAAAAATCCAGATGAATTCTACTACAAAATGACTCGGGTTAAACTCCAGGATGGAGT

SEQ ID NO: 4024 ACGCGGGGGAGTCACTGCTGCTCTTTGAGGCAATGCGCAAGGGCAAAGTTTTTC
AGAGGGCGAGGCCACACTACGGATGAAGCTGGTGATGGAGGATGGCAAGATGGACCTGTAGCC
TATCGAGTCAAGTATACACCACACCACCGCACAGGGGACAAATGGTGATCTATCCACCTACGA
CTACACACACTGCCTCTGTGACTCCATCGAGCACATCACTCACTCACTCTGCACCAAGGAATTCCA
GGCCCGACGCTCTTCTACTTCTGGCTTTGCAATGCACTGGACGTCTATTGCCCTGTGCAGTGGGA
GTATGGCCGCTCAACCTGCATATGCTGTGTCTCTAAGANGAAGATCCTCCANCTTGANCAAC
TGGTGCTGTGCGGGACTGGGGATGACCCACGGCTTTTAACTCACGGCCCTGCGACGGCGGGGCTT
CCACCTGATGGCCATCAACACTTNTGTGCCGGGTGGGAAGTGANTGTGGCACAAACCAACAATG
GANCCCCATCTTCTNAAAAGCCTGTGTGCGTTANTGTGCTAAATACACANCCCCCNACCATGGCT
TGGCTOGAAGTAATTACGGGTAATTNATACCAANTTTCTGTTGCCAANTCCTTGGGAATTTC

SEQ ID NO: 4025 ACAGGCAGAGCAACCATCCTCTTCGTCACCCAGACGCAAGACAGTAAAGGA
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CCCAGGGAGGGGCANAAGCTCCCCAAATCCAGGACGGCCTACTCTGGTGGAGCATAGGACCTAG
AGAGGGAGCTGAAGAAGGAGAAACCAATCACGAGCACAAGTCCTCAAGCAGGAGGGAGGCAA
GAGAAGAAAAGACCAAGGATTAGGGACAGAGGGCGGAGCTCAGATGCACATTTCTANCTGGTATA
ATGGGCGTTTTAAGGGCGTATTTTANAAGTAGAAGTAGGAGCCGAATAAATCCCATANGCATAAA
AGGGCCGACNCTCCCGGAGCGGGAGTCTTCGAATCNCAGTGACCGTTGGCCGCTCACT

SEQ ID NO: 4026 ACAAGTATTTATATCAATGAAAAATTTCCATTGGTGATTTTTTGGCAGAATATT
GGTCTTGACTCTGTGGAATAAATGACGACGTAAACGTAGCTGCACAGGGGTGTTCCTGTATAATGC
TTGAATCAATTGTGTGTGAAAGCATCATGCAAAATGGCTAATTAAATTTGGGTGATGACTGAAAGGTT
ATAAATCCTTCAATCCAGCTCCAGAGCAGATCCCTTCTCCAAGTGTGTCTCCAGCTTGACAGTC
ACAGATTTACCCGTGCCAGTTTTCCAGCTGTCAATACTATTCTNGCATTATCATGGCTTAAATCN
CACAAATTNCTTGACCTTCTGTACCC

SEQ ID NO: 4027 ACCTAAATAATGTCCTTCATTTTGTCTTAGCTTGCAAAGCCTCTAATATTGCT
ACCTGCCCTTTTCAAAAAAAAAAAAAAAAAAAAAAAAAANAAAGGCTTGTCACCTCTCTACTAAAAANA
AACTCAAGGGTCTATGTCTGTCTGTTTGTATTTTCATCTGCATTGCCAAATGCAGTGGCTCCTCTG
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AGNTAAATTTTATAAATAAAGGGATAGGAAAAATGCTGATTATTCTGNGTGNCNGNGCTTTNAAT
ATAAGGCCANTTCNNACATGC

SEQ ID NO: 4028 GGGTACTCTGGTGAGTCAACACTTCAGGGCTTTACTCCGTAACAGATTTTGT
GGCATAGCTCTGGGGTGGGCAGTTTTTTGAAAATGGGCTCAACCAGAAAAGCCCAAGTTCATGCA
GCTGTGGCAGAGTTACAGTTCTGTGGTTTCATGTTAGTTACCTTATAGTTACTGTGTAATTAGTGCC
ACTTAATGTATGTTACCAAAAAATAATATATCTACCCAGACTAGATGTANGTATTTTTGTATAA
TTGGATTTTCTAATACTGTCTATCTCAAGAAAGTGATNNGTTTTTTAAAAAAGAAAGTGATTTT
GGAAATAAAAGTCATGATGGAAAAATTCATTTNTTTAAATTTCCCCGGTTTNTCACTTTNTTNGATT
ANAAGATGGGCCATATNNCCCTTTTTTGGCCCCATGGATTAA

SEQ ID NO: 4029 ACTTTTTTTTTTTTTTTTTTTTTTTTNGCAAGCCATATCTGAAAAGCCATCTCTG
CCCTTCCCCTGCCTGCCCANACCATGAGCCGGGCACCGCCAATGCATTNAGGNGGGGA
CNCATTTCTGCGGTGGCTGTCTTTGANAGACCCACATGTTATTTTCATGGAANACGGAGTTGGTG
ACTTNAGGAAACTCCTTNTGGANAACATGGGANGCNCCTTNATAANTCTTGAAAGTT

SEQ ID NO: 4030 ACGCGGGGGCGTCTTGTTCTTGCTGGTGTCGGTGGTTAGTTTCTGCGACTTG
TGTTGGGACTGCTGATAGGAAGATGTCTTCAGGAAATGCTAAAAATTGGGCACCCTGCCCCAACTT
CAAAGCCACAGCTGTTATGCCAGATGGTCAGTTTAAAGATATCAGCCTGTCTGACTACAAAGGAA

AATATGTTGTGTTCTTCTTTTACCCTCTTGAAGCTTACCTTTGTGTGCCCCACGGAGATCATTGCTTTC
 AGTGATAGGGCAGAAAGAAATTTAAGAACTCAACTGCCAAAGTGATTGGTGCTTCTGTGGATTCTC
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 CCTTTGGTATCAAACCCGAAGCGACCATTTGCTCATGATTATTGGGGTCTTAAAGGCTGATGAAA
 GCATCTCGTTCAGGGGCCCTTTTATCATTGNATGATAAA

SEQ ID NO: 4031 ACCCTCCAGAAATTGGTGACTTTGCTTTTGTGACTGACAACACTTATACTAAG
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 ACCTTTGCACTTCTTTCGGAGAGCATCTAAGATTGGAGAGGTTGATGTCGAGCAACATACCTTTANC
 CAAATACCTGATGGAACTAACTATGTTGGACTATGACATGGTGCACTTCTCTCTTCTCAAATTGC
 AANCANGAGCTTTTGTCTAGCACTGAAAATTCTGGATAATGGNGAATGGACACCAACTCTACAA
 CATTACCTGTATATACTGAAGAATCTTNTTCTTCCAGTTATGCAGCACCTGGCTAAAAATGTNNT
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 ATGCTAANATCANCTCTNTTACCACTAGCTGAATTNTGGCACTTATTTNAAGATTTACCAANGCTN
 GGGCAATGNGTAACTTGTAANCTTGAGTTGGA

SEQ ID NO: 4032 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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 CAGGCAATGGAGAGAGGGCAGAAAGGTTGANAAGCTGAAGGGGGCTAGANGCTTACTCTGAGT
 TTCTTCTTCTGNCTTNAATCTTTACTTCTTATGGCCAAAAACCCAGCTGTTTTATAGGCTGGAG
 ATGCACTNTTCTATACTGCTNNAGACAGCCAGAAACAGGGGANGAGGGAAGATTG

SEQ ID NO: 4033 ACTGCAGCTAAACCAGCGGCTTCAATAACAAGTAAGCCTGCTACACTTACAA
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 CAATGCCACCTCATGGTCAGTATGGTGGTCATCATCAAGGCATGCCAGGATACTTCTGGTGCTA
 TGCCCCGTTGGGCAGGGACCGCAATGGTGCCCCCTTACCAGGGTGGGCCTNCTCGACCTCCGAT
 GGGAAATGAGACCTCCTGTNATGTGCGAAGGTGGGCCGNTACTGGATCTTACTTCATCCAGTCTAAT
 AGGNTTTGGAGATTAAACNTTTCTTAACCTTGCTGTTATATAGCCAAGCTC

SEQ ID NO: 4034 ACCTGGGGGGAGTTGTAACACTCCANAAGGTCCAACTCCTCTCTTGGCATGG
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 GCGCCCTGAGTGTCTGCGGCANAAAGAGTCGGAACAGGTTTTTGTAAAGGTCCATGANTCTTCAAT
 TCACACTTCCCCCCTAATGGANGANAAGGGAGCNTGGTCAAATTACNANGAATCGNNTACCTC
 TCNNGGCCGGATACAATTACNATACAAGTCATTNAAANAGGT

SEQ ID NO: 4035 ACGCGGGGGAGCCAGCGCGGAGCACCTGCGCCCGCGGCTGACACCTTCGCTC
 GCAGTTTGTTCGCAGTTTACTCGCACACCANNTTCCCCACCGCGCTTTGGATTAGTGTGATCTCAG
 CTCAAGGCAAAGGTGGGATATCATGGCATCTATCTGGGTTGGACACCGAGGAACAGTAAGAGATT
 ATCCAGACTTTAGCCCATCAGTGGATGCTGAAGCTATTGAGAAAGCAATCATGAGGAATTGGAAC
 TGATNAGAAAATGCTCATCAGCATTTCTGACTGAGAGGTCAAATGCACANTCGGCTGNTGATTGTT
 NAGGAATATCAAGCAGCATTATGGAAGGAGCTTGNAAAGATGACTTGAAGGGGTGATCTCTCG
 GCCACTTTGAGCATCTCATGGGTGGCCCTANTGACTCCNCATCAGNCTTTGATGCAAAAGCAACTAA
 AAGAAATTCATTGAAGGGCCNCGGGAACAACTGNAAGATGCCTTGATTGAAATCTTANTTACC
 TGGACAAGNCAAGCTNATGAAANGATNTTTTTCANCTTATTAT

SEQ ID NO: 4036 CCGGGGGTAGACGGAACCTTCGCTTTCTCTCGGCCTTAGCGCCATTTTTTTGG
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 AGAAAGATGAGGCAGAGGTCCAAGTAAACCGCTAGCTTGTTCACCCGTGGAGGCCACAGGAGC
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 AANCTTATCAAAATGGGCTGNTCTTCTCAAGCCTT

SEQ ID NO: 4037 ACTACTGCTGTTTTCTGAAGACGCGAGGGCAAGTGCAGCCAGCCGTTTCTTTT
 CCTTCTTTAAGCGTTTCTTCTCTGTTTCTCCAGCTTCTAGTAATCTCAGCAGCCGCTTCTCTGCC
 TGAACCATGCTTCTTCTCATGACATCCAGATTCTTTCGTGGTATCTCTCCAGTCTCATAGAAGGACA
 GTCGCTCTTCAACTTGTCTCGAAGCTTCTCCCCGAATACACTCGTGGGCACCTCAGAGAAGCAAT
 CGATTCTGTAGGCAATACTGCATTGTGTTGCCAGGTATCGGGAGATCGGGCCTTTTGTCTTGCCA
 GCTGCTCGGCCAATGAAGGTGGAAGTGAAAAATGAGTCCATATTTGGGGTGGTTACCCCTNNGC

TNTNAGGGGCTCTGAACAGGGCCTTTTCANCCCCAAGGATCTGCACTGGGGATGCTGGATACTTGC
CANGTNTGTGNAGTNGCAACATTGTGCAATGAGANATG

SEQ ID NO: 4038 ACCTAGAAGAGAGGGCGGGTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTCAT
AGGCTATCCCATCACCCCTTTATTTGGAGAAGGAACGAGAGAAGGAAATTAGTGATGATGAGGCAG
AGGAAGAGAAAAGGTGAGAAAAGAAGAGGAAGATAAAGATGATGAAGAAAAACCAAGATCGAAG
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AGAGAAATACATTGATCAGGAAGAATAACAAGACCAAGCCTATTTGGACCAGAAAACCTGATG
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GCAGTCAAGCACTTTTCTGTAGAAGGTCANTTGGGNTTTCANGGGCATTGCTTTTTNTTCCCTCGNC
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SEQ ID NO: 4039 ACACATGAGAGAAAAATCTTTCCAATGTAATGAGAGTGGCAAAGCCTTTAAT
TATAGTCTCAGTCTTAAGGAAACATCAGATAATCCATTTAGGAGCGAAACAATATAAATGTGATGT
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ACCTTACAAGTGTAATGATTGTGGCAAGACCTTCAGTCAGGAGTTAACCTTACATGCCATCATAG
ACTTCATACTGGAGAGAAACATTACAAGTGCAGTGAGTGTGGCAAGACCTTCAGTCGAAATTCAG
CCCTTGTAATTCTAAGGCAATTCATACTGGAGAGAAATCTTACAAGTNGTAATGAATGTGGCAA
GACCTTCAGTCAAACGGTCNTACCTTGGGT

SEQ ID NO: 4040 ACGCGGGGTCCGCCGCTAGTCTCCAGCTCCAAAATGGCGGCTGCCACTGTGG
GGCTTCTGCCGGCCGGTAGTCCCTGGCGCTGCTGACCCAGCATCGGCTTTTCTACGTCTTGAACCT
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AGAACTCTTCAGAAATCCTGGTGTTCATCATATATACGACTAAGATATCAACTCTTCTAGCTTGCT
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TCTGCCCTTTGCTATCTTCTCCAAGTNGATGANTTTAGATTTTTATTGGACTGTGGCTGGGATGAA
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SEQ ID NO: 4041 ACTTGCAGCCCTCGGCCAAACGGCCAGACGCCGACGTCGACCAGCAGAGACT
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TAAACAACCAACCAACATTGATGCTTAAGGACCACACTGGAAGGAAAAAAAAAGAGGGGACTTN
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GGGAAATTGTTNNTNNGTGGCAGGGGGTTTGANNAAGTCCCCCTTNCGGTTGAAAA

SEQ ID NO: 4042 ACATGACAAGGTGCGGCTCCCTAGGCCCTCCCCTCTTCAAGGGGTCTACAT
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GTGAGGGTCTCTCTCTTCTCTTGTGCTCTTGCTGGGGCTGGTGGTCCAGGGGTCTTACTCCTTGG
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GAGCTTGACAAAGTGGTGGTGGAGGCAATGCCAGCCCCAGCGTCAAAGGTGGAGGAGTGGGTGT
CGCTGTTGAAGTCAGAGGANACCACTGGTGCTCAGTGTACCCAAGATGCCCTTGANGGGGCCCT
CNACGCCTGCTTACCAACCTTCTTGATGTCATCATATTTGGCAAGGTTTTCTANACNGCAGGTCA
NGTCCACCCACTGACACATTTGGCATTGGGGACACGGAANGCCATGCCANTGAACTTNCCCCTTT
AACTNAGGGATNACCTTGCCACACCTTGGCANC

SEQ ID NO: 4043 ACNCGGGAGAAGAAGAGTAAGAAGGACAAGAAGGCCAAAGCTGGTCTGGAG
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ATTGAGAAAACATGTTATAGATCCTTTTGTGCTGAGAGAGTGGAACATAGGTCTAGACAGGGT
GAANAGTTCTGGCACATTTTAGCTGCTCTTGAGACCTCGGTGATGTTACCTGNTGTGGTCACTCC
ATCTTGTCTGTTTTAAGGATTTGGGCNNGGNATANATGAAAGAGGC

SEQ ID NO: 4044 GTTTTTNTNTTTTTTTGGCCCAAATTTATTTTTATTTTGACACATAGGAAAC
AGGATCCTATCAAAAGANAACAAAAAGAGAAACNAGCCANTTGTGTCAGAGGAAAAGCATGCAC
ANATCTGCTTNAAGTTTACTCTGAACACGGACNCTCCGGGAATTCNACACACAGGAGCTGNNTC
ACTCCAGGAAGTGGGCACAACCCACCATCCACACAATGGAAACAAGATGGCCAGGAAATGTCA
CCGAAGTGAGACTTCCATATGCAGGATCAGCGTTCACAGTAGCACAAATCTAACCAAGTTCAAGG
GAAAAACAACTTNTGTCTCACACAAACATGGGAATCAAAATTTGTTGACCCTAGCCATCACTGCTCT
TAACATAATTTGCTTCAAAAAGACAAACGAAATTTANTCCGGACTTTGGGTGCCTATTCAACTGC

ACCCGATTCCAGGGGCAGCTTAGTGTGCTTTTTCATTACAAAAATAAAGACNTTTAAAAATGCAA
ACAAATTACCTGGAGGAANAAGAGTGTGGACCACNCATTGTCTTGGTTGNAACAAGGGAACATT
GGCCTTGGTGGCCATTAAATGGAGGCTTCAGCATTGGAAGGACCTGCCNGCGGGCCTTTNAA

SEQ ID NO: 4045 ACCAAACGGGCAAGGACATCTCTACAAATTACTATGCGAGTCAGAAGAAAAAC
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SEQ ID NO: 4046 ACTTTTTTTTTTTTTTTTTTTTNGCATCAAAAAGCTTTATTTCCATTGTTGTC
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SEQ ID NO: 4047 ACTTTTTTTTTTTTTTTTTTTTTTTTNGGTTATTTTTAGTTAAAGAAAAACA
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SEQ ID NO: 4048 ACTCTGCCACAACTGATCACACTGCTTCTGGTAAGGGTCTGGCAGGAAGCT
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SEQ ID NO: 4049 ACCGACCATAGAGCAAGAATCAAGATTCTGCTAACTCCTGCACAGCCCCGTC
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SEQ ID NO: 4050 ACTGTTGTCCATTTTCATGAGAGTAGGCTTGAGGACACCATGGGCAAGGATCT
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SEQ ID NO: 4051 ACTGAGGACAAATCAGTTCTCTGTGACCAGACATGAGAAGGTTGCCAATGGG
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SEQ ID NO: 4052 ACTTCCCACTTTTCATAACGAGTNGGAGCCTAGAGTTGATCGACTCCAGCGAC
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CCCGCT

SEQ ID NO: 4053 ACCAGAAGTATAAGTTTATGGAACCTCAACCTTGCTCAAAAGAAAAAGAGGCT
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SEQ ID NO: 4054 ACGCGGGGAAGGGGAGAGTTTAAAAACCCAAACCGTTGTGGTTTTAAGGTG
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GCAN

SEQ ID NO: 4055 ACAAAAAAATTAATTTGCTTTAGTTATAAAAGAGCTCTGTCAATATACACA
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SEQ ID NO: 4056 ACCCTGATGCCGTTGACAAGTATCTCGAGACACCTGGGGATGAGAATGAAC
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SEQ ID NO: 4057 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACAGTGGTCTTA
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SEQ ID NO: 4058 ACGGTTTGGCCTGCAATGCTAATGGTCTCACAAGCAGTCAAGGTATTTTGCTA
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SEQ ID NO: 4059 ACAGAACATGATCAAGGGTGTTACACTGGGCTTCCGTTACAAGATGAGGTCT
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SEQ ID NO: 4060 ACCACAAAGAATAGTCTCATTTGACAGAGAGACTCAAAATATTGGACTCTAGC
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CCA

SEQ ID NO: 4061 ACTTTTTTTTTTTTTTTTTTTTTTTTCCAAAGCAGTATGTCTCAATAGTGGCCT
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SEQ ID NO: 4062 ACACACACGGGAAAGAACTCTGCGAGTCTGATGTGTGTCAGAGTTCAGTC
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SEQ ID NO: 4063 ACCCAAAGCCTCCCCAAGGCCACAGTAGTCATGCTCCCGGGCAGTATCTGCC
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SEQ ID NO: 4064 ACAGTTTGCAGAATATATTAGAAAAACGTGCAACTTTATAAGATGCGAAAT
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SEQ ID NO: 4065 ACGACCTCATTTGCCGTGTCCAATCATTATGGAGCCATGGGGGTGGCCACTAC
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SEQ ID NO: 4066 ACAGGTTTCACTATTACAAATATATGATGTTAACTAACAACTCATGACCTT
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SEQ ID NO: 4067 ACAGCCTACCAAGAGGCCAGAAGGCAGAACTTATGCTGACTACGAATCTGTG
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SEQ ID NO: 4068 ACAGGTGCATCGTGCACATAAGCCTCGTTATCCCATGTGTGCGAAGAAGATAG
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SEQ ID NO: 4069 ACATTTACTGGATTGTTTTTTCAGTTTGCAGCTGCCCTCTTGACATCCCAAATA
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SEQ ID NO: 4070 ACTTTTTTTTTTTTTTTTTTTTTTTTNGCAGTAAGAGTAGCCAGGTGTAGCCAC
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SEQ ID NO: 4071 ACATTGAAGCTCGGGTGACAAAAGGTGAGACACTCACCTAGAACAGTGCCGT
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C

SEQ ID NO: 4072 ACGCGGGAGCCAAGAGGGCGGATAAGTGCCCCACCTTAGAACAGTATGCCAT
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CAGACATTGCT

SEQ ID NO: 4073 ACTTTTTTTTTTTTTTTTTTTTTTTTCCAANATTTGTTTTATTTATTATG
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SEQ ID NO: 4074 ACGCGGGGGGGCGACTGAGCGGACAAACGGAAGTGTAGGTTACGGTCTGAG
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SEQ ID NO: 4075 ACAAATCATATGTTAGGTCACAGAACAGGTCTTACTAAATTTTTAAAAATCA
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SEQ ID NO: 4076 CCCTAATGATAACCATTTTTAGAAATTCATCATCACTGTAGAAATCAGAGTCTG
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SEQ ID NO: 4077 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCCATATCATTCATGACCAAAAAA
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SEQ ID NO: 4078 ACTTTTTTTTTTTTTTTTTTTTTTTTTTCTCAAGCACGTGCACTTTATTGAATGAC
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TTGGCGGTGGAGGCATAGGCCTGGGCCCCGGTCACTNCGCCAACCATCTTCTGTCCCTAGACTTC
ACGGAGTAGGCAAAATGCTATGAAGCCCAACAGCACCAAGTTCAAGAAGAGGGTGTGAACAGGG
ACCAAACNACATGGTGGCACGGAGGTCTCGCTGTGGATGTTGATCACCGGTGGACCTTGAAG

SEQ ID NO: 4079 ACAAATGTTTTTATTCAA AAAANGCAAAATAAAATATCTGTAGGCATGGACA
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GACTACCA

SEQ ID NO: 4081 ACTTGCAATGGGGCCACCATGTTTTCTCCCATAGCCAGCCCCATTATCATATG
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AGCTGGATGCATGCCAAAGGCAAGCCATCCACAGTCTGCTGGAAGGGTGGTGCAGACTCTAAC
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[illegible]

SEQ ID NO: 4085 ACAATGAAGCTTTTCTCAAGCAATAATTGTTTCCAAGTGTCTGGGAATT
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CACCAACTCCATCAATACCACCCAAAGTGTTTANGCAGTGAATAAAATCAAATAATGCATCTTA
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SEQ ID NO: 4086 ACGGGGGGCGCGTCTTGTTCTTGCTGGTGTGGTGGTGTAGTTTCTGCGACTT
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ACCTCCCTGTTGGCCGCTCTGTGGATGANACTTTGAACTAGTTCAGGCCTTCCAGTTCACCTGAC
AAACATGGGGGAANTGTCCANCCTGGCTGGAACCTGCCAGTGATACCATCAAGCCCTTGATGT
CCAAAAA

SEQ ID NO: 4087 ACAAATGATGAAACGGAAAGACGAAGGAAATTTTCCATTTTGAAGAAAA
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TANGGCCACCT

SEQ ID NO: 4088 ACTCTTTTAAATGTGTTTATATTGGAGGTGAGGGTAGAATGTTTATAAAAGGA
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SEQ ID NO: 4089 ACGCGGGGACTGCNCAGGCGCTTACAGTGCACCAAGATGGCCGCCCCGTGG
ATCTAGAGCTGAAGAAGGCCTTCACAGAGCTTCAAGCCAAAGTTATTGACACTCAACAGAAAGGTG
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SEQ ID NO: 4090 ACAAATCAACCAGGTCTGAACTGATTGGTGATAAGAGCACACAGATCAGTC
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SEQ ID NO: 4091 ACTGCTATCTCGCATTCTTCTCAGGTTGCCAGGAAATGTTTCTCTAACCCTTTC
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CAATAAGAACTGTTCCCTCTGTGGATGTAGTGATTGATCCTTACCTTGATATCATCTTCGACCA
CATCAGAAAGAAGGAATCATATTCTTTATGAATGTGTAATGGGAATGAGAATGAATGGCAGATG
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CCTGCAGTGTCAAGGACCCATATGGAGGCAAGCCAGTAATAAAGAAGACACTAATTGTCACACCTG
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ATTTACTGTTGATCAGGACCACAAAGTTGAAGAATTCATCAAGTCTATATTTATTCTGGTCTTATT
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GNGACGANGGG

SEQ ID NO: 4092 ACAGCACTTCGGAAGAGTTTGTAGTTGGCCCTTTGCTGGTTGGGCTGAGTTT
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CTCCAGAATATGGAGGCACCAAAAGTAGTTCTAGATGACAAGGATTATTCCTATTTANAAAAT
GGTGACATTCTTGAAAAGTACCTCGGNCGGGAACACCNTAAGGGCNAATTCCANCACACTGGC
NGGCCGTACTAG

SEQ ID NO: 4093 ACGCGGGGTTGCTTTATTTCCATCAAAGCCCTCTGAGAAGTGAGACCTCAGC
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SEQ ID NO: 4094 ACATTCGTGTTTCATGTTTACAANNCTCTCCATATATTTACAAATTTACGAT
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CAACANAT

SEQ ID NO: 4095 ACGCGGGGTCGCGCGCGTGGATCTGCCGCCGGGTTGCTGTGCGACTATTCT
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AAAAGTGCCCCGATCTGCTTCTGCTTCCACCAGGCCGACATTAAGGAAGCA

SEQ ID NO: 4096 ACAGGAGTTGTTGCATATTCATGAGGCTGGTGTGCGGAAGCAGGGACCCAC
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SEQ ID NO: 4097 ACTTTTTTTTTTTTTTTTTNNNTTGGGGTATAAACTACTATGCTTTAATGAGC
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CCTNAAAANGGA

SEQ ID NO: 4098 ACTTGAGGTAACAGTCATGGAGATCGAGATAACGACCATATCCCTCTTCATCT
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SEQ ID NO: 4099 ACATGATCAGCTCTTTCTATTTTTACTCGTAAAAATTATGGAAATGAATAATT
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SEQ ID NO: 4100 ACTGCGAGCAGTTCTTCCAATTTCGATGAATATAATCCTCTGAGGAGTTAGGGT
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TC

SEQ ID NO: 4101 ACTGGCCTTTATGTGTCTATTTCATAGCAGTGGACTGGGCTGCTCGCACCAGAC
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NAATCT

SEQ ID NO: 4102 ACCTATAAATGTTGTTGAGACACTGAGAACACGTGGGGCCCCCACC GGATA
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TAATNNCTATGCTGTCTTTACCGGAATCTCTAAACACAAATTTGTAAGATTTTCATGGACACTTA
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NCTGANGAGGATGTTTGTACCTCAGGACCATGTGATAATTNNNTTAACTGCANAAAATTTGTA
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ANGGAATAAAAAA

SEQ ID NO: 4103 ACAACAAAAAGATTAGGAAGCAAAATGTGAATAAGCTTGTATTTCAGAATATACCTATATGTGTGTGCAAAGACAATACACTCATCATATACCTCAGTTAGGTTCCCTTTATGATGCATAATTCCTTAATCATTCAATTTGTGAAACAAGAATGAATATTAAGAAACATGAAATCCAAATTGCACTTATTTTACAATATCAATGCTAAACTCAAAATAGCAACTTCATTGACTCTCAATGGTAAATTTCAAAATGGAAGCAATCTTAATTTTTTAACCCCTTTGACTAGGGTCTGTAAAAAACGGTGGATTATTTACTGTACAGCATTCTGGAATAAGCAAGAGTGTTCAATTCACACACACAGTAGCTTCAAAACTGTTCGATCTGTTTGTTCCTATGTAGTTTTCTAAAGATGGAAAAAAGGACTTTTGGTCATCAAGACTACTGTGGCCATATTAGATTACTGGAACATCTAAGCATCAGTGTGTGACCATGCGAACAAAAGACTTCGGGGAGTGTCTATTTTTAAAAAGGTTTATGTGTGTGAGGCAGTTGTAAAAGATTTACTGCAGAATCAAGCCCTTTTANGCTTAGGACCAGGTTCTAACTATCTAAAAATATTGACTGATAACAAAAAGTGGTCTTAAATGT

SEQ ID NO: 4104 ACGCGGGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAAAAACCCAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAGAGTCTTCAGTTCTGAAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATGTGTTAATGATGAGAAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTGGTCTTCCTTGCACGCAGTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAAAAAAGGATCCATCAGACGCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGGAAGGAGGAATTGTCTAAGTGTAGAAATCAATGAAAAGACTTAACANCCCTTCAATATCCAGAAAAAGTGTCTGAACAAGGGAGGGATGATTTGGAAGATATCTGAAANATAAACAGCTAGCAGTTTGCCTGAAATATGCTGGAAATTTTTGCAGAAAAATGCCAAAANATGCTTGATGGAAAAANAATNTATTTTAATACCAAATCTGTTGGGCTTCTTTNAAAAAAGCAATGACTTATTNCCCCCAACCANGTTAGTAGAAANGGCTGTTGTTCAAATATGGNTN

SEQ ID NO: 4105 ACCTGGCCATCCTGGGCAGTGTGACGTTTCTGGCTGGCAATCGGATGCTGGCCAGCAGGCAGTCAAGAGAACAGCACATTAGTTCCAGAGAAAGATGGAAATCTGAAAACTGAAATGTCAAGAAAAGGAGTCAAGAACAAATTCACAGTATGAGAAGAAAAATGGAAAAAACTTTATTAAAAAAGAAAAAGTCCAGATTGTAGTTATACTTTTGCTTGTTTTTTCAGTTTCCCCAACACACAGCAGATACCTGGTGAGCTCAGATAGTCTCTTCTGACACTGTGTAAGAAGCTGTGAATATTCCTAAGTACCCAGATGTTGCTTTTGAAAAAGTTGAAATGTGTAATGTTTTTGAATAAAGAGGGTAACAAAGTNNAAAAAANAAAAAAGGTCCCTGCCTATTTAGAAATCCTAGAGAACATTTTCAATGTAANAACTAGTCCATTATTAAGTGTCCAGTATTTTTCATTTTCAGTGGGTCCAAGATGCNAAAGTTCCAGACACAATCTTGGTCTCTAATACTGCTCCAGGGTGGGATATCAATCTGTCTCATGATTTGCAATGATGATAACCGTTCCCTTAAATGAAACATTTTTTCCAAATGTCCACATNTCTGNAACTGNGGAG

SEQ ID NO: 4106 ACAACATGACATTACAGAGTATCTTATAAAATACAAAGACAAATATAAAAAGACTATGATGCTTTAAGTCTGAAAACTATTGGCCAAATATTTAGGTTTAAATTTACAGTTCCTGGGTATGAGAATCATATTACTATATACATCTCCCAAACAGTAGGTAGTATTTTCCAATTAACCATGTGTGTATCATCTTCTACAAAGTCTTTGGCCATCTCTGCTGTGATCACAATATGACTAACCTTATTCTGAACTTTACACCATAGAAATTTGTCAGCTGACTCAAGCAGTTCAGGCCTAAAAGTAGTTGTAATAAAGTCAATGATG

SEQ ID NO: 4107 ACGCGGGGACGGTTCGTTTTTGCTTTAGTCAGGAAGGACGTTGGTGTGAGGTAGCATACGTATCAAGGACAGTAACTACCATGGCTCCTGAAGTTTTGCCAAAACCTCGGATGCGTGGCCTTCTGGCCAGGCGTCTGCNAAATCATATGGCTGTAGCATTGCTGCTATCCCTGGGGTTGCANGCTTTGTATAAAAGTTTCTTGTGGCTGATCAAAAANAANAAGGCATACTCAGATTTCTACAGAACTACAATTGTTATNGAAAGATTTTGANNGANATNAGGAAGGCTGGTATCTTTNANANTGTAGAAGTATCTTTGGAATATAAAAGAATTNCTCCANGTTGANTAAANTAACTGANCTAGT

SEQ ID NO: 4108 ACTGGCCTGCTGCTGGCCGAGGCTTCTCAATAGGTTTGGCATGGACAAGATCTATGAAGGCCAAGTGGAGGTGACTGGTGTGATGAATACAATGTGGAAAGCATTGATGGTCAGCCAGGTGCCTTACCTGCTATTTGGATGCAGGCCTTGCCAGAACTACCACTGGCAATAAAGTTTTTGGTGGCCTGAAGGGAGCTGTGGATGGAGGCTTGCTATCCCTCACAGTACATCCAAAACCATAAAGGAAATATTCTGATGCCAGATGATGAAGACTGGGGTGAATTAAGTCCACACATTTATTTCAAGTTGTTAAAGAGTTTGTGGGCCACGCAATGGTCCCTCGCATGCAAGAAGTCAAAGAGCTCCTCCGTGCAATCCTCTTCTGTATGTGATCGAGAGGATACAGCTCATCAGAGCTAGCCGCTCCCGGGCTTTACACATTTCTCCAAGTCTCGCATGCTCTCTCACTGTTGTTAGGGGATCCACTAATTCCTCTCTTCTTCTCCTCCTNAGGATCTCCGATTGCGTAAGCATCTTTGCTCGTCTCATCCCATGTTGGCTACGGTTCTAGATTCAACACGAANCAGCAACAGCGGCACCTACCCANTTCANGATCAAAAAAGGACTTGTAAAGGTC

SEQ ID NO: 4109 ACGCGGGGGCGGCCAACATGGCGGAACGCAGGAGACACAAGAAGCGGATCC
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SEQ ID NO: 4110 ACAGTAAGGCAGTAATCCATTAGCATCCTGCTGTGGTTTTCTTTCAAGTTA
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CAGC

SEQ ID NO: 4111 ACGCGGGGAGCCGGGTGCTGATGCGAGTCCGTGGCAGCGAGGACATTTCTG
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SEQ ID NO: 4112 ACCATACCACTTATAAAGTGGAACTCTTGACCAAGATTTGGATTAATTTGT
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SEQ ID NO: 4113 ACGCGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCA
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SEQ ID NO: 4114 ACGCGGGGGCTGTGCTCACTCAGATTGTCCGTTTGCTATGCCGAATGCAGCC
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CCATTGGCTCTGCAGGGCAGGGGTGAGGCAGGTTTCTGCTCATAAGTGCTTTTGGAAAGTCACCTAC
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CCCCGAATATTGGTAAAGATCGANCAATGGCTTCAGGACATGGGTTCTTCTCTCTGTGATCATTC
AAGTGCTTACTGCATGAAAGACTGGCTTGTCTCAAGTGTTCACCCCTCACCAGGGGCTGGCTNTT
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TGNCCC

SEQ ID NO: 4115 ACTAAGAGAAAAGCACGAAGCTGTGGATCATAGTTCCCAGCATGAGGAAAA
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ATGGGACAGATACTTCTTTCTCTGGAAGACTTATTCAGTTGCTTTCATCACAGCCTGAAAATTC
ACTGGAGGGCATCTCATTGGGAGATATTCCCTCTTCCAGGCAGTATCAGTGATGGCATGGAATTCCTC
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SEQ ID NO: 4116 ACTTTTTTTTTTTTTTTTTTTTTTTTTTGCACAAGCAGTGCACCTTATTGAATG
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TACCAGTAACAGGATGAATCCCAATGGTCATGAGGATGCCANAATCAGGGCCCAAATGTTCAAGC
ACTTGGCGGTGGAGGCATAGGCCCTGGGCCCGGTACGTCGCCAACCATNTTCTGTCCCTAGACT
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SEQ ID NO: 4117 ACGCGGTATAAACTATGGAGAAAAGTCTAAAGGGTATCCCTGACCTTTA
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SEQ ID NO: 4118 ACAAAGACAAACACCTAAAACACACTGCGTCAAGTGCAGCACCGACTTTGGT
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GCTGCTTTGTCTAGGAATGGCCTATATTTCTCCAGATGGGACCTGTGCTGCAGGCAGCAATCAG
CATCTTTGGCATGGTTGGGGACCGCTGCTGGGACTCTTCTGCTTGGAAATGTTCTTCCATGTGCT
ACCCTCCTGGTGCTGTTGTGGGCCTGTTGGCTTGGGCTCGTCATGGCCTTNTGGATTGGCATCGGG
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SEQ ID NO: 4119 ACTTGCAGCCCTCGGCCAAACGGCCAGACGCCGACGTCGACCAGCAGAGACT
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SEQ ID NO: 4120 ACTTGATATGGAAAGAAGCTTTTTTCTCTCAAGTTGGATGCAGAACTGAGT
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TCTGCACATGTCTGGGTGATAATTCAATCAATGTAACGTAAGGACCTTTATTAGCTCCAT
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GGGTT

SEQ ID NO: 4121 ACCTATATGGCTCCCCCAATTAATCACAATTCAGCAGCATCCACTCCCCATAT
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SEQ ID NO: 4122 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTCGCTCTATTGGCAG
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SEQ ID NO: 4123 ACTTTTTTTTTTTTTTTTTTTTTTTTNGACAGTGCTTTCTACTTTAATAACATCAA
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TCAC

SEQ ID NO: 4124 ACGCGGGATCTGAAGAAAACCAAGAAGAACTAAGCATTGATAACTGCATTGT
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TAATT

SEQ ID NO: 4125 ACAAGTATTTATATCAATGAAAAATTTCCAATTGGTGATTTTTTGGCAGAATATT
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ATAAATCCTTCATTCCAGCTCCACGAGCAGATCCCTTCTCCAACCTGTCTCCAGCTTGACAGTG
CACAGATTTACCGTGCCAGTTTTCCAGCTGTCTACTATTCTGCATTTTCATGGCTTCAATCACA
CAAATTTCTTGACCTTCTGCTACCGGT

SEQ ID NO: 4126 ACTGGTGTCCCTGGGTGCCAGTGAGAACTATCCTTGCTCTCTGCGGGAATC
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GTG

SEQ ID NO: 4127 ACCCATGATCACAGGCCCTTTGGAGCACTTTTACTCTCTGAGAAGAACTGGAG
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SEQ ID NO: 4129 ACTATCATGTTGTTGAAACTGGGTCCATGGGAGCAAGATTAGTGGCTGCTAA
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SEQ ID NO: 4130 ACCGTGTCCTGTTCTTAGTGCTCGAATGTCCCAACCTGAAGCTGAAGAAGCC
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GGGCATCAGAGGCCAGTAGCTTTCTGGCCTACAGAGTAAATGGACAATATATTATGGAAGGACT
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AAGGTTGNACT

SEQ ID NO: 4131 ACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA
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AGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTNTCCANCAAGCACAACCTAGCAG
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SEQ ID NO: 4132 ATGNCAATTGCTTCGNAGCCGGGCCCGCCAGTNGTGGNATGGGNATTATTCT
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SEQ ID NO: 4138 ACACAATGGTTTATTAAAGGAATGTGTGGCCCATCAACCTANCAAGGATT
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SEQ ID NO: 4141 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACACAAAAACACTTTAATTGACAGTAT
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ATAAAT

SEQ ID NO: 4142 ACTTGGCCAAGCGCTCAGATCGGCAAGGGGCACAGTCTTGATCTGCCAGT
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SEQ ID NO: 4143 ACGACGTGATCGTGCTGGGCACCGGCCTGACGGAATGTATCCTGTGAGGTAT
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SEQ ID NO: 4144 ACTTATTCAACAATCTTAGAGATGCTAGCTAGTGTGAAGCTAAAAATAGC
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SEQ ID NO: 4145 ACTGCTACTTCTATAAACGGACAGCCGTAAGACTAGGCGATCCTCACTTCTAC
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SEQ ID NO: 4146 ACTGTTTCTTACATGCGAATCTACAATTATCTCAAAATAAAAAAGTCTAATTTA
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SEQ ID NO: 4148 ACCTATTTGACTTACCATGGAGTTAACATCATGAATTTATTGCACATTGTTCA
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SEQ ID NO: 4158 ACGCGGGGCCAGTAACAGGCATCGAACGGTGCAGACTGAAGACGCCCTCC
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SEQ ID NO: 4160 ACCAGTGGAGGAAGGCCTTCCGCGGAACATGGCAGTGAAGTGTCTCCGAGAT
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SEQ ID NO: 4162 ACCACTCAATCTTTTAAAAAATGAAAAAGAAAAAAGCGGCTCCAAAG
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CC

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CACCCAGATAAAGGTGGATCTCCTTACGTAGCAGCCAAAAATAAATGAAGCAAAAGACTTGCTAGA
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AAAAAAGCCCTGCAAAATATTCTAAACATGGTCTTCTTAATTTTCTATATGGATTGACCACAGT
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SEQ ID NO: 4172 ACGCGGGGGGAGTTAGGCGACCAAAACAGTGAGAGCCCCAATCCCTGCAGTT
TTGTGGCTTCAAGTGTGGGTGGACAGTCCTAATGGGGATCTCCAGCTCCTTCTGTGGGCTGCCAC
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CCTACGAAATCATTTGTTTCTAAGTTGTGTTTATTCCTGGAGTGACATGCCACCCGAATGGCTCAC
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TCCTT

SEQ ID NO: 4173 ACCAACAGACGTGGATAAGTGGTTCCATCACCAGAAAACTAATGAGATTTC
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SEQ ID NO: 4174 ACGTGCAACCTTGTGCTACGGCCACTATTCTTCATTTTGGTAGAGCCGAAT
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GCTTACAGCAGCAGAGTGACCAAAAGGAGGCGATGGAGAGCTGGACACTGATGAGGCTGGGTCA
CTTATGGGCATAAAAAACCTGGGCCCTCTGGGTAAAGCTGTTTGTGATCTCCTTATCCAACCTCACATC
CATTTTCATTATTATCATCCAAGTAAAGCACCTTCACTGGTCCCTTTTCACCAATTTGGTAAGAAAC
CTCAATGGGTGATCAAAACACTAAGATCCTGTGGCAGATTGCCACGAACATCATCAATGTCCA
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SEQ ID NO: 4175 ACGCGGGGAGACGCGCGGGCGGGAAGATGGCGGCTGGGTTCAAAACCGTGG
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SEQ ID NO: 4176 ACGCGGGGGCTGACTCTCTTTTCAGACTCAGCCCACTTGACCCCAAGTGAATT
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AAGAAATCCACTGCGACCTCGGGTCTCAGACCAGCCCAAGGAACATCTCACCATTTCAAATC

SEQ ID NO: 4181 ACITTTTTTTTTTTTTTTTTTTTTTTTTTAAAGATTTTGAAACTTTTATTATA
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CTTTGTGAATGTTTCACTCTTACTGTAGGATCTTGAATATGTTTTACAATAATGAAGCTCAAAAGTT
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GATT

SEQ ID NO: 4182 ACAAATTTAATAAAGCCTTTGATCACATCTCAATCCATAAGTTAGCTACAAAA
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GTTTGGGT

SEQ ID NO: 4183 ACTTTTTTTTTTTTTTTTTTTTTTTTTCNAATCTGAAGTCTTGTTGTTTACTAAT
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CAAGTTGAGTTTCTTAAATCTTCTGCCCTATCACTGAAAGCANTGATCTCCGTGGGGCACACAAA
GGTGAAGTCAAAAAGGTTAAAAANAACACACATTTTCTTTTAGTCAAAACAGGCTGATTNTT
TAAACTG

SEQ ID NO: 4184 ACCTGGGTGTTCCCCACCTTGGGCATCATGCACCACAACAAACAGGCCACTG
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ATTAACAGCCCCAGTTCCGGGCTGTCTTGGGGGAAGTGAAGTGTGTGAGAAGATGGCCAGTT
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CGGGAAGAGAAAGCAGAAAGCCCCAGGCTGAGCGGAAGGAGGAGAAAAAGGCGGCTGCCCTGCTC
CTGAGGAGGAGATGGGGGTCATTAAAGGAACTGAACATTGGATAA

SEQ ID NO: 4185 ACAAGTAACTGTTTAGAGCAAGTAAGTAGTTTGGTCCAATATTATCTTAATGT
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ACAACATAAAGGCTATAATACAGCTATGCAGCATAAATGGTCAACACTGCTGATCCTAAAGTGA
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SEQ ID NO: 4186 ACGTGACAGCGGTGGTAGTTCTGGAGTCTGGAAGCCACGAGGTGCTCATCC
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GCACATCGTGCTCACAGTTCCGTCCGTAGAAAGGAGGAGGGCAGGCACAAAAGGACCCAGCAT
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CCGCGT

SEQ ID NO: 4187 ACTTTAGGGGCTGCCATTGGGTATTCTTCTGGAAGGAATAGTTCAAGTTTAAA
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SEQ ID NO: 4188 ACGCGGGGGGATGGTTCATCATGGCGTCAATGCAGAAACGACTACAGAAA
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SEQ ID NO: 4189 ACATGATCTAAATGTTTAAATGCTAAAGGTATATCGTAAGGGTAGTGTGTTT
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SEQ ID NO: 4190 ACTTCGTCTTCTAATTTCAAAAATATAACTTAAAAATGTAAATATTCTATATG
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SEQ ID NO: 4191 ACTTGTCTAGCTCCTCTCGGTTCTTCCGAGCCAGCTCGTCATATTGGGCCCGG
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SEQ ID NO: 4192 TCGGCCGCGGGCAGGTACATTTGAGAAGACAACAAATAAAATTACTCTCAG
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SEQ ID NO: 4193 ACATGATCTAAATGTTTAAATGCTAAAGGTATATCGTAAGGGTAGTGTGTTT
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CNTGG

SEQ ID NO: 4194 CGGCCGCGGGCAGGACGCGGGGACAAAATGGATACATAAAGACTAAGTAG
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SEQ ID NO: 4195 ACCTAAGTATATGATTGCGAGTGGAAAAATAGGGGACAGAAATCAGGTATTG
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SEQ ID NO: 4196 ACTTTTTTTTTTTTTTTTTTTTTTTTATGTTTCTTTGGTTTTATTATTACAAAC
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CATANCA

SEQ ID NO: 4197 ACTTTTTTTTTTTTTTTTTTTTTTTTGCACAATGGTTTATTAAAGGAATGTA
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SEQ ID NO: 4198 ACNAAGGGCTGAGGCAAACTGNTTTTAAAGTTGGTAGATATGCTCATGAGC
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SEQ ID NO: 4199 ACAGGGAAAAGGGGAAGGGAGAAGGAAACAAAACCTTTACAAATCCTGCT
AATACTGTCTTACCCAAAAAGACCATAATGCTTTGTCCCATATTCAAGTCACTTATATAATAAACCA
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SEQ ID NO: 4200 ACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACCAAGTGGTCTTA
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SEQ ID NO: 4201 ACGTGGGCCTGTAATGCACCTTCTGAGGCACCTCCAGCTGCCCCCGGCCGGG
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SEQ ID NO: 4202 ACGCGGGCATCACTGAGTGCAAGGAGGAGGACATCATGTGCATGTATGAAGC
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SEQ ID NO: 4203 ACGCGGGCACAGTCAAGCTTTAAAGAAAGTGTGTTGCTGAAAATAAAGAAATC
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SEQ ID NO: 4204 ACTACTCGTAAAGAGCTTCAAGAAGCTTTCTCATCCATTAAAGACCTTGTCT
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SEQ ID NO: 4205 ACTTTTTTTTTTTTTTTTTTTTGGCAGGAAATATTTTATTGACAACCAAGGGACA
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SEQ ID NO: 4206 ACTTTGCCCTCAGCATCTCCCTTCATGTCTGGGTCATGAACCTTACGCTGAAAA
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SEQ ID NO: 4207 ACATGTTTGAAATGAGTTAGATACTTGAAAAGTCTAAACACACTGATTTAG
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CAGCNTCATAAGATCC

SEQ ID NO: 4208 ACGCGGGGCTCTTTTCCGGCTGGAACCATGGAGGGTGTAGAAGAGAAGAAG
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SEQ ID NO: 4211 ACTCAGGCTCATCATCTAACCAGCCTTCGGGTTTTGTGGCCTCTTCATCTGGA
ATCTTAGCAGGGGCATCTTCATCCCAGTCATCTGGCTTGACAGCTTCTGGATCTGGGATTTTTGGTG
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TATCTGGATTCAAGATTAGTGTGTAAGATGTGTTTTCTTATCAGTAAAAATAGGTCTTCAGATCTG
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SEQ ID NO: 4212 ACGCGGGGCCCTGGAGCTGTCTCTGGAAAGTAGCTGGCGAGGTTACCTTAAC
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CATCACTTTGTGTTGCATAAAGTATACGGTTTTGTTAAGGCCTTTGTTCTGTGAGATGCAAAACAGCT
GCTAGTCTGCAACCTAGTTTTCCCTCTCACCTTTAACTGACGTTTTCTCAATAATTACACAAGGAC
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SEQ ID NO: 4213 ACTGGAAGGGTAGTGGAACGAGTAAAGGCCTTACCACATTGTTTACACTTAT
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SEQ ID NO: 4214 ACGCGGGGTGAGAAGCTTGGACCGCATCCTAGCCGCCGACTCACACAAGGCA
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CCAGACCCTCTCCAGAGGTTGGGGTGACCAACTCATCTGGACTCAGACATATGAAGAAGCTCTAT
ATAAATCCCAAGACAAGCAACAAACCCTTGATGATTATTCATCACTTGGATGAGTGCCACACAGT
CAAGCTTTAAAGAAAGTGTGTTGCTGAAAATAAANAATCCANAAATTCAGAGCAGTTTGNCCCT
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SEQ ID NO: 4215 ACCTATGGGCTTCCCTGGCACTGTCCCTTCAAAGAAGGAACCTACTCACTGCC
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SEQ ID NO: 4216 ACCGCCTATTCAATTTCTTGAACCTTCTCATAATGATAGTCATCAGTTGCCCTTCT
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SEQ ID NO: 4217 ACGCGGGACCAAACGGAAAAAAACGGAATTATCGAATGGAATCGAAGAGAA
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SEQ ID NO: 4218 ACGCGGGGGGAGCGGGCGGGCGGTGGCGGCTTGTGCAGCAATGGCCAAG
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AGGTGGAGCTGTCCAGCTGCGCGTCGCCAAAGTGACAGGCGGTGCGGCCTCCAAGCTCTCTAAG
ATCCGAGTCGTCCGGAATCCATTGCCGTGTTCTCACAGTTATTAACCAGACTCANAAAGAAAACC
TCAGGAAATTTACAAGGGCAAGAGTCCTCNGC

SEQ ID NO: 4219 TCGAAGCCGGCCGCCGGGCAGGTACGCGGGGACAGANGGAGGAAGGACAGC
ANGGCCAACANTCACAGCAGCCCTGACCAGAGCATTCCTGGAGCTCAAGCTCCTCTACAAAGAGG
TGGACAGAGAAGACAGCATTAGACCATGGGACCCCTCAGCCCTCCCTGCAGATTGCATGTCC
CCTGGAAGGAGGTCTGCTCACATANTCACTTCTAACCTTCTNGAACCCATCCANAC

SEQ ID NO: 4220 ACTAAAGCATTTCATGGAGGCTCTTCAGGCTGGTGCAGACATCTCCATGATTG
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TNCGGGGTGAGTAAAATAANTTGGGGTATAAAAAATCTGAACCTTTACATCTGGCANAAGGCAAAA
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SEQ ID NO: 4221 ACATCAAAGATTACATGAAATCAATCAAAGGGAAACTTGAAGAACAGAGAC
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CGTGAGGATGGTGTGACCCCATATATGATTTCTTTAAGGATGGTTAGAAATGAAAAATGTAA
CAAATGTGGCAATTATTTGGATCTATCACCTGTCATCATAACTGGCTTCTGCTTGTACCCACACA
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TCCTGGAGAAGCTAGAGCCTGATTGTAGGCTCTACTCATCAATTAACCTTCTACAGTGAGACTACT
TCTGGGACTGGAATATAAAAAANAATCAAAGGTCTGATTTTGAAGTGAATAAAGGGAAAGACCA
TGCTCATAGCAGTGGCCAACCTTNTGAAGTGTGGAGCCTTACCCTTTTATTAACCTACA

SEQ ID NO: 4222 ACTATGGTAGAAATGGCGCCATCTTCCTTTTCATGCTTAAAAACCACCCTG
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CAATCTAGGAAGAGCTGTAGCAACACAGTTTACAAAGTCTTCGGAGATCCCATTTTGAGTTAG
CCTCACTAACATGATATTATTTATTTGCATAATGAAGAGCCATGTCTGCCACTTTGCCACCTGTT
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TACTAAAAATTCATCAATTTCTCAGCAGTCTTTATCAACACTGTTCCCTTAGTTTCTGTTATCATGCC
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SEQ ID NO: 4223 ACACAATGGTTTATTAAAGGAATGTATGGCCACATCAACCTAGCAAGGATT
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TGCATCTTCTAGACTGCTCGAGACAGCCAGTGTAGTAGGGCCCTTATCACTCTTAGTTTGTAGG
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SEQ ID NO: 4224 ACGCGGGGCTCACTGAGCACCGTCCAGCATCCGACACCACAGCGGCCCTT
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ACCGTGATCAACATCCACAGCGAGACCTCCGTGCCGACCATGTGCTGGTCCCTGTTCAACACC
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GGTTGGGACGTGACCGGGGGCCANGCCTATGCCTCCACCGCAAGTGCCTGAACATCTGGGCCCT

GATTCTGGGCATCCTATGACCATTGGATTTCCTGTTACTGGTATTTCGGCTCTGTGACAGTCTACC
ATATTATGTTACAGATAATACAGGAAAAACGGGGTTACTAGTANCCCGCCCATAGCCTGCAACCT
TTGCACTCCACTGTGCAATGCTGGCCCTGACGCTTGGGGCTGTTGCCCTGCCCTTGGTCTCGCC
CNTAAATCAGCANTTTATACCCANACACCTGTCTAAGTGTNTTCAATAAAGTGACAGTGTGNG
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SEQ ID NO: 4225 ACANAATGGATTTTGGGAAGAGGGAGTCACCACTGGACCTCCAAGGAAGCCAC
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AATCAN

SEQ ID NO: 4226 ACTGTGTGGAAAAGTGGTGTGCTGATTACTTCCTCAACTGTTTCAGCACTCAGA
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SEQ ID NO: 4227 ACAGATTTTGAATATGGTGAAGGCAAGGGGCACTTTGGGCTAATACTCTA
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SEQ ID NO: 4228 ACGGGGGAGGCATTGAGGCAGCCAGCGCAGGGGCTTCTGCTGAGGGGGCAG
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SEQ ID NO: 4229 ACTTTTTTTTTTTTTTTTTTTTTTTTAAAGTTTAAATGCATTTTATTTTAGACA
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SEQ ID NO: 4230 ACCAACAGAATTATTTGTGAGAAGAATGAACAAATTTTGATAAAGTATGAAT
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SEQ ID NO: 4231 ACATGGCCACAGATCATCAAACCAACATTTTTTGTGAAATCATGAACAAGAT
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GTAGAGGATCCCCAATTCACATCTGGTTTTTTGTAGGTAACATAAATATACAGCCCAAGGACTATC
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SEQ ID NO: 4232 ACTGCTACCATTACATGGTTCCTTATTAATTTGAAAAGTGCTGAAAGTTTG
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SEQ ID NO: 4233 ACTCCTTACTCAGGTTCTCCATATATTTCTGTAGTGTCTTATGCTTCCAGAGCA
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SEQ ID NO: 4234 ACCCAGCATCAGGTCAAAAACCTGAATCGTTGCAGTGTGCCAGTAGATCAGG
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SEQ ID NO: 4235 ACGCGGGGTCTGCAGGTTGTGCTTCCGGTGCAGGAGGTGAGGACAAAGATGG
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SEQ ID NO: 4236 ACTGCTCCCCACCTAGTTCTTCACAACCTAACATAGAAAAATTGTTGAAAAGTA
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SEQ ID NO: 4237 ACGCGGGGGTCATAGCGACTTTTGGGATAGTTTGTATCGACAAAAGGGAGAC
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CGCNACCC

SEQ ID NO: 4238 ACCGGGGGTAGAGGTATATGAAAAGATGAGAAGCTCACACTGGGCTTCTTC
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ATAAGA

SEQ ID NO: 4239 ACGCGGGGCACAAAATACATGCAGAAGATGGTGGCAGATCTGGTGGAAAAT
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SEQ ID NO: 4240 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCTAGGAAATATTTTATATTAAT
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SEQ ID NO: 4241 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGCATCAAAAAGCTTTATTTCCATTG
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SEQ ID NO: 4242 ACGCGGGGGAGGAGCCTGAGGAAGAGGGCGGCGACGGTGGTGGTACTGAG
CGGAGCCCGGTGACAGGATGTTGGTGTGGTATTAGGAGATCTGCACATCCACACCGGTGCAAC
AGTTTGCCAGCTAAATTCAAAAAATCCTGGTGCCAGGAAAAATTCAGCACATTCTCTGCACAGG
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AGGAGACTTCNATGAAAATCTNAATTATCCANAACAGAAAGTTGTGACTGTTGGACANTTNAAAA
TTGGTCTGATCCATGGACATNAANTTATCCATGGGGAGATATGGCCAGCTTACCCTGTTGCNTAG
GCAATTTNATNTGGACATTCTTTCTT

SEQ ID NO: 4243 ACGCGGGGCTGTTGAGGATCAAATACAAAATTAATATACTAGGCCGAGCGCA
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GTTTGAGGCCAGCGTGGTCAACATGGTAAAGCCGCTCTCTACTAAAAATACAAAATTTGGCCTGGC
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GGAGGTGGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCCAGCCTGGGTGACAGAGTGAGA
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CCA

SEQ ID NO: 4244 ACTCTCTCTGAAACAGCTACAAACATCTTGTTTTGCAAAATATACAATGTTT
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SEQ ID NO: 4245 ACTTATACCCCTAAATATATAAAACATTTTTTAAAGAAAAAAGGAAGAA
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SEQ ID NO: 4246 ACATAAGCATAATCAGTTATGGACAGCTTCTTGATAAAATGCTATTTCAGCAA
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TCTGAAAATATGGGCACATTTTAAACATATTAAGACAGTTCTGTAAACCATAATAGTCCACAGT
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ATAATCATATATTGCAACAACCTTTCTCAATATAATTCTTGGGGGCCCAAGCAAGGATCCCCATCTG
GANTATGGGANCATTATACTTGAACACTGTCAGCCTNCTNATCTTCATAATCCAAGTGGTGGGTGGT
GGNGGGGGA

SEQ ID NO: 4247 ACCAGGGCGCGCGTGGTCTACGCCGAGTGACAGAGACGCTCAGGCTGTGTT
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TTGGGAAGTGGAGCACCGATGATGTGCAGATCAATGACATTTCCCTGCAGGATTACATTGCAGTG
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GGGCTACGAGCCGTCTCCTGAAGATGCAAAACAGCGGTGGCGGCGCGCTCTCTTCCAGGACATC
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GACCCCTTGACAACCTTCACAGGCTGGGTGGGCCGAGGNTGGGCTTGGGC

SEQ ID NO: 4248 ACAGCCGCCACAGCTACACTCCAACCACGTCCCGCTCTCCCCAGCATTTCACAGACCTGATCAAGGAATCAACATTTACCGAAAGCCACCCATCTACAAACAGCATGCTGCCTTGGCAGCCCAGAGCAAGTCTCAGAAGATATCATCAAGTTTCCAAAGTTCCAGCAGCCCAGGCACACAGACCCAGCGAGACACCAAAGATTGAGACGGACCACTGGCCTGGTCCCCCTCATTTGCTGTGTAAGACCTGACATGAAACGCAGATCTAGTGGCAGAGAGGAAGATGATGAGGAACTCTGAGACGCTGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAACCTCAGGCCTGGGACAGTTGATCTTGAAAGAAAGATGGAGAAAGAGAGCGGGAAGGTCATCTCTGTAGCCAGTCGCTACGATTCTCCCATCACTCAGCTTCACATATTCATCATCTAAAACCTGCATCTCTCCTGGCTATGGAAGAAAATGGGCTTCCCGGCTGTTTCTACCGACTTTTCGCTCAGTATACAGCTATTGGGGATGTCAACGGGGGAGTGGCAGATTACCCAGACACTCCCAGATGGCCCATGCGGATTTCAGGCAATGAAATGGACCCGAGGAGTGTATTGCCAACTNTTGGAAACCAAGAAATTTTCATTTGAAATGCTCATGGGGACCNACCGAAGGGGCNAACA

SEQ ID NO: 4249 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGANATGGAGTTTCTCCTTGTAAGCCAGGTGGAGTGCAATGGTGTGAGCTCGGCTCACTGCAACTTCCACCTCCAGGTTCAAGTGAGTCTCATGCTCANCTTCCCAAGTAGCTGAGTTACAGGCATGTGCCACCACCCAGCTAAATTTTGTATTTTAGTGGANACGGGATTTCCGCATNTTGGCCAAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCACCTNCGCCTNCCAAATGCTGGGATTTCAGGCAATGAGCCACCGCNCGCGAGTGTATTATTTATTAATACTAACGTTTACATCTTNTATTCTANAAGGGCAAACCCNGAAAAAATGGTGA

SEQ ID NO: 4250 ACCATATCAATGCCAACCTTTTATTATAAATGAATAACCAAAAAAATAAGTGAAAAATGAGGGCACGATCTCTTTACACCTCTTCAACTCTCCAGCATCTAAACCTTCTCTGTGCAAGTCTGCTCTGGAGACTTTTTTCATCTGCAAGGACAGTGCTTTATTCCATGACTAACTCTCCATGTGCTCTGGATAATGGTTGGTACTATAACCTTGAAAAATTTTCGACCTGGTGTCTAGTGTAAAGTGAAGTAATGCATTTTTTTAAGTGAAAAAGCTTCTTACATTATTTACAGACAGTATTACCCACCCACATTATGAATAGTTAGATATATTTTATGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAATGAGTCTTTTATTCTCTTGGNAATCTCTTCCAGTTAACTACTTCCGNTGGAGGTGATGAAATGGGTAAGGCTCCCACTTCAAATGTTGGCACTGCTATGANCATGGTCTTCCCTTTATTGCACTCAAAATCANAACCTTGTATTCTTTTTTATATTCCAGCCCAAAAGTAGCTCACTGGNAAAAGTAAATTGATGAAGTA

SEQ ID NO: 4251 ACCAGCTGTAACCAATACGATTCTGGGGCAGGTTGTGGGCGAGTAGAAGAACCTCCTTCCCTCTGCGACATTGAACGGCGTGGATTCAATAGTGAGCTTGGCAGTGGTGGGTGGGTTCCAGAAGGTTAGAAGTGAGGCTGTGAGCAGGACCTCCTTCCAGGGGACATGCAATCTGCAGGGAGGGGCTGAGGGGGTCCCATGGTCTCTGCTGTCTTCTCTGTCCACCTCTTTGTAGAGGAGCCTGAGCTCCAGGAATGCTCTGGTCAGGGCTGTGTGACTGTTGGCCCTGCTGTCTTCTCCTCTCTGTCCCCACGT

SEQ ID NO: 4252 ACGCGGGGCTTTCCGGCGGTGACGACCTACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGACAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCAGGATGCTATAAAATCACCACGGTCTTAGCCATGCACAAACGGTAGTTTTGTGTGTGGCTGCTCCACTGTCTCTGCTAGCCTACAGGAGAAAAAGCAAGGCTTACAGAAGGATGTTCTTCCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGCGGGAACCATCTCAATAAACACATTTTGGATAAAAAAAAAAAAAAAAAAGTACGCGGGGGAACCCAAAGAGCCCTCCTTAGCCAAACACGCTAACTCCGAAGCCTCCCTTACCCCCAACCAACAAGGCGCGACACCTGATTACGCGCACAAACACAGGTCCCTTCTGTCCGGATACAATTACGCGGGAAAAACACACTTAACCTGCGCGGGGCACCAAAACAGCTATGAGTCTTACACTCCATATTTAATTCTCCTGGGAATGGCTGTTGGGGATACAAGGCTGCAAAATCATCATCGTGCCGCCAAATTTTTTTAAAGCCATTTTTT

SEQ ID NO: 4253 ACTCTCCTACTTCTGGGCATGGGGTGACTTGAGGAATGTTGAAGCCATTCTGACCACCATCCCGATCGGCCATGCTGTCAAAGAAGAGCCAGGCAGAATCGTCTTCCCATACTTCACAAAAGCAACATAGTGGCTTGTCTATGCAGAGAACAGCAAAATACTCCATATTCTGGCAAGGGAAGCAGCCGTGTCTCCAGTCCAGTCGGGTAAGTCTTTGGGAAGTGACACTGGGTATATTTATGATTCAGCCTCTTCGGATGAAGGTGGACTTGAGTGTTCAGGTTTTACAAAACCTGCTGATTTTTCCAGCTGAGATGTCCGGATCGTGTGAGCATTTCTTACACTCATACATTGCAAGCCCTCCACATATCCGGCACTGTCTGGGAGTGTCTTCAAGTAAATCTGTTATATTTAATCCAGAGAAGGAAAAATTTTTTAAATAGTTTTAAAGTCTTTTCCAAATCGAGGCATCTGAATAATCAGACATGATGGTGCCTCTGCAAAATTCANGTACTGTTGATAAAAAAGACCAATCTAACTGCTGAATTGTGGGAACGCCAACTTTCTCATTTTTTNCATAAAAAATTTGATAGAAATAACAATCTTGG

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SEQ ID NO: 4256 ACGAATACACAGAGTGGTCTTTTCAACACTCCTCCCCCTACTCCACCGGACCT
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SEQ ID NO: 4257 ACGCGGGGGATCGCTGCTCTCTGCGGCTCTGGCGGCCGACCGAGAACG
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CGCNACAA

SEQ ID NO: 4259 ACAGATCAGCAGAGCAGGACAGTTGGCAGCAGTGACCTCAGTAGGGAACAT
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SEQ ID NO: 4260 ACATACCCTTTCACTAGTGTGAGTGGCACAAGCCACATTTACCATGAGAAA
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SEQ ID NO: 4261 ACCGCCAGCTCTCTGCTCTCCACAGGGCTCCCCGCCCCACCCGGCCTGATAAA
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SEQ ID NO: 4262 ACGCGGGGGAGGTGACTTCTGGTCTATCCTGNTGACCCCTNCGNTTCCAC
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SEQ ID NO: 4263 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGATTTANCTGTTCTTTATTGACATG
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 AATNCAACCAAGGCACCT

SEQ ID NO: 4264 AACTAAAGGGTGTTCCTCAAGAATAGAGGTGAAGATATTTTCATTTTGTTTA
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SEQ ID NO: 4265 ACTTTTTTTTTTTTTTTTTTTTTTTTGANACAGGGTCTAGCTCTATGGCCAGGCT
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GCC

SEQ ID NO: 4269 ACCAAAAAGAAAAAGAAAAAGGAAAAAGGTTTCTACTGCTGTATTATCTATAACT
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SEQ ID NO: 4270 ACGCGGGGTTTCAACTGACCTCTGGACGCAGAACTTCAGCCATGAAGGTAAC
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SEQ ID NO: 4273 ATACGCGGGGAGTCACGGGGGAGCGAGGCCTGCTGGGCTTGGCAACGAGGG
ACTCGGCCTCGGAGCGGACCCAGACCACACAGACACTGGGTCAAGGAGTAAGCAGAGGATAAAC
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SEQ ID NO: 4274 ACCTCTCTAAGTTTTTCATGCCCTGCTATCTGGAACACTTCCCCACTTCCCTGCC
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SEQ ID NO: 4275 ACCAGCTGTGGGATTTTCGTCTTCGGATTCAATTGTTGCTTTAACTTGGGCTTTT
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SEQ ID NO: 4277 ACTACCAGAGCGAGGAGCAGGCAGAGGAGGAGCTCCTGGACATGGCGGTGC
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SEQ ID NO: 4279 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTNGATCCGTATCTTTTGTCTTCTAAAG
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SEQ ID NO: 4280 ACCCCTCAACCCCTTCTCCTTACCCTTAGCGGCAAGTCCCGCTTTCCTAGGG
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SEQ ID NO: 4281 ACTGGTATTACTTGA AAAAATAAAAAATTA AAAATATATTGTCAATCATGCATT
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SEQ ID NO: 4282 TTATCATCCTAATGTAGACAAGTTGGGAAGAATATGTTTAGATATTTTGAAG
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CATANAAACAGCTAGAGCATGGACTAGGCTATATGCCATGAATAATTTAAATTTGATACGATC
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SEQ ID NO: 4283 ACCGGGATGTTCCAACACTACATCCGACATCAGAAGAGCTAACAAATTGCTGG
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SEQ ID NO: 4284 ACTTTTTTTTTTTTTTTTTTTTTTTCAGAAAGAGTAGCCAGGTGTTAGCCAC
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SEQ ID NO: 4286 ACTGCAGAAGAAAAAGCAATCGTTCAGCAGTGTTAGAAATACAGGGTCACTC
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SEQ ID NO: 4287 ACGAGCCGGTAGAGGAATCCTGTTTGATCTGGAAATTTCCGTGGAGAGCCC
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SEQ ID NO: 4289 ACAAATGTTTTTTATTCAAAAATACAAAATAAATTATCTGTAGGCATGGACA
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GACCT

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SEQ ID NO: 4307 ACTGAAATAGATGTATAGACCAATGGAACAGAACAGAGGCCTCAGAAATAA
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SEQ ID NO: 4308 ACTTGCTGGTCTCAAATTTCCACAAGGAGATATCAATGGTGATACCACGTTCA
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SEQ ID NO: 4310 ACCTGTGAACCAAGTGTTTGGGCAGGATGAGATGATCGACGTCATCGGGGTG
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SEQ ID NO: 4311 ACTCGAAGATCTAGATTTCAATTTCTCCATCTACAACTTGGTCAACCAACAAAGA
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TGTA

SEQ ID NO: 4312 ACTAAAATTGTGTTGGGAGCAGGGATTTGGAAATTTCTGAGAGATGTGTAGT
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SEQ ID NO: 4313 ACTTAGCATCGGAACCTGCAATGTTAGGAGCAGGGTTGTGTGTTGGATTGAC
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SEQ ID NO: 4314 ACCAGTTTTCTGAGGACCATGATGTGGAATATTTTCTTCGGCTGGCTCATGAG
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SEQ ID NO: 4315 ACAAGTCTGGCTAGGGCTAAAAATGTGAAGAATGAGAAGATGTTACCTGGGAA
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SEQ ID NO: 4316 ACTTCAAGAACCTGCACAGATTACTCATATTCCTTCAGGAAAGTGTTTAGAT
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T

SEQ ID NO: 4317 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTACAGGAAATCTGCCTATTTTATTTT
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CTTTAATTTTACTCAAGTAAAANCANAATCACATAACGGACATCAAAACTAAATAGTTCACATCAT
TAGTTTAAAT

SEQ ID NO: 4318 GTACGCGGGGACTTCTGAGAAANTGAAACGACAGGGGAAAGGAGGTCTCAC
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SEQ ID NO: 4319 ACGCGGGGGGCTTGCAAATCTCTTGCAATTGAAGGCAGGAAAAAGCAACAT
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NCAG

SEQ ID NO: 4321 ACATTTCAAGTGAATAAGTAATTCTAGATAGGACAATTTAAATTGGATAAT
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